

GAM150923 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM150923 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM150923 target RNA into GAM150923 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM177788 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM177788 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM177788 target RNA into GAM177788 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4354 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4354 gene: GAM150923 target protein and GAM177788 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM150923 and GAM177788

GR4355 BF222847 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4355(GR4355) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4355 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4355 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4355 gene encodes GR4355 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4355 precursor RNA folds spatially, forming GR4355 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4355 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4355 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4355 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM64215 precursor RNA and GAM148210 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM64215 RNA and GAM148210 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM64215 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM64215 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM64215 target RNA into GAM64215 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM148210 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM148210 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM148210 target RNA into GAM148210 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4355 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4355 gene: GAM64215 target protein and GAM148210 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM64215 and GAM148210

GR4356 AI925028 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4356(GR4356) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4356 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4356 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4356 gene encodes GR4356 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4356 precursor RNA folds spatially, forming GR4356 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4356 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4356 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4356 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM43825 precursor RNA and GAM178076 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM43825 RNA and GAM178076 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM43825 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM43825 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM43825 target RNA into GAM43825 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM178076 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM178076 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM178076 target RNA into GAM178076 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4356 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4356 gene: GAM43825 target protein and GAM178076 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference,

with references to GAM43825 and GAM178076

GR4357 AW882806 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4357 (GR4357) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4357 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4357 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4357 gene encodes GR4357 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4357 precursor RNA folds spatially, forming GR4357 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4357 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4357 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4357 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2387 precursor RNA, GAM4112 precursor RNA and GAM37724 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2387 RNA, GAM4112 RNA and GAM37724 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2387 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2387 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2387 target RNA into GAM2387 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM4112 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM4112 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4112 target RNA into GAM4112 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM37724 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM37724 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM37724 target RNA into GAM37724 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4357 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4357 gene: GAM2387 target protein, GAM4112 target protein and GAM37724 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2387, GAM4112 and GAM37724

GR4358 AA602517 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4358(GR4358) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4358 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4358 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4358 gene encodes GR4358 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4358 precursor RNA folds spatially, forming GR4358 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4358 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4358 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4358 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1354 precursor RNA and GAM209361 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1354 RNA and GAM209361 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1354 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1354 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1354 target RNA into GAM1354 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM209361 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM209361 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM209361 target RNA into GAM209361 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4358 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4358 gene: GAM1354 target protein and GAM209361 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1354 and GAM209361

GR4359 AA468004 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4359(GR4359) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4359 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4359 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4359 gene encodes GR4359 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4359 precursor RNA folds spatially, forming GR4359 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4359 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4359 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4359 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM40227 precursor RNA and GAM64192 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM40227 RNA and GAM64192 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM40227 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM40227 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM40227 target RNA into GAM40227 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM64192 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM64192 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM64192 target RNA into GAM64192 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4359 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4359 gene: GAM40227 target protein and GAM64192 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM40227 and GAM64192

GR4360 BF573681 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4360(GR4360) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4360 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4360 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4360 gene encodes GR4360 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4360 precursor RNA folds spatially, forming GR4360 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4360 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4360 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4360 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM44811 precursor RNA and GAM70951 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM44811 RNA and GAM70951 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM44811 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM44811 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM44811 target RNA into GAM44811 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM70951 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM70951 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM70951 target RNA into GAM70951 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4360 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4360 gene: GAM44811 target protein and GAM70951 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM44811 and GAM70951

GR4361 BG427826 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4361 (GR4361) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4361 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4361 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4361 gene encodes GR4361 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4361 precursor RNA folds spatially, forming GR4361 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4361 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4361 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4361 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5708 precursor RNA and GAM163719 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5708 RNA and GAM163719 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5708 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5708 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5708 target RNA into GAM5708 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM163719 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM163719 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM163719 target RNA into GAM163719 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4361 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4361 gene: GAM5708 target protein and GAM163719 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5708 and GAM163719

GR4362 BG292228 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4362(GR4362) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4362 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4362 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4362 gene encodes GR4362 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4362 precursor RNA folds spatially, forming GR4362 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4362 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4362 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4362 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM43 precursor RNA, GAM455 precursor RNA and GAM253537 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM43 RNA, GAM455 RNA and GAM253537 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM43 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM43 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM43 target RNA into GAM43 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM455 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM455 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM455 target RNA into GAM455 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM253537 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM253537 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM253537 target RNA into GAM253537 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4362 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4362 gene: GAM43 target protein, GAM455 target protein and GAM253537 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM43, GAM455 and GAM253537

GR4363 BG504861 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4363(GR4363) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4363 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4363 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4363 gene encodes GR4363 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4363 precursor RNA folds spatially, forming GR4363 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4363 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4363 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4363 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM88705 precursor RNA and GAM98085 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM88705 RNA and GAM98085 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM88705 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM88705 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM88705 target RNA into GAM88705 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM98085 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM98085 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM98085 target RNA into GAM98085 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4363 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4363 gene: GAM88705 target protein and GAM98085 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM88705 and GAM98085

GR4364 AI733285 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4364(GR4364) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4364 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4364 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4364 gene encodes GR4364 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4364 precursor RNA folds spatially, forming GR4364 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4364 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4364 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4364 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM82424 precursor RNA and GAM183004 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM82424 RNA and GAM183004 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM82424 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM82424 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM82424 target RNA into GAM82424 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM183004 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM183004 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM183004 target RNA into GAM183004 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4364 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4364 gene: GAM82424 target protein and GAM183004 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM82424 and GAM183004

GR4365 AA343609 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4365(GR4365) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4365 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4365 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4365 gene encodes GR4365 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4365 precursor RNA folds spatially, forming GR4365 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4365 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4365 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4365 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4346 precursor RNA and GAM315836 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4346 RNA and GAM315836 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4346 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4346 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4346 target RNA into GAM4346 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM315836 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM315836 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM315836 target RNA into GAM315836 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4365 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4365 gene: GAM4346 target protein and GAM315836 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4346 and GAM315836

GR4366 AV652352 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4366(GR4366) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4366 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4366 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4366 gene encodes GR4366 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4366 precursor RNA folds spatially, forming GR4366 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4366 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4366 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4366 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2623 precursor RNA, GAM300589 precursor RNA and GAM326118 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2623 RNA, GAM300589 RNA and GAM326118 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2623 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2623 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2623 target RNA into GAM2623 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM300589 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM300589 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM300589 target RNA into GAM300589 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM326118 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM326118 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM326118 target RNA into GAM326118 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4366 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4366 gene: GAM2623 target protein, GAM300589 target protein and GAM326118 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2623, GAM300589 and GAM326118

GR4367 AW072067 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4367(GR4367) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4367 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4367 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4367 gene encodes GR4367 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4367 precursor RNA folds spatially, forming GR4367 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4367 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4367 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4367 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3900 precursor RNA, GAM7959 precursor RNA and GAM54787 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3900 RNA, GAM7959 RNA and GAM54787 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3900 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3900 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3900 target RNA into GAM3900 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7959 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7959 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7959 target RNA into GAM7959 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM54787 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM54787 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM54787 target RNA into GAM54787 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4367 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4367 gene: GAM3900 target protein, GAM7959 target protein and GAM54787 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3900, GAM7959 and GAM54787

GR4368 BF195020 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4368(GR4368) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4368 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4368 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4368 gene encodes GR4368 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4368 precursor RNA folds spatially, forming GR4368 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4368 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4368 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4368 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM87583 precursor RNA, GAM243656 precursor RNA and GAM295560 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM87583 RNA, GAM243656 RNA and GAM295560 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM87583 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM87583 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM87583 target RNA into GAM87583 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM243656 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM243656 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM243656 target RNA into GAM243656 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM295560 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM295560 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM295560 target RNA into GAM295560 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4368 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4368 gene: GAM87583 target protein, GAM243656 target protein and GAM295560 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM87583, GAM243656 and GAM295560

GR4369 AA721296 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4369(GR4369) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4369 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4369 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4369 gene encodes GR4369 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4369 precursor RNA folds spatially, forming GR4369 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4369 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4369 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4369 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM13553 precursor RNA and GAM335809 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM13553 RNA and GAM335809 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM13553 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM13553 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM13553 target RNA into GAM13553 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM335809 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM335809 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM335809 target RNA into GAM335809 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4369 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4369 gene: GAM13553 target protein and GAM335809 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM13553 and GAM335809

GR4370 AA620828 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4370(GR4370) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4370 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4370 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4370 gene encodes GR4370 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4370 precursor RNA folds spatially, forming GR4370 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4370 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4370 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4370 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM270329 precursor RNA and GAM281608 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin

shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM270329 RNA and GAM281608 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM270329 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM270329 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM270329 target RNA into GAM270329 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM281608 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM281608 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM281608 target RNA into GAM281608 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4370 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4370 gene: GAM270329 target protein and GAM281608 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM270329 and GAM281608

GR4371 BE397472 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4371(GR4371) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4371 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4371 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4371 gene encodes GR4371 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4371 precursor RNA folds spatially, forming GR4371 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4371 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4371 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4371 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM108730 precursor RNA and GAM255626 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM108730 RNA and GAM255626 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM108730 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM108730 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM108730 target RNA into GAM108730 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM255626 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM255626 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM255626 target RNA into GAM255626 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4371 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4371 gene: GAM108730 target protein and GAM255626 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM108730 and GAM255626

GR4372 AI626029 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4372(GR4372) gene, which encodes an `operon-like` cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4372 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4372 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4372 gene encodes GR4372 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4372 precursor RNA folds spatially, forming GR4372 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4372 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4372 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4372 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM12023 precursor RNA, GAM222190 precursor RNA and GAM283343 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM12023 RNA, GAM222190 RNA and GAM283343 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM12023 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM12023 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM12023 target RNA into GAM12023 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM222190 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM222190 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM222190 target RNA into GAM222190 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM283343 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM283343 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM283343 target RNA into GAM283343 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4372 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4372 gene: GAM12023 target protein, GAM222190 target protein and GAM283343 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM12023, GAM222190 and GAM283343

GR4373 BF507817 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4373(GR4373) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4373 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4373 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4373 gene encodes GR4373 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4373 precursor RNA folds spatially, forming GR4373 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4373 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4373 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4373 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7620 precursor RNA and GAM163754 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7620 RNA and GAM163754 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7620 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7620 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7620 target RNA into GAM7620 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM163754 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM163754 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM163754 target RNA into GAM163754 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4373 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4373 gene: GAM7620 target protein and GAM163754 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7620 and GAM163754

GR4374 AI935841 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4374(GR4374) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4374 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4374 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4374 gene encodes GR4374 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4374 precursor RNA folds spatially, forming GR4374 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated

that GR4374 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4374 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4374 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM178372 precursor RNA and GAM336599 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM178372 RNA and GAM336599 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM178372 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM178372 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM178372 target RNA into GAM178372 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336599 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336599 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336599 target RNA into GAM336599 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4374 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4374 gene: GAM178372 target protein and GAM336599 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM178372 and GAM336599

GR4375 BM926390 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4375(GR4375) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR4375 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4375 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4375 gene encodes GR4375 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4375 precursor RNA folds spatially, forming GR4375 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4375 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4375 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4375 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM85349 precursor RNA, GAM221172 precursor RNA, GAM275732 precursor RNA and GAM333801 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM85349 RNA, GAM221172 RNA, GAM275732 RNA and GAM333801 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM85349 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM85349 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM85349 target RNA into GAM85349 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM221172 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM221172 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM221172 target RNA into GAM221172 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM275732 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM275732 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM275732 target RNA into GAM275732 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM333801 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM333801 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM333801 target RNA into GAM333801 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4375 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4375 gene: GAM85349 target protein, GAM221172 target protein, GAM275732 target protein and GAM333801 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM85349, GAM221172, GAM275732 and GAM333801

GR4376 AA826769 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4376(GR4376) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4376 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4376 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4376 gene encodes GR4376 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4376 precursor RNA folds spatially, forming GR4376 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4376 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4376 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4376 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM42687 precursor RNA and GAM71377 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM42687 RNA and GAM71377 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM42687 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM42687 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM42687 target RNA into GAM42687 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM71377 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM71377 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM71377 target RNA into GAM71377 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4376 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4376 gene: GAM42687 target protein and GAM71377 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM42687 and GAM71377

GR4377 BF592545 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4377(GR4377) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4377 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4377 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4377 gene encodes GR4377 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4377 precursor RNA folds spatially, forming GR4377 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4377 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4377 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4377 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM115857 precursor RNA, GAM241607 precursor RNA and GAM263626 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM115857 RNA, GAM241607 RNA and GAM263626 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM115857 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM115857 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM115857 target RNA into GAM115857 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM241607 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM241607 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM241607 target RNA into GAM241607 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM263626 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM263626 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM263626

target RNA into GAM263626 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4377 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4377 gene: GAM115857 target protein, GAM241607 target protein and GAM263626 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM115857, GAM241607 and GAM263626

GR4378 BE731520 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4378(GR4378) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4378 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4378 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4378 gene encodes GR4378 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4378 precursor RNA folds spatially, forming GR4378 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4378 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4378 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4378 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM218387 precursor RNA and GAM231558 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM218387 RNA and GAM231558 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM218387 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM218387 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM218387 target RNA into GAM218387 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM231558 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM231558 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM231558 target RNA into GAM231558 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4378 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4378 gene: GAM218387 target protein and GAM231558 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM218387 and GAM231558

GR4379 N25480 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4379(GR4379) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4379 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4379 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4379 gene encodes GR4379 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4379 precursor RNA folds spatially, forming GR4379 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4379 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4379 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4379 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM762 precursor RNA and GAM92524 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM762 RNA and GAM92524 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM762 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM762 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM762 target RNA into GAM762 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM92524 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM92524 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM92524 target RNA into GAM92524 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4379 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4379 gene: GAM762 target protein and GAM92524 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM762 and GAM92524

GR4380 AV734026 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4380(GR4380) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4380 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4380 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4380 gene encodes GR4380 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4380 precursor RNA folds spatially, forming GR4380 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4380 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4380 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4380 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM121336 precursor RNA, GAM129505 precursor RNA, GAM208094 precursor RNA and GAM240381 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM121336 RNA, GAM129505 RNA, GAM208094 RNA and GAM240381 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM121336 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM121336 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM121336 target RNA into GAM121336 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM129505 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM129505 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM129505 target RNA into GAM129505 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM208094 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM208094 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM208094 target RNA into GAM208094 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM240381 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM240381 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM240381 target RNA into GAM240381 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4380 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4380 gene: GAM121336 target protein, GAM129505 target protein, GAM208094 target protein and GAM240381 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM121336, GAM129505, GAM208094 and GAM240381

GR4381 R21894 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4381(GR4381) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4381 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4381 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4381 gene encodes GR4381 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4381 precursor RNA folds spatially, forming GR4381 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4381 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4381 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4381 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM196306 precursor RNA and GAM216376 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM196306 RNA and GAM216376 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM196306 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM196306 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM196306 target RNA into GAM196306 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM216376 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM216376 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM216376 target RNA into GAM216376 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4381 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4381 gene: GAM196306 target protein and GAM216376 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM196306 and GAM216376

GR4382 AI828117 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4382(GR4382) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4382 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4382 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4382 gene encodes GR4382 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4382 precursor RNA folds spatially, forming GR4382 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated

that GR4382 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4382 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4382 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6353 precursor RNA and GAM240586 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6353 RNA and GAM240586 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6353 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6353 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6353 target RNA into GAM6353 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM240586 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM240586 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM240586 target RNA into GAM240586 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4382 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4382 gene: GAM6353 target protein and GAM240586 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6353 and GAM240586

GR4383 BF879472 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4383(GR4383) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR4383 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4383 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4383 gene encodes GR4383 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4383 precursor RNA folds spatially, forming GR4383 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4383 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4383 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4383 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM121150 precursor RNA, GAM251338 precursor RNA and GAM320040 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM121150 RNA, GAM251338 RNA and GAM320040 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM121150 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM121150 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM121150 target RNA into GAM121150 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM251338 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM251338 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM251338 target RNA into GAM251338 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM320040 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM320040 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM320040 target RNA into GAM320040 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4383 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4383 gene: GAM121150 target protein, GAM251338 target protein and GAM320040 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM121150, GAM251338 and GAM320040

GR4384 AI393777 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4384(GR4384) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4384 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4384 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4384 gene encodes GR4384 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4384 precursor RNA folds spatially, forming GR4384 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4384 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4384 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4384 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7650 precursor RNA and GAM56529 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7650 RNA and GAM56529 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7650 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7650 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7650 target RNA into GAM7650 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM56529 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM56529 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM56529 target RNA into GAM56529 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4384 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4384 gene: GAM7650 target protein and GAM56529 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7650 and GAM56529

GR4385 BI459072 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4385(GR4385) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4385 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4385 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4385 gene encodes GR4385 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4385 precursor RNA folds spatially, forming GR4385 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4385 folded precursor RNA comprises a plurality of what is known in the

art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4385 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4385 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM89378 precursor RNA and GAM219378 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM89378 RNA and GAM219378 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM89378 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM89378 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM89378 target RNA into GAM89378 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM219378 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM219378 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM219378 target RNA into GAM219378 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4385 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4385 gene: GAM89378 target protein and GAM219378 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM89378 and GAM219378

GR4386 AW250482 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4386(GR4386) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR4386 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4386 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4386 gene encodes GR4386 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4386 precursor RNA folds spatially, forming GR4386 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4386 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4386 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4386 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM33968 precursor RNA, GAM187315 precursor RNA and GAM194147 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM33968 RNA, GAM187315 RNA and GAM194147 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM33968 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM33968 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM33968 target RNA into GAM33968 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM187315 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM187315 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM187315 target RNA into GAM187315 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM194147 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM194147 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM194147 target RNA into GAM194147 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4386 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4386 gene: GAM33968 target protein, GAM187315 target protein and GAM194147 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM33968, GAM187315 and GAM194147

GR4387 BG336826 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4387(GR4387) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4387 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4387 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4387 gene encodes GR4387 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4387 precursor RNA folds spatially, forming GR4387 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4387 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4387 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4387 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2248 precursor RNA and GAM20515 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2248 RNA and GAM20515 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2248 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2248 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2248 target RNA into GAM2248 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM20515 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM20515 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM20515 target RNA into GAM20515 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4387 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4387 gene: GAM2248 target protein and GAM20515 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2248 and GAM20515

GR4388 BG569519 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4388(GR4388) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4388 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4388 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4388 gene encodes GR4388 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4388 precursor RNA folds spatially, forming GR4388 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4388 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR4388 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4388 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2704 precursor RNA and GAM29039 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2704 RNA and GAM29039 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2704 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2704 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2704 target RNA into GAM2704 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM29039 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM29039 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM29039 target RNA into GAM29039 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4388 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4388 gene: GAM2704 target protein and GAM29039 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2704 and GAM29039

GR4389 AA975040 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4389(GR4389) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4389 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4389 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4389 gene encodes GR4389 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4389 precursor RNA folds spatially, forming GR4389 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4389 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4389 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4389 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM18756 precursor RNA and GAM216530 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM18756 RNA and GAM216530 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM18756 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM18756 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM18756 target RNA into GAM18756 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM216530 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM216530 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM216530 target RNA into GAM216530 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4389 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4389 gene: GAM18756 target protein and GAM216530 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM18756 and GAM216530

GR4390 BI791470 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4390(GR4390) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4390 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4390 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4390 gene encodes GR4390 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4390 precursor RNA folds spatially, forming GR4390 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4390 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4390 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4390 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3319 precursor RNA, GAM50930 precursor RNA and GAM72209 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3319 RNA, GAM50930 RNA and GAM72209 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3319 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3319 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig. 8, thereby inhibiting translation of GAM3319 target RNA into GAM3319 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM50930 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM50930 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM50930 target RNA into GAM50930 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM72209 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM72209 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM72209 target RNA into GAM72209 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4390 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4390 gene: GAM3319 target protein, GAM50930 target protein and GAM72209 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3319, GAM50930 and GAM72209

GR4391 AV719046 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4391 (GR4391) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4391 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4391 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4391 gene encodes GR4391 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4391 precursor RNA folds spatially, forming GR4391 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4391 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4391 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4391 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM102704 precursor RNA and GAM210486 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM102704 RNA and GAM210486 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM102704 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM102704 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM102704 target RNA into GAM102704 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM210486 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM210486 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM210486 target RNA into GAM210486 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4391 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4391 gene: GAM102704 target protein and GAM210486 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM102704 and GAM210486

GR4392 BE834615 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4392(GR4392) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4392 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4392 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4392 gene encodes GR4392 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4392 precursor RNA folds spatially, forming GR4392 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4392 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4392 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4392 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM290 precursor RNA, GAM178194 precursor RNA and GAM280592 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM290 RNA, GAM178194 RNA and GAM280592 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM290 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM290 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM290 target RNA into GAM290 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM178194 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM178194 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM178194 target RNA into GAM178194 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM280592 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM280592 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM280592 target RNA into GAM280592 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4392 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4392 gene: GAM290 target protein, GAM178194 target protein and GAM280592 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM290, GAM178194 and GAM280592

GR4393 BE545209 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4393(GR4393) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4393 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4393 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4393 gene encodes GR4393 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4393 precursor RNA folds spatially, forming GR4393 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4393 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4393 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4393 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM841 precursor RNA and GAM262106 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM841 RNA and GAM262106 RNA, herein schematically

represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM841 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM841 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM841 target RNA into GAM841 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM262106 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM262106 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM262106 target RNA into GAM262106 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4393 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4393 gene: GAM841 target protein and GAM262106 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM841 and GAM262106

GR4394 AI141166 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4394(GR4394) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4394 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4394 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4394 gene encodes GR4394 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4394 precursor RNA folds spatially, forming GR4394 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4394 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4394 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4394 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1723 precursor RNA, GAM1738 precursor RNA and GAM77426 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1723 RNA, GAM1738 RNA and GAM77426 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1723 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1723 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1723 target RNA into GAM1723 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM1738 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1738 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1738 target RNA into GAM1738 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM77426 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM77426 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM77426 target RNA into GAM77426 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4394 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4394 gene: GAM1723 target protein, GAM1738 target protein and GAM77426 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1723, GAM1738 and

GR4395 AW206714 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4395(GR4395) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4395 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4395 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4395 gene encodes GR4395 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4395 precursor RNA folds spatially, forming GR4395 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4395 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4395 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4395 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM164842 precursor RNA, GAM177920 precursor RNA and GAM319815 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM164842 RNA, GAM177920 RNA and GAM319815 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM164842 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM164842 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM164842 target RNA into GAM164842 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM177920 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM177920 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM177920 target RNA into GAM177920 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM319815 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM319815 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM319815 target RNA into GAM319815 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4395 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4395 gene: GAM164842 target protein, GAM177920 target protein and GAM319815 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM164842, GAM177920 and GAM319815

GR4396 AA403295 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4396(GR4396) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4396 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4396 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4396 gene encodes GR4396 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4396 precursor RNA folds spatially, forming GR4396 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4396 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4396 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4396 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3491 precursor RNA and GAM263714 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3491 RNA and GAM263714 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3491 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3491 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3491 target RNA into GAM3491 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM263714 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM263714 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM263714 target RNA into GAM263714 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4396 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4396 gene: GAM3491 target protein and GAM263714 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3491 and GAM263714

GR4397 BE261388 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4397(GR4397) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4397 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4397 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4397 gene encodes GR4397 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4397 precursor RNA folds spatially, forming GR4397 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4397 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4397 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4397 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM245981 precursor RNA and GAM268167 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM245981 RNA and GAM268167 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM245981 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM245981 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM245981 target RNA into GAM245981 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM268167 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM268167 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM268167 target RNA into GAM268167 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4397 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4397 gene: GAM245981 target protein and GAM268167 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM245981 and GAM268167

GR4398 BI457191 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4398(GR4398) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4398 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4398 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4398 gene encodes GR4398 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4398 precursor RNA folds spatially, forming GR4398 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4398 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4398 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4398 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7279 precursor RNA and GAM22788 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7279 RNA and GAM22788 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7279 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7279 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7279 target RNA into GAM7279 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM22788 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM22788 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM22788 target RNA into GAM22788 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4398 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4398 gene: GAM7279 target protein and GAM22788 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7279 and GAM22788

GR4399 AI970620 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4399(GR4399) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4399 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4399 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4399 gene encodes GR4399 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4399 precursor RNA folds spatially, forming GR4399 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4399 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4399 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4399 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM50951 precursor RNA and GAM276217 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM50951 RNA and GAM276217 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM50951 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM50951 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM50951 target RNA into GAM50951 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM276217 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM276217 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM276217 target RNA into GAM276217 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4399 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4399 gene: GAM50951 target protein and GAM276217 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM50951 and GAM276217

GR4400 BM811172 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4400(GR4400) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4400 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4400 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4400 gene encodes GR4400 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4400 precursor RNA folds spatially, forming GR4400 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4400 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4400 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4400 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM5223 precursor RNA, GAM47071 precursor RNA, GAM221167 precursor RNA and GAM316330 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5223 RNA, GAM47071 RNA, GAM221167 RNA and GAM316330 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5223 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5223 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5223 target RNA into GAM5223 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM47071 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM47071 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM47071 target RNA into GAM47071 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM221167 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM221167 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM221167 target RNA into GAM221167 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM316330 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM316330 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM316330 target RNA into GAM316330 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4400 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4400 gene: GAM5223 target protein, GAM47071 target protein, GAM221167 target protein and GAM316330 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5223, GAM47071, GAM221167 and GAM316330

GR4401 BF246314 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4401 (GR4401) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4401 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4401 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4401 gene encodes GR4401 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4401 precursor RNA folds spatially, forming GR4401 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4401 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4401 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4401 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM284931 precursor RNA and GAM301851 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM284931 RNA and GAM301851 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM284931 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM284931 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM284931 target RNA into GAM284931 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM301851 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM301851 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM301851 target RNA into GAM301851 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4401 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4401 gene: GAM284931 target protein and GAM301851 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM284931 and GAM301851

GR4402 AW969332 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4402(GR4402) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4402 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4402 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4402 gene encodes GR4402 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4402 precursor RNA folds spatially, forming GR4402 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4402 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4402 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4402 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6437 precursor RNA and GAM307171 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin

shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6437 RNA and GAM307171 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6437 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6437 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6437 target RNA into GAM6437 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM307171 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM307171 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM307171 target RNA into GAM307171 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4402 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4402 gene: GAM6437 target protein and GAM307171 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6437 and GAM307171

GR4403 BF183225 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4403(GR4403) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4403 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4403 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4403 gene encodes GR4403 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4403 precursor RNA folds spatially, forming GR4403 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4403 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4403 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4403 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2381 precursor RNA and GAM334416 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2381 RNA and GAM334416 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2381 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2381 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2381 target RNA into GAM2381 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM334416 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM334416 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM334416 target RNA into GAM334416 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4403 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4403 gene: GAM2381 target protein and GAM334416 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2381 and GAM334416

GR4404 AI758404 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4404(GR4404) gene, which encodes an `operon-like` cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4404 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4404 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4404 gene encodes GR4404 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4404 precursor RNA folds spatially, forming GR4404 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4404 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4404 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4404 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6335 precursor RNA and GAM54268 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6335 RNA and GAM54268 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6335 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6335 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6335 target RNA into GAM6335 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM54268 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM54268 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM54268 target RNA into GAM54268 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4404 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4404 gene: GAM6335 target protein and GAM54268 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6335 and GAM54268

GR4405 BM835171 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4405(GR4405) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4405 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4405 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4405 gene encodes GR4405 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4405 precursor RNA folds spatially, forming GR4405 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4405 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4405 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4405 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7059 precursor RNA and GAM77079 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7059 RNA and GAM77079 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7059 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7059 target RNA, herein schematically represented by

GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7059 target RNA into GAM7059 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM77079 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM77079 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM77079 target RNA into GAM77079 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4405 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4405 gene: GAM7059 target protein and GAM77079 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7059 and GAM77079

GR4406 BG473293 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4406(GR4406) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4406 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4406 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4406 gene encodes GR4406 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4406 precursor RNA folds spatially, forming GR4406 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4406 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4406 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4406 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM119298 precursor RNA, GAM243447 precursor RNA

and GAM248685 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM119298 RNA, GAM243447 RNA and GAM248685 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM119298 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM119298 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM119298 target RNA into GAM119298 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM243447 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM243447 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM243447 target RNA into GAM243447 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM248685 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM248685 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM248685 target RNA into GAM248685 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4406 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4406 gene: GAM119298 target protein, GAM243447 target protein and GAM248685 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM119298, GAM243447 and GAM248685

GR4407 BM683760 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4407(GR4407) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR4407 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4407 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4407 gene encodes GR4407 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4407 precursor RNA folds spatially, forming GR4407 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4407 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4407 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4407 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM5438 precursor RNA, GAM8173 precursor RNA, GAM19798 precursor RNA and GAM312669 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5438 RNA, GAM8173 RNA, GAM19798 RNA and GAM312669 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5438 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5438 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5438 target RNA into GAM5438 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8173 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8173 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8173 target RNA into GAM8173 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM19798 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM19798 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM19798 target RNA into GAM19798 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM312669 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM312669 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM312669 target RNA into GAM312669 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4407 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4407 gene: GAM5438 target protein, GAM8173 target protein, GAM19798 target protein and GAM312669 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5438, GAM8173, GAM19798 and GAM312669

GR4408 BF514482 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4408(GR4408) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4408 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4408 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4408 gene encodes GR4408 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4408 precursor RNA folds spatially, forming GR4408 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4408 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4408 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4408 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM125105 precursor RNA, GAM231153 precursor RNA and GAM310078 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM125105 RNA, GAM231153 RNA and GAM310078 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM125105 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM125105 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM125105 target RNA into GAM125105 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM231153 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM231153 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM231153 target RNA into GAM231153 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM310078 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM310078 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM310078 target RNA into GAM310078 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4408 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4408 gene: GAM125105 target protein, GAM231153 target protein and GAM310078 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM125105, GAM231153 and GAM310078

GR4409 BF924157 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4409(GR4409) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4409 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4409 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4409 gene encodes GR4409 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4409 precursor RNA folds spatially, forming GR4409 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4409 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4409 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4409 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4689 precursor RNA, GAM30619 precursor RNA and GAM287271 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4689 RNA, GAM30619 RNA and GAM287271 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4689 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4689 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4689 target RNA into GAM4689 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM30619 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM30619 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM30619 target RNA into GAM30619 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM287271 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM287271 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM287271 target RNA into GAM287271 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4409 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4409 gene: GAM4689 target protein, GAM30619 target protein and GAM287271 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4689, GAM30619 and GAM287271

GR4410 BE563399 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4410(GR4410) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4410 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4410 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4410 gene encodes GR4410 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4410 precursor RNA folds spatially, forming GR4410 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4410 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4410 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4410 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4276 precursor RNA, GAM213478 precursor RNA

and GAM255616 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4276 RNA, GAM213478 RNA and GAM255616 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4276 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4276 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4276 target RNA into GAM4276 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM213478 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM213478 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM213478 target RNA into GAM213478 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM255616 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM255616 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM255616 target RNA into GAM255616 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4410 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4410 gene: GAM4276 target protein, GAM213478 target protein and GAM255616 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4276, GAM213478 and GAM255616

GR4411 BG955095 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4411(GR4411) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR4411 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4411 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4411 gene encodes GR4411 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4411 precursor RNA folds spatially, forming GR4411 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4411 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4411 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4411 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM90228 precursor RNA and GAM134827 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM90228 RNA and GAM134827 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM90228 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM90228 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM90228 target RNA into GAM90228 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM134827 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM134827 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM134827 target RNA into GAM134827 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4411 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4411 gene: GAM90228 target protein and GAM134827 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM90228 and GAM134827

GR4412 AA112195 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4412(GR4412) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4412 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4412 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4412 gene encodes GR4412 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4412 precursor RNA folds spatially, forming GR4412 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4412 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4412 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4412 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM89057 precursor RNA, GAM212356 precursor RNA and GAM303284 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM89057 RNA, GAM212356 RNA and GAM303284 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM89057 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM89057 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM89057 target RNA into GAM89057 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM212356 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM212356 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM212356 target RNA into GAM212356 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM303284 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM303284 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM303284 target RNA into GAM303284 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4412 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4412 gene: GAM89057 target protein, GAM212356 target protein and GAM303284 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM89057, GAM212356 and GAM303284

GR4413 BG743513 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4413(GR4413) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4413 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4413 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4413 gene encodes GR4413 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4413 precursor RNA folds spatially, forming GR4413 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4413 folded precursor RNA comprises a plurality of what is known in the

art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4413 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4413 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM59618 precursor RNA, GAM224479 precursor RNA and GAM315261 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM59618 RNA, GAM224479 RNA and GAM315261 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM59618 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM59618 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM59618 target RNA into GAM59618 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM224479 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM224479 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM224479 target RNA into GAM224479 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM315261 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM315261 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM315261 target RNA into GAM315261 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4413 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4413 gene: GAM59618 target protein, GAM224479 target protein and GAM315261 target protein, herein

schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM59618, GAM224479 and GAM315261

GR4414 BM702157 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4414(GR4414) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4414 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4414 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4414 gene encodes GR4414 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4414 precursor RNA folds spatially, forming GR4414 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4414 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4414 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4414 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1048 precursor RNA and GAM59348 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1048 RNA and GAM59348 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1048 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1048 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1048 target RNA into GAM1048 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM59348 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM59348 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM59348 target RNA into GAM59348 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4414 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4414 gene: GAM1048 target protein and GAM59348 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1048 and GAM59348

GR4415 AI476198 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4415(GR4415) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4415 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4415 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4415 gene encodes GR4415 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4415 precursor RNA folds spatially, forming GR4415 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4415 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4415 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4415 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM41601 precursor RNA and GAM125495 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM41601 RNA and GAM125495 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM41601 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM41601 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM41601 target RNA into GAM41601 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM125495 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM125495 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM125495 target RNA into GAM125495 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4415 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4415 gene: GAM41601 target protein and GAM125495 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM41601 and GAM125495

GR4416 AW591912 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4416(GR4416) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4416 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4416 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4416 gene encodes GR4416 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4416 precursor RNA folds spatially, forming GR4416 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4416 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR4416 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4416 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM242929 precursor RNA and GAM245853 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM242929 RNA and GAM245853 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM242929 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM242929 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM242929 target RNA into GAM242929 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM245853 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM245853 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM245853 target RNA into GAM245853 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4416 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4416 gene: GAM242929 target protein and GAM245853 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM242929 and GAM245853

GR4417 H26168 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4417(GR4417) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4417 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4417 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4417 gene encodes GR4417 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4417 precursor RNA folds spatially, forming GR4417 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4417 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4417 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4417 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8691 precursor RNA and GAM330630 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8691 RNA and GAM330630 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8691 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8691 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8691 target RNA into GAM8691 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM330630 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM330630 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM330630 target RNA into GAM330630 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4417 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4417 gene: GAM8691 target protein and GAM330630 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8691 and GAM330630

GR4418 BF699770 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4418(GR4418) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4418 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4418 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4418 gene encodes GR4418 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4418 precursor RNA folds spatially, forming GR4418 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4418 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4418 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4418 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM149207 precursor RNA and GAM166503 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM149207 RNA and GAM166503 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM149207 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM149207 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM149207

target RNA into GAM149207 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM166503 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM166503 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM166503 target RNA into GAM166503 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4418 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4418 gene: GAM149207 target protein and GAM166503 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM149207 and GAM166503

GR4419 BF306764 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4419(GR4419) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4419 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4419 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4419 gene encodes GR4419 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4419 precursor RNA folds spatially, forming GR4419 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4419 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4419 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4419 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2431 precursor RNA and GAM282150 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2431 RNA and GAM282150 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2431 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2431 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2431 target RNA into GAM2431 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM282150 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM282150 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM282150 target RNA into GAM282150 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4419 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4419 gene: GAM2431 target protein and GAM282150 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2431 and GAM282150

GR4420 AA834877 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4420(GR4420) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4420 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4420 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4420 gene encodes GR4420 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4420 precursor RNA folds spatially, forming GR4420 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated

that GR4420 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4420 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4420 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM167992 precursor RNA, GAM179303 precursor RNA and GAM202678 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM167992 RNA, GAM179303 RNA and GAM202678 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM167992 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM167992 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM167992 target RNA into GAM167992 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM179303 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM179303 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM179303 target RNA into GAM179303 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM202678 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM202678 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM202678 target RNA into GAM202678 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4420 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4420 gene: GAM167992 target

protein, GAM179303 target protein and GAM202678 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM167992, GAM179303 and GAM202678

GR4421 BE881166 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4421 (GR4421) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4421 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4421 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4421 gene encodes GR4421 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4421 precursor RNA folds spatially, forming GR4421 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4421 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4421 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4421 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM85183 precursor RNA, GAM110152 precursor RNA and GAM324391 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM85183 RNA, GAM110152 RNA and GAM324391 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM85183 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM85183 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM85183

target RNA into GAM85183 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM110152 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM110152 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM110152 target RNA into GAM110152 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM324391 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM324391 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM324391 target RNA into GAM324391 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4421 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4421 gene: GAM85183 target protein, GAM110152 target protein and GAM324391 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM85183, GAM110152 and GAM324391

GR4422 AV704985 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4422(GR4422) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4422 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4422 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4422 gene encodes GR4422 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4422 precursor RNA folds spatially, forming GR4422 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4422 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4422 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4422 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM6006 precursor RNA, GAM112300 precursor RNA and GAM209434 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6006 RNA, GAM112300 RNA and GAM209434 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6006 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6006 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6006 target RNA into GAM6006 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM112300 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM112300 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM112300 target RNA into GAM112300 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM209434 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM209434 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM209434 target RNA into GAM209434 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4422 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4422 gene: GAM6006 target protein, GAM112300 target protein and GAM209434 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6006, GAM112300 and

GR4423 AW630228 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4423(GR4423) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4423 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4423 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4423 gene encodes GR4423 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4423 precursor RNA folds spatially, forming GR4423 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4423 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4423 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4423 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM256193 precursor RNA and GAM327880 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM256193 RNA and GAM327880 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM256193 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM256193 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM256193 target RNA into GAM256193 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM327880 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM327880 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM327880 target RNA into GAM327880 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4423 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4423 gene: GAM256193 target protein and GAM327880 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM256193 and GAM327880

GR4424 N58024 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4424(GR4424) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4424 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4424 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4424 gene encodes GR4424 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4424 precursor RNA folds spatially, forming GR4424 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4424 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4424 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4424 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM38266 precursor RNA and GAM300415 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM38266 RNA and GAM300415 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding

to GAM RNA of Fig. 8.

GAM38266 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM38266 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM38266 target RNA into GAM38266 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM300415 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM300415 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM300415 target RNA into GAM300415 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4424 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4424 gene: GAM38266 target protein and GAM300415 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM38266 and GAM300415

GR4425 BF570160 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4425(GR4425) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4425 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4425 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4425 gene encodes GR4425 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4425 precursor RNA folds spatially, forming GR4425 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4425 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4425 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR4425 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM146 precursor RNA, GAM60715 precursor RNA, GAM253032 precursor RNA and GAM319446 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM146 RNA, GAM60715 RNA, GAM253032 RNA and GAM319446 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM146 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM146 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM146 target RNA into GAM146 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM60715 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM60715 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM60715 target RNA into GAM60715 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM253032 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM253032 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM253032 target RNA into GAM253032 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM319446 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM319446 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM319446 target RNA into GAM319446 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly

utilities, of GR4425 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4425 gene: GAM146 target protein, GAM60715 target protein, GAM253032 target protein and GAM319446 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM146, GAM60715, GAM253032 and GAM319446

GR4426 BF895553 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4426(GR4426) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4426 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4426 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4426 gene encodes GR4426 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4426 precursor RNA folds spatially, forming GR4426 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4426 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4426 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4426 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM93498 precursor RNA, GAM208923 precursor RNA and GAM218652 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM93498 RNA, GAM208923 RNA and GAM218652 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM93498 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM93498 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM93498 target RNA into GAM93498 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM208923 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM208923 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM208923 target RNA into GAM208923 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM218652 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM218652 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM218652 target RNA into GAM218652 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4426 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4426 gene: GAM93498 target protein, GAM208923 target protein and GAM218652 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM93498, GAM208923 and GAM218652

GR4427 BI260618 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4427(GR4427) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4427 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4427 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4427 gene encodes GR4427 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4427 precursor RNA folds spatially, forming GR4427 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4427 folded precursor RNA comprises a plurality of what is known in the

art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4427 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4427 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4994 precursor RNA, GAM5962 precursor RNA and GAM81236 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4994 RNA, GAM5962 RNA and GAM81236 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4994 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4994 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4994 target RNA into GAM4994 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5962 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5962 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5962 target RNA into GAM5962 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM81236 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM81236 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM81236 target RNA into GAM81236 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4427 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4427 gene: GAM4994 target protein, GAM5962 target protein and GAM81236 target protein, herein

schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4994, GAM5962 and GAM81236

GR4428 BG614346 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4428(GR4428) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4428 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4428 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4428 gene encodes GR4428 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4428 precursor RNA folds spatially, forming GR4428 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4428 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4428 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4428 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1413 precursor RNA and GAM239821 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1413 RNA and GAM239821 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1413 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1413 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1413 target RNA into GAM1413 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM239821 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM239821 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM239821 target RNA into GAM239821 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4428 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4428 gene: GAM1413 target protein and GAM239821 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1413 and GAM239821

GR4429 BG938559 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4429(GR4429) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4429 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4429 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4429 gene encodes GR4429 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4429 precursor RNA folds spatially, forming GR4429 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4429 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4429 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4429 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM32582 precursor RNA, GAM35354 precursor RNA, GAM257818 precursor RNA and GAM272953 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM32582 RNA, GAM35354 RNA, GAM257818 RNA and GAM272953 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM32582 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM32582 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM32582 target RNA into GAM32582 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM35354 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM35354 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM35354 target RNA into GAM35354 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM257818 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM257818 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM257818 target RNA into GAM257818 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM272953 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM272953 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM272953 target RNA into GAM272953 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4429 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4429 gene: GAM32582 target protein, GAM35354 target protein, GAM257818 target protein and GAM272953 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM32582, GAM35354, GAM257818 and GAM272953

bioinformatically detected regulatory gene, referred to here as Genomic Record 4430(GR4430) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4430 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4430 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4430 gene encodes GR4430 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4430 precursor RNA folds spatially, forming GR4430 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4430 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4430 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4430 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM111960 precursor RNA and GAM135837 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM111960 RNA and GAM135837 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM111960 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM111960 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM111960 target RNA into GAM111960 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM135837 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM135837 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM135837

target RNA into GAM135837 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4430 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4430 gene: GAM111960 target protein and GAM135837 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM111960 and GAM135837

GR4431 BG099361 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4431(GR4431) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4431 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4431 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4431 gene encodes GR4431 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4431 precursor RNA folds spatially, forming GR4431 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4431 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4431 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4431 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM135944 precursor RNA and GAM320717 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM135944 RNA and GAM320717 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM135944 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM135944 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM135944 target RNA into GAM135944 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM320717 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM320717 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM320717 target RNA into GAM320717 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4431 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4431 gene: GAM135944 target protein and GAM320717 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM135944 and GAM320717

GR4432 AU123084 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4432(GR4432) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4432 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4432 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4432 gene encodes GR4432 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4432 precursor RNA folds spatially, forming GR4432 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4432 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4432 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4432 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM73905 precursor RNA, GAM234624 precursor RNA and GAM325935 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM73905 RNA, GAM234624 RNA and GAM325935 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM73905 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM73905 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM73905 target RNA into GAM73905 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM234624 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM234624 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM234624 target RNA into GAM234624 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM325935 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM325935 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM325935 target RNA into GAM325935 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4432 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4432 gene: GAM73905 target protein, GAM234624 target protein and GAM325935 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM73905, GAM234624 and GAM325935

4433(GR4433) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4433 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4433 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4433 gene encodes GR4433 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4433 precursor RNA folds spatially, forming GR4433 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4433 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4433 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4433 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM70467 precursor RNA, GAM114083 precursor RNA and GAM219362 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM70467 RNA, GAM114083 RNA and GAM219362 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM70467 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM70467 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM70467 target RNA into GAM70467 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM114083 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM114083 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM114083

target RNA into GAM114083 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM219362 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM219362 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM219362 target RNA into GAM219362 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4433 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4433 gene: GAM70467 target protein, GAM114083 target protein and GAM219362 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM70467, GAM114083 and GAM219362

GR4434 BM014129 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4434(GR4434) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4434 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4434 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4434 gene encodes GR4434 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4434 precursor RNA folds spatially, forming GR4434 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4434 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4434 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4434 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM275963 precursor RNA and GAM334207 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin

shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM275963 RNA and GAM334207 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM275963 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM275963 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM275963 target RNA into GAM275963 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM334207 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM334207 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM334207 target RNA into GAM334207 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4434 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4434 gene: GAM275963 target protein and GAM334207 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM275963 and GAM334207

GR4435 BG250255 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4435(GR4435) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4435 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4435 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4435 gene encodes GR4435 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4435 precursor RNA folds spatially, forming GR4435 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4435 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4435 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4435 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3981 precursor RNA and GAM196627 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3981 RNA and GAM196627 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3981 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3981 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3981 target RNA into GAM3981 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM196627 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM196627 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM196627 target RNA into GAM196627 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4435 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4435 gene: GAM3981 target protein and GAM196627 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3981 and GAM196627

GR4436 BI463319 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4436(GR4436) gene, which encodes an `operon-like` cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4436 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4436 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4436 gene encodes GR4436 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4436 precursor RNA folds spatially, forming GR4436 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4436 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4436 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4436 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM764 precursor RNA and GAM143202 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM764 RNA and GAM143202 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM764 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM764 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM764 target RNA into GAM764 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM143202 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM143202 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM143202 target RNA into GAM143202 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4436 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4436 gene: GAM764 target protein and GAM143202 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM764 and GAM143202

GR4437 BQ002503 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4437(GR4437) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4437 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4437 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4437 gene encodes GR4437 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4437 precursor RNA folds spatially, forming GR4437 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4437 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4437 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4437 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM227580 precursor RNA and GAM296382 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM227580 RNA and GAM296382 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM227580 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM227580 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM227580 target RNA into GAM227580 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM296382 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM296382 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM296382 target RNA into GAM296382 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4437 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4437 gene: GAM227580 target protein and GAM296382 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM227580 and GAM296382

GR4438 BF694446 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4438(GR4438) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4438 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4438 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4438 gene encodes GR4438 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4438 precursor RNA folds spatially, forming GR4438 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4438 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4438 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4438 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM277474 precursor RNA and GAM326249 precursor

RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM277474 RNA and GAM326249 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM277474 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM277474 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM277474 target RNA into GAM277474 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM326249 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM326249 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM326249 target RNA into GAM326249 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4438 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4438 gene: GAM277474 target protein and GAM326249 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM277474 and GAM326249

GR4439 BI018972 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4439(GR4439) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4439 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4439 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4439 gene encodes GR4439 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4439 precursor RNA folds spatially, forming GR4439 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4439 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4439 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4439 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2787 precursor RNA, GAM5363 precursor RNA and GAM37719 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2787 RNA, GAM5363 RNA and GAM37719 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2787 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2787 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2787 target RNA into GAM2787 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5363 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5363 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5363 target RNA into GAM5363 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM37719 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM37719 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM37719 target RNA into GAM37719 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly

utilities, of GR4439 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4439 gene: GAM2787 target protein, GAM5363 target protein and GAM37719 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2787, GAM5363 and GAM37719

GR4440 BI759699 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4440(GR4440) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4440 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4440 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4440 gene encodes GR4440 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4440 precursor RNA folds spatially, forming GR4440 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4440 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4440 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4440 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM668 precursor RNA and GAM71807 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM668 RNA and GAM71807 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM668 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM668 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds

to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM668 target RNA into GAM668 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM71807 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM71807 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM71807 target RNA into GAM71807 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4440 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4440 gene: GAM668 target protein and GAM71807 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM668 and GAM71807

GR4441 AW298094 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4441 (GR4441) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4441 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4441 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4441 gene encodes GR4441 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4441 precursor RNA folds spatially, forming GR4441 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4441 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4441 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4441 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1340 precursor RNA and GAM6324 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3

FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1340 RNA and GAM6324 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1340 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1340 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1340 target RNA into GAM1340 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6324 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6324 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6324 target RNA into GAM6324 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4441 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4441 gene: GAM1340 target protein and GAM6324 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1340 and GAM6324

GR4442 BE900393 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4442(GR4442) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4442 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4442 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4442 gene encodes GR4442 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4442 precursor RNA folds spatially, forming GR4442 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4442 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4442 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4442 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4772 precursor RNA, GAM6528 precursor RNA and GAM6834 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4772 RNA, GAM6528 RNA and GAM6834 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4772 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4772 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4772 target RNA into GAM4772 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6528 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6528 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6528 target RNA into GAM6528 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6834 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6834 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6834 target RNA into GAM6834 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4442 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4442 gene: GAM4772 target protein, GAM6528 target protein and GAM6834 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4772, GAM6528 and GAM6834

GR4443 BF131980 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4443(GR4443) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4443 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4443 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4443 gene encodes GR4443 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4443 precursor RNA folds spatially, forming GR4443 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4443 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4443 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4443 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4117 precursor RNA and GAM160372 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4117 RNA and GAM160372 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4117 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4117 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig. 8, thereby inhibiting translation of GAM4117 target RNA into GAM4117 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM160372 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM160372 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM160372 target RNA into GAM160372 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4443 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4443 gene: GAM4117 target protein and GAM160372 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4117 and GAM160372

GR4444 BF310041 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4444(GR4444) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4444 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4444 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4444 gene encodes GR4444 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4444 precursor RNA folds spatially, forming GR4444 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4444 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4444 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4444 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM5476 precursor RNA, GAM5877 precursor RNA and GAM7812 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded

precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5476 RNA, GAM5877 RNA and GAM7812 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5476 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5476 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5476 target RNA into GAM5476 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5877 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5877 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5877 target RNA into GAM5877 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7812 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7812 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7812 target RNA into GAM7812 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4444 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4444 gene: GAM5476 target protein, GAM5877 target protein and GAM7812 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5476, GAM5877 and GAM7812

GR4445 BG117888 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4445(GR4445) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4445 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4445 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4445 gene encodes GR4445 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4445 precursor RNA folds spatially, forming GR4445 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4445 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4445 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4445 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM49715 precursor RNA and GAM174505 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM49715 RNA and GAM174505 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM49715 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM49715 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM49715 target RNA into GAM49715 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM174505 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM174505 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM174505 target RNA into GAM174505 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4445 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4445 gene: GAM49715 target protein and GAM174505 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM49715 and GAM174505

GR4446 BE794640 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4446(GR4446) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4446 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4446 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4446 gene encodes GR4446 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4446 precursor RNA folds spatially, forming GR4446 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4446 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4446 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4446 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM158879 precursor RNA, GAM232119 precursor RNA and GAM252291 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM158879 RNA, GAM232119 RNA and GAM252291 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM158879 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM158879 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM158879 target RNA into GAM158879 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM232119 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM232119 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM232119 target RNA into GAM232119 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM252291 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM252291 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM252291 target RNA into GAM252291 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4446 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4446 gene: GAM158879 target protein, GAM232119 target protein and GAM252291 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM158879, GAM232119 and GAM252291

GR4447 AI446812 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4447(GR4447) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4447 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4447 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4447 gene encodes GR4447 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4447 precursor RNA folds spatially, forming GR4447 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4447 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4447 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4447 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM192964 precursor RNA and GAM301316 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM192964 RNA and GAM301316 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM192964 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM192964 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM192964 target RNA into GAM192964 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM301316 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM301316 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM301316 target RNA into GAM301316 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4447 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4447 gene: GAM192964 target protein and GAM301316 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM192964 and GAM301316

GR4448 AI564599 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4448(GR4448) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4448 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4448 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4448 gene encodes GR4448 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4448 precursor RNA folds spatially, forming GR4448 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4448 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4448 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4448 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM25590 precursor RNA and GAM36043 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM25590 RNA and GAM36043 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM25590 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM25590 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM25590 target RNA into GAM25590 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM36043 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM36043 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM36043 target RNA into GAM36043 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4448 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR4448 gene: GAM25590 target protein and GAM36043 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM25590 and GAM36043

GR4449 T66045 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4449(GR4449) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4449 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4449 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4449 gene encodes GR4449 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4449 precursor RNA folds spatially, forming GR4449 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4449 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4449 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4449 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM112496 precursor RNA and GAM294206 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM112496 RNA and GAM294206 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM112496 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM112496 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM112496 target RNA into GAM112496 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM294206 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM294206 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM294206 target RNA into GAM294206 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4449 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4449 gene: GAM112496 target protein and GAM294206 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM112496 and GAM294206

GR4450 AA630640 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4450(GR4450) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4450 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4450 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4450 gene encodes GR4450 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4450 precursor RNA folds spatially, forming GR4450 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4450 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4450 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4450 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM45890 precursor RNA, GAM55329 precursor RNA and GAM93138 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM45890 RNA, GAM55329 RNA and GAM93138 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM45890 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM45890 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM45890 target RNA into GAM45890 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM55329 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM55329 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM55329 target RNA into GAM55329 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM93138 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM93138 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM93138 target RNA into GAM93138 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4450 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4450 gene: GAM45890 target protein, GAM55329 target protein and GAM93138 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM45890, GAM55329 and GAM93138

GR4451 BG682690 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4451(GR4451) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4451 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR4451 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4451 gene encodes GR4451 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4451 precursor RNA folds spatially, forming GR4451 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4451 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4451 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4451 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM111 precursor RNA, GAM7027 precursor RNA and GAM102744 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM111 RNA, GAM7027 RNA and GAM102744 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM111 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM111 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM111 target RNA into GAM111 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7027 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7027 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7027 target RNA into GAM7027 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM102744 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM102744 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM102744 target RNA into GAM102744 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4451 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4451 gene: GAM111 target protein, GAM7027 target protein and GAM102744 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM111, GAM7027 and GAM102744

GR4452 BE613754 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4452(GR4452) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4452 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4452 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4452 gene encodes GR4452 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4452 precursor RNA folds spatially, forming GR4452 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4452 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4452 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4452 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM59184 precursor RNA, GAM70762 precursor RNA, GAM231501 precursor RNA and GAM257768 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM59184 RNA, GAM70762 RNA, GAM231501 RNA and GAM257768

RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM59184 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM59184 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM59184 target RNA into GAM59184 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM70762 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM70762 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM70762 target RNA into GAM70762 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM231501 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM231501 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM231501 target RNA into GAM231501 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM257768 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM257768 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM257768 target RNA into GAM257768 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4452 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4452 gene: GAM59184 target protein, GAM70762 target protein, GAM231501 target protein and GAM257768 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM59184, GAM70762, GAM231501 and GAM257768

GR4453 AU132310 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4453(GR4453) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR4453 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4453 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4453 gene encodes GR4453 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4453 precursor RNA folds spatially, forming GR4453 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4453 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4453 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4453 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3515 precursor RNA and GAM43980 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3515 RNA and GAM43980 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3515 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3515 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3515 target RNA into GAM3515 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM43980 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM43980 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM43980 target RNA into GAM43980 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4453 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4453 gene: GAM3515 target protein and GAM43980 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3515 and GAM43980

GR4454 BM670679 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4454(GR4454) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4454 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4454 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4454 gene encodes GR4454 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4454 precursor RNA folds spatially, forming GR4454 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4454 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4454 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4454 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4369 precursor RNA, GAM247397 precursor RNA and GAM256084 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4369 RNA, GAM247397 RNA and GAM256084 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4369 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4369 target RNA, herein schematically represented by

GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4369 target RNA into GAM4369 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM247397 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM247397 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM247397 target RNA into GAM247397 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM256084 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM256084 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM256084 target RNA into GAM256084 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4454 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4454 gene: GAM4369 target protein, GAM247397 target protein and GAM256084 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4369, GAM247397 and GAM256084

GR4455 AA454970 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4455(GR4455) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4455 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4455 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4455 gene encodes GR4455 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4455 precursor RNA folds spatially, forming GR4455 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4455 folded precursor RNA comprises a plurality of what is known in the

art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4455 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4455 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6017 precursor RNA and GAM30014 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6017 RNA and GAM30014 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6017 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6017 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6017 target RNA into GAM6017 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM30014 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM30014 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM30014 target RNA into GAM30014 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4455 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4455 gene: GAM6017 target protein and GAM30014 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6017 and GAM30014

GR4456 BE300452 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4456(GR4456) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR4456 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4456 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4456 gene encodes GR4456 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4456 precursor RNA folds spatially, forming GR4456 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4456 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4456 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4456 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2424 precursor RNA, GAM5416 precursor RNA and GAM108254 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2424 RNA, GAM5416 RNA and GAM108254 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2424 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2424 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2424 target RNA into GAM2424 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5416 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5416 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5416 target RNA into GAM5416 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM108254 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM108254 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM108254 target RNA into GAM108254 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4456 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4456 gene: GAM2424 target protein, GAM5416 target protein and GAM108254 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2424, GAM5416 and GAM108254

GR4457 BM800864 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4457(GR4457) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4457 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4457 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4457 gene encodes GR4457 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4457 precursor RNA folds spatially, forming GR4457 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4457 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4457 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4457 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2412 precursor RNA, GAM49576 precursor RNA and GAM290539 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2412 RNA, GAM49576 RNA and GAM290539 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2412 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2412 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2412 target RNA into GAM2412 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM49576 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM49576 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM49576 target RNA into GAM49576 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM290539 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM290539 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM290539 target RNA into GAM290539 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4457 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4457 gene: GAM2412 target protein, GAM49576 target protein and GAM290539 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2412, GAM49576 and GAM290539

GR4458 AA777067 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4458(GR4458) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4458 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4458

gene was detected is described hereinabove with reference to Figs. 8-18.

GR4458 gene encodes GR4458 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4458 precursor RNA folds spatially, forming GR4458 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4458 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4458 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4458 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM156180 precursor RNA and GAM180470 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM156180 RNA and GAM180470 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM156180 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM156180 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM156180 target RNA into GAM156180 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM180470 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM180470 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM180470 target RNA into GAM180470 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4458 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4458 gene: GAM156180 target protein and GAM180470 target protein, herein schematically represented by GAM1

TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM156180 and GAM180470

GR4459 BI520516 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4459(GR4459) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4459 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4459 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4459 gene encodes GR4459 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4459 precursor RNA folds spatially, forming GR4459 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4459 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4459 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4459 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1676 precursor RNA and GAM241110 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1676 RNA and GAM241110 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1676 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1676 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1676 target RNA into GAM1676 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM241110 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM241110 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM241110 target RNA into GAM241110 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4459 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4459 gene: GAM1676 target protein and GAM241110 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1676 and GAM241110

GR4460 BG760738 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4460(GR4460) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4460 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4460 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4460 gene encodes GR4460 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4460 precursor RNA folds spatially, forming GR4460 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4460 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4460 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4460 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM63984 precursor RNA, GAM64623 precursor RNA and GAM69862 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM63984 RNA, GAM64623 RNA and GAM69862 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM63984 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM63984 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM63984 target RNA into GAM63984 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM64623 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM64623 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM64623 target RNA into GAM64623 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM69862 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM69862 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM69862 target RNA into GAM69862 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4460 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4460 gene: GAM63984 target protein, GAM64623 target protein and GAM69862 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM63984, GAM64623 and GAM69862

GR4461 BI602337 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4461(GR4461) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4461 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4461 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4461 gene encodes GR4461 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4461 precursor RNA folds spatially, forming GR4461 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4461 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4461 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4461 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM47630 precursor RNA and GAM240459 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM47630 RNA and GAM240459 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM47630 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM47630 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM47630 target RNA into GAM47630 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM240459 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM240459 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM240459 target RNA into GAM240459 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4461 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4461 gene: GAM47630 target protein and GAM240459 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes

is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM47630 and GAM240459

GR4462 AW749576 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4462(GR4462) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4462 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4462 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4462 gene encodes GR4462 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4462 precursor RNA folds spatially, forming GR4462 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4462 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4462 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4462 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4350 precursor RNA and GAM6298 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4350 RNA and GAM6298 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4350 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4350 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4350 target RNA into GAM4350 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6298 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM6298 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6298 target RNA into GAM6298 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4462 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4462 gene: GAM4350 target protein and GAM6298 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4350 and GAM6298

GR4463 BE512695 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4463(GR4463) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4463 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4463 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4463 gene encodes GR4463 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4463 precursor RNA folds spatially, forming GR4463 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4463 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4463 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4463 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7653 precursor RNA and GAM91636 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7653 RNA and GAM91636 RNA, herein schematically

represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7653 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7653 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7653 target RNA into GAM7653 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM91636 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM91636 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM91636 target RNA into GAM91636 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4463 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4463 gene: GAM7653 target protein and GAM91636 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7653 and GAM91636

GR4464 BI836106 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4464(GR4464) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4464 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4464 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4464 gene encodes GR4464 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4464 precursor RNA folds spatially, forming GR4464 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4464 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4464 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4464 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM271297 precursor RNA and GAM280941 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM271297 RNA and GAM280941 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM271297 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM271297 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM271297 target RNA into GAM271297 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM280941 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM280941 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM280941 target RNA into GAM280941 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4464 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4464 gene: GAM271297 target protein and GAM280941 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM271297 and GAM280941

GR4465 BE253640 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4465(GR4465) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4465 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR4465 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4465 gene encodes GR4465 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4465 precursor RNA folds spatially, forming GR4465 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4465 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4465 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4465 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM59201 precursor RNA and GAM273593 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM59201 RNA and GAM273593 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM59201 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM59201 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM59201 target RNA into GAM59201 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM273593 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM273593 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM273593 target RNA into GAM273593 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4465 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4465 gene: GAM59201 target

protein and GAM273593 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM59201 and GAM273593

GR4466 AW129462 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4466(GR4466) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4466 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4466 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4466 gene encodes GR4466 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4466 precursor RNA folds spatially, forming GR4466 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4466 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4466 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4466 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3340 precursor RNA, GAM17471 precursor RNA and GAM191582 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3340 RNA, GAM17471 RNA and GAM191582 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3340 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3340 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3340 target RNA into GAM3340 target protein, herein schematically represented by GAM1 TARGET

PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM17471 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM17471 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM17471 target RNA into GAM17471 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM191582 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM191582 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM191582 target RNA into GAM191582 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4466 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4466 gene: GAM3340 target protein, GAM17471 target protein and GAM191582 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3340, GAM17471 and GAM191582

GR4467 H16444 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4467(GR4467) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4467 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4467 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4467 gene encodes GR4467 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4467 precursor RNA folds spatially, forming GR4467 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4467 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4467 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR4467 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM202592 precursor RNA and GAM323644 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM202592 RNA and GAM323644 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM202592 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM202592 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM202592 target RNA into GAM202592 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM323644 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM323644 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM323644 target RNA into GAM323644 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4467 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4467 gene: GAM202592 target protein and GAM323644 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM202592 and GAM323644

GR4468 BM728108 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4468(GR4468) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4468 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4468

gene was detected is described hereinabove with reference to Figs. 8-18.

GR4468 gene encodes GR4468 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4468 precursor RNA folds spatially, forming GR4468 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4468 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4468 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4468 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM981 precursor RNA, GAM34476 precursor RNA and GAM245122 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM981 RNA, GAM34476 RNA and GAM245122 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM981 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM981 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM981 target RNA into GAM981 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM34476 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM34476 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM34476 target RNA into GAM34476 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM245122 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM245122 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM245122 target RNA into GAM245122 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4468 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4468 gene: GAM981 target protein, GAM34476 target protein and GAM245122 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM981, GAM34476 and GAM245122

GR4469 BG769337 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4469(GR4469) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4469 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4469 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4469 gene encodes GR4469 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4469 precursor RNA folds spatially, forming GR4469 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4469 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4469 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4469 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8433 precursor RNA and GAM270670 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8433 RNA and GAM270670 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8433 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8433 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8433 target RNA into GAM8433 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM270670 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM270670 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM270670 target RNA into GAM270670 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4469 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4469 gene: GAM8433 target protein and GAM270670 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8433 and GAM270670

GR4470 BM789696 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4470(GR4470) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4470 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4470 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4470 gene encodes GR4470 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4470 precursor RNA folds spatially, forming GR4470 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4470 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4470 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4470 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM128888 precursor RNA and GAM134672 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM128888 RNA and GAM134672 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM128888 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM128888 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM128888 target RNA into GAM128888 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM134672 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM134672 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM134672 target RNA into GAM134672 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4470 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4470 gene: GAM128888 target protein and GAM134672 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM128888 and GAM134672

GR4471 BI676499 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4471(GR4471) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4471 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4471 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4471 gene encodes GR4471 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4471 precursor RNA folds spatially, forming GR4471 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4471 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4471 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4471 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3259 precursor RNA and GAM310508 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3259 RNA and GAM310508 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3259 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3259 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3259 target RNA into GAM3259 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM310508 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM310508 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM310508 target RNA into GAM310508 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4471 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4471 gene: GAM3259 target protein and GAM310508 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes

is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3259 and GAM310508

GR4472 BI253214 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4472(GR4472) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4472 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4472 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4472 gene encodes GR4472 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4472 precursor RNA folds spatially, forming GR4472 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4472 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4472 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4472 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4099 precursor RNA, GAM126973 precursor RNA and GAM254406 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4099 RNA, GAM126973 RNA and GAM254406 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4099 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4099 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4099 target RNA into GAM4099 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM126973 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM126973 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM126973 target RNA into GAM126973 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM254406 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM254406 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM254406 target RNA into GAM254406 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4472 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4472 gene: GAM4099 target protein, GAM126973 target protein and GAM254406 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4099, GAM126973 and GAM254406

GR4473 AL121306 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4473(GR4473) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4473 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4473 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4473 gene encodes GR4473 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4473 precursor RNA folds spatially, forming GR4473 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4473 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4473 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4473 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6544 precursor RNA and GAM175709 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6544 RNA and GAM175709 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6544 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6544 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6544 target RNA into GAM6544 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM175709 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM175709 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM175709 target RNA into GAM175709 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4473 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4473 gene: GAM6544 target protein and GAM175709 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6544 and GAM175709

GR4474 BM662990 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4474(GR4474) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4474 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4474 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4474 gene encodes GR4474 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4474 precursor RNA folds spatially, forming GR4474 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4474 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4474 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4474 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1232 precursor RNA and GAM218559 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1232 RNA and GAM218559 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1232 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1232 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1232 target RNA into GAM1232 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM218559 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM218559 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM218559 target RNA into GAM218559 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4474 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4474 gene: GAM1232 target protein and GAM218559 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference,

with references to GAM1232 and GAM218559

GR4475 AI796994 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4475(GR4475) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4475 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4475 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4475 gene encodes GR4475 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4475 precursor RNA folds spatially, forming GR4475 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4475 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4475 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4475 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM38192 precursor RNA and GAM244639 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM38192 RNA and GAM244639 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM38192 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM38192 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM38192 target RNA into GAM38192 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM244639 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM244639 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM244639 target RNA into GAM244639 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4475 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4475 gene: GAM38192 target protein and GAM244639 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM38192 and GAM244639

GR4476 BI493666 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4476(GR4476) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4476 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4476 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4476 gene encodes GR4476 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4476 precursor RNA folds spatially, forming GR4476 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4476 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4476 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4476 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM1707 precursor RNA, GAM126117 precursor RNA, GAM324742 precursor RNA and GAM333595 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1707 RNA, GAM126117 RNA, GAM324742 RNA and GAM333595

RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1707 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1707 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1707 target RNA into GAM1707 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM126117 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM126117 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM126117 target RNA into GAM126117 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM324742 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM324742 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM324742 target RNA into GAM324742 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM333595 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM333595 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM333595 target RNA into GAM333595 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4476 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4476 gene: GAM1707 target protein, GAM126117 target protein, GAM324742 target protein and GAM333595 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1707, GAM126117, GAM324742 and GAM333595

GR4477 AV760037 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4477(GR4477) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR4477 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4477 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4477 gene encodes GR4477 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4477 precursor RNA folds spatially, forming GR4477 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4477 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4477 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4477 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM44406 precursor RNA and GAM232895 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM44406 RNA and GAM232895 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM44406 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM44406 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM44406 target RNA into GAM44406 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM232895 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM232895 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM232895 target RNA into GAM232895 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4477 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4477 gene: GAM44406 target protein and GAM232895 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM44406 and GAM232895

GR4478 BM846398 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4478(GR4478) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4478 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4478 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4478 gene encodes GR4478 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4478 precursor RNA folds spatially, forming GR4478 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4478 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4478 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4478 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6575 precursor RNA and GAM48704 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6575 RNA and GAM48704 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6575 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6575 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds

to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6575 target RNA into GAM6575 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM48704 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM48704 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM48704 target RNA into GAM48704 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4478 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4478 gene: GAM6575 target protein and GAM48704 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6575 and GAM48704

GR4479 BE770943 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4479(GR4479) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4479 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4479 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4479 gene encodes GR4479 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4479 precursor RNA folds spatially, forming GR4479 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4479 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4479 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4479 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM69885 precursor RNA, GAM279518 precursor RNA and GAM289461 precursor RNA, herein schematically represented by GAM1 FOLDED

PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM69885 RNA, GAM279518 RNA and GAM289461 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM69885 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM69885 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM69885 target RNA into GAM69885 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM279518 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM279518 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM279518 target RNA into GAM279518 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM289461 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM289461 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM289461 target RNA into GAM289461 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4479 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4479 gene: GAM69885 target protein, GAM279518 target protein and GAM289461 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM69885, GAM279518 and GAM289461

GR4480 BM310193 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4480(GR4480) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR4480 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4480 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4480 gene encodes GR4480 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4480 precursor RNA folds spatially, forming GR4480 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4480 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4480 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4480 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM5789 precursor RNA, GAM274772 precursor RNA and GAM312531 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5789 RNA, GAM274772 RNA and GAM312531 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5789 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5789 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5789 target RNA into GAM5789 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM274772 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM274772 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM274772 target RNA into GAM274772 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM312531 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM312531 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM312531 target RNA into GAM312531 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4480 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4480 gene: GAM5789 target protein, GAM274772 target protein and GAM312531 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5789, GAM274772 and GAM312531

GR4481 AW367727 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4481 (GR4481) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4481 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4481 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4481 gene encodes GR4481 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4481 precursor RNA folds spatially, forming GR4481 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4481 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4481 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4481 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM90345 precursor RNA and GAM285727 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM90345 RNA and GAM285727 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM90345 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM90345 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM90345 target RNA into GAM90345 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM285727 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM285727 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM285727 target RNA into GAM285727 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4481 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4481 gene: GAM90345 target protein and GAM285727 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM90345 and GAM285727

GR4482 AA129884 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4482(GR4482) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4482 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4482 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4482 gene encodes GR4482 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4482 precursor RNA folds spatially, forming GR4482 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4482 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR4482 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4482 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5885 precursor RNA and GAM131844 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5885 RNA and GAM131844 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5885 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5885 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5885 target RNA into GAM5885 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM131844 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM131844 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM131844 target RNA into GAM131844 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4482 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4482 gene: GAM5885 target protein and GAM131844 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5885 and GAM131844

GR4483 AA765258 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4483(GR4483) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4483 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4483 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4483 gene encodes GR4483 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4483 precursor RNA folds spatially, forming GR4483 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4483 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4483 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4483 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM95391 precursor RNA and GAM109015 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM95391 RNA and GAM109015 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM95391 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM95391 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM95391 target RNA into GAM95391 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM109015 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM109015 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM109015 target RNA into GAM109015 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4483 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4483 gene: GAM95391 target protein and GAM109015 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM95391 and GAM109015

GR4484 AI903552 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4484(GR4484) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4484 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4484 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4484 gene encodes GR4484 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4484 precursor RNA folds spatially, forming GR4484 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4484 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4484 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4484 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3562 precursor RNA and GAM126952 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3562 RNA and GAM126952 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3562 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3562 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3562 target RNA into

GAM3562 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM126952 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM126952 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM126952 target RNA into GAM126952 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4484 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4484 gene: GAM3562 target protein and GAM126952 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3562 and GAM126952

GR4485 AW953003 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4485(GR4485) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4485 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4485 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4485 gene encodes GR4485 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4485 precursor RNA folds spatially, forming GR4485 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4485 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4485 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4485 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM24736 precursor RNA, GAM163225 precursor RNA and GAM180498 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED

PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM24736 RNA, GAM163225 RNA and GAM180498 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM24736 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM24736 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM24736 target RNA into GAM24736 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM163225 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM163225 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM163225 target RNA into GAM163225 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM180498 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM180498 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM180498 target RNA into GAM180498 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4485 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4485 gene: GAM24736 target protein, GAM163225 target protein and GAM180498 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM24736, GAM163225 and GAM180498

GR4486 AI174721 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4486(GR4486) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4486 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4486 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4486 gene encodes GR4486 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4486 precursor RNA folds spatially, forming GR4486 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4486 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4486 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4486 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM759 precursor RNA and GAM298320 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM759 RNA and GAM298320 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM759 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM759 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM759 target RNA into GAM759 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM298320 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM298320 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM298320 target RNA into GAM298320 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4486 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR4486 gene: GAM759 target protein and GAM298320 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM759 and GAM298320

GR4487 T34364 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4487(GR4487) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4487 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4487 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4487 gene encodes GR4487 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4487 precursor RNA folds spatially, forming GR4487 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4487 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4487 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4487 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4840 precursor RNA, GAM22531 precursor RNA and GAM292122 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4840 RNA, GAM22531 RNA and GAM292122 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4840 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4840 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4840 target RNA into

GAM4840 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM22531 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM22531 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM22531 target RNA into GAM22531 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM292122 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM292122 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM292122 target RNA into GAM292122 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4487 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4487 gene: GAM4840 target protein, GAM22531 target protein and GAM292122 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4840, GAM22531 and GAM292122

GR4488 BF116037 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4488(GR4488) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4488 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4488 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4488 gene encodes GR4488 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4488 precursor RNA folds spatially, forming GR4488 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4488 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4488 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4488 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3714 precursor RNA, GAM101848 precursor RNA and GAM116792 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3714 RNA, GAM101848 RNA and GAM116792 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3714 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3714 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3714 target RNA into GAM3714 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM101848 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM101848 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM101848 target RNA into GAM101848 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM116792 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM116792 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM116792 target RNA into GAM116792 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4488 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4488 gene: GAM3714 target protein, GAM101848 target protein and GAM116792 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3714, GAM101848 and

GR4489 AW511262 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4489 (GR4489) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4489 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4489 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4489 gene encodes GR4489 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4489 precursor RNA folds spatially, forming GR4489 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4489 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4489 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4489 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM262227 precursor RNA and GAM289371 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM262227 RNA and GAM289371 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM262227 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM262227 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM262227 target RNA into GAM262227 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM289371 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM289371 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM289371 target RNA into GAM289371 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4489 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4489 gene: GAM262227 target protein and GAM289371 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM262227 and GAM289371

GR4490 AA648538 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4490(GR4490) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4490 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4490 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4490 gene encodes GR4490 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4490 precursor RNA folds spatially, forming GR4490 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4490 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4490 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4490 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM125505 precursor RNA and GAM143262 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM125505 RNA and GAM143262 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding

to GAM RNA of Fig. 8.

GAM125505 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM125505 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM125505 target RNA into GAM125505 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM143262 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM143262 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM143262 target RNA into GAM143262 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4490 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4490 gene: GAM125505 target protein and GAM143262 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM125505 and GAM143262

GR4491 AV764305 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4491 (GR4491) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4491 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4491 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4491 gene encodes GR4491 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4491 precursor RNA folds spatially, forming GR4491 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4491 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4491 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR4491 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM16787 precursor RNA and GAM172539 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM16787 RNA and GAM172539 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM16787 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM16787 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM16787 target RNA into GAM16787 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM172539 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM172539 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM172539 target RNA into GAM172539 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4491 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4491 gene: GAM16787 target protein and GAM172539 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM16787 and GAM172539

GR4492 AI522296 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4492(GR4492) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4492 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4492

gene was detected is described hereinabove with reference to Figs. 8-18.

GR4492 gene encodes GR4492 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4492 precursor RNA folds spatially, forming GR4492 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4492 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4492 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4492 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM129883 precursor RNA, GAM222523 precursor RNA and GAM249386 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM129883 RNA, GAM222523 RNA and GAM249386 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM129883 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM129883 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM129883 target RNA into GAM129883 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM222523 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM222523 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM222523 target RNA into GAM222523 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM249386 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM249386 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM249386 target RNA into GAM249386 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4492 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4492 gene: GAM129883 target protein, GAM222523 target protein and GAM249386 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM129883, GAM222523 and GAM249386

GR4493 AA442926 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4493(GR4493) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4493 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4493 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4493 gene encodes GR4493 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4493 precursor RNA folds spatially, forming GR4493 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4493 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4493 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4493 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM108671 precursor RNA, GAM223774 precursor RNA and GAM237321 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM108671 RNA, GAM223774 RNA and GAM237321 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs

corresponding to GAM RNA of Fig. 8.

GAM108671 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM108671 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM108671 target RNA into GAM108671 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM223774 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM223774 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM223774 target RNA into GAM223774 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM237321 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM237321 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM237321 target RNA into GAM237321 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4493 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4493 gene: GAM108671 target protein, GAM223774 target protein and GAM237321 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM108671, GAM223774 and GAM237321

GR4494 H38866 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4494(GR4494) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4494 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4494 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4494 gene encodes GR4494 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR4494 precursor RNA folds spatially, forming GR4494 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4494 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4494 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4494 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5731 precursor RNA and GAM318659 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5731 RNA and GAM318659 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5731 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5731 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5731 target RNA into GAM5731 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM318659 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM318659 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM318659 target RNA into GAM318659 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4494 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4494 gene: GAM5731 target protein and GAM318659 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5731 and GAM318659

GR4495 BF362851 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4495(GR4495) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4495 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4495 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4495 gene encodes GR4495 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4495 precursor RNA folds spatially, forming GR4495 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4495 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4495 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4495 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4235 precursor RNA and GAM9753 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4235 RNA and GAM9753 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4235 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4235 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4235 target RNA into GAM4235 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM9753 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM9753 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig. 8, thereby inhibiting translation of GAM9753 target RNA into GAM9753 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4495 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4495 gene: GAM4235 target protein and GAM9753 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4235 and GAM9753

GR4496 BE783109 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4496(GR4496) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4496 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4496 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4496 gene encodes GR4496 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4496 precursor RNA folds spatially, forming GR4496 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4496 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4496 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4496 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2377 precursor RNA and GAM6908 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2377 RNA and GAM6908 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2377 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2377 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2377 target RNA into GAM2377 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6908 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6908 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6908 target RNA into GAM6908 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4496 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4496 gene: GAM2377 target protein and GAM6908 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2377 and GAM6908

GR4497 AL039521 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4497(GR4497) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4497 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4497 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4497 gene encodes GR4497 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4497 precursor RNA folds spatially, forming GR4497 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4497 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4497 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4497 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM26796 precursor RNA and GAM60282 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM26796 RNA and GAM60282 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM26796 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM26796 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM26796 target RNA into GAM26796 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM60282 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM60282 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM60282 target RNA into GAM60282 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4497 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4497 gene: GAM26796 target protein and GAM60282 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM26796 and GAM60282

GR4498 BF735775 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4498(GR4498) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4498 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4498 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4498 gene encodes GR4498 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4498 precursor RNA folds spatially, forming GR4498 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4498 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4498 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4498 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM6478 precursor RNA, GAM164262 precursor RNA and GAM247987 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6478 RNA, GAM164262 RNA and GAM247987 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6478 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6478 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6478 target RNA into GAM6478 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM164262 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM164262 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM164262 target RNA into GAM164262 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM247987 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM247987 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM247987 target RNA into GAM247987 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4498 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4498 gene: GAM6478 target protein, GAM164262 target protein and GAM247987 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6478, GAM164262 and GAM247987

GR4499 AW772090 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4499(GR4499) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4499 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4499 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4499 gene encodes GR4499 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4499 precursor RNA folds spatially, forming GR4499 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4499 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4499 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4499 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6149 precursor RNA and GAM31041 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6149 RNA and GAM31041 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6149 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6149 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6149 target RNA into GAM6149 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM31041 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM31041 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM31041 target RNA into GAM31041 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4499 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4499 gene: GAM6149 target protein and GAM31041 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6149 and GAM31041

GR4500 W73765 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4500(GR4500) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4500 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4500 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4500 gene encodes GR4500 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4500 precursor RNA folds spatially, forming GR4500 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4500 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4500 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4500 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM21266 precursor RNA and GAM212968 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM21266 RNA and GAM212968 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM21266 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM21266 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM21266 target RNA into GAM21266 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM212968 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM212968 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM212968 target RNA into GAM212968 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4500 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4500 gene: GAM21266 target protein and GAM212968 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM21266 and GAM212968

GR4501 BM988723 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4501(GR4501) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4501 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4501 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4501 gene encodes GR4501 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4501 precursor RNA folds spatially, forming GR4501 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4501 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4501 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4501 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM123635 precursor RNA and GAM276879 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM123635 RNA and GAM276879 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM123635 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM123635 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM123635 target RNA into GAM123635 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM276879 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM276879 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM276879 target RNA into GAM276879 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4501 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4501 gene: GAM123635 target protein and GAM276879 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM123635 and GAM276879

GR4502 BF529703 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4502(GR4502) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4502 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4502 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4502 gene encodes GR4502 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4502 precursor RNA folds spatially, forming GR4502 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4502 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4502 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4502 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM109415 precursor RNA and GAM335648 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM109415 RNA and GAM335648 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM109415 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM109415 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM109415 target RNA into GAM109415 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM335648 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM335648 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM335648 target RNA into GAM335648 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4502 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4502 gene: GAM109415 target protein and GAM335648 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM109415 and GAM335648

GR4503 BM721545 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4503(GR4503) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4503 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4503 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4503 gene encodes GR4503 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4503 precursor RNA folds spatially, forming GR4503 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4503 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4503 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4503 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM405 precursor RNA and GAM3559 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM405 RNA and GAM3559 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM405 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM405 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM405 target RNA into GAM405 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM3559 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3559 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3559 target RNA into GAM3559 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4503 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4503 gene: GAM405 target protein and GAM3559 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM405 and GAM3559

GR4504 AA890447 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4504(GR4504) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4504 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4504 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4504 gene encodes GR4504 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4504 precursor RNA folds spatially, forming GR4504 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4504 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4504 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4504 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4825 precursor RNA and GAM60737 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4825 RNA and GAM60737 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4825 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4825 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4825 target RNA into GAM4825 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM60737 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM60737 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM60737 target RNA into GAM60737 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4504 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4504 gene: GAM4825 target protein and GAM60737 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4825 and GAM60737

GR4505 BE908152 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4505(GR4505) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4505 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4505 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4505 gene encodes GR4505 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4505 precursor RNA folds spatially, forming GR4505 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4505 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4505 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4505 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM120053 precursor RNA, GAM225208 precursor RNA and GAM238740 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM120053 RNA, GAM225208 RNA and GAM238740 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM120053 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM120053 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM120053 target RNA into GAM120053 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM225208 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM225208 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM225208 target RNA into GAM225208 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM238740 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM238740 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM238740

target RNA into GAM238740 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4505 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4505 gene: GAM120053 target protein, GAM225208 target protein and GAM238740 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM120053, GAM225208 and GAM238740

GR4506 BF990682 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4506(GR4506) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4506 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4506 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4506 gene encodes GR4506 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4506 precursor RNA folds spatially, forming GR4506 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4506 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4506 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4506 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2824 precursor RNA and GAM79012 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2824 RNA and GAM79012 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2824 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2824 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2824 target RNA into GAM2824 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM79012 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM79012 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM79012 target RNA into GAM79012 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4506 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4506 gene: GAM2824 target protein and GAM79012 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2824 and GAM79012

GR4507 H08010 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4507(GR4507) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4507 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4507 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4507 gene encodes GR4507 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4507 precursor RNA folds spatially, forming GR4507 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4507 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4507 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4507 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM56477 precursor RNA and GAM94473 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM56477 RNA and GAM94473 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM56477 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM56477 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM56477 target RNA into GAM56477 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM94473 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM94473 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM94473 target RNA into GAM94473 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4507 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4507 gene: GAM56477 target protein and GAM94473 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM56477 and GAM94473

GR4508 BI038756 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4508(GR4508) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4508 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4508 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4508 gene encodes GR4508 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4508 precursor RNA folds spatially, forming GR4508 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4508 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4508 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4508 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7088 precursor RNA and GAM9230 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7088 RNA and GAM9230 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7088 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7088 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7088 target RNA into GAM7088 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM9230 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM9230 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM9230 target RNA into GAM9230 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4508 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4508 gene: GAM7088 target protein and GAM9230 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference,

with references to GAM7088 and GAM9230

GR4509 BM009944 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4509 (GR4509) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4509 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4509 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4509 gene encodes GR4509 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4509 precursor RNA folds spatially, forming GR4509 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4509 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4509 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4509 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7114 precursor RNA and GAM158071 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7114 RNA and GAM158071 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7114 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7114 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7114 target RNA into GAM7114 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM158071 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM158071 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM158071 target RNA into GAM158071 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4509 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4509 gene: GAM7114 target protein and GAM158071 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7114 and GAM158071

GR4510 BG256154 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4510(GR4510) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4510 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4510 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4510 gene encodes GR4510 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4510 precursor RNA folds spatially, forming GR4510 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4510 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4510 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4510 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM8252 precursor RNA, GAM11993 precursor RNA and GAM181054 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8252 RNA, GAM11993 RNA and GAM181054 RNA, herein

schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8252 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8252 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8252 target RNA into GAM8252 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM11993 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM11993 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM11993 target RNA into GAM11993 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM181054 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM181054 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM181054 target RNA into GAM181054 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4510 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4510 gene: GAM8252 target protein, GAM11993 target protein and GAM181054 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8252, GAM11993 and GAM181054

GR4511 AI673467 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4511(GR4511) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4511 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4511 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4511 gene encodes GR4511 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4511 precursor RNA folds spatially, forming GR4511 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4511 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4511 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4511 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6924 precursor RNA and GAM107625 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6924 RNA and GAM107625 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6924 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6924 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6924 target RNA into GAM6924 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM107625 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM107625 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM107625 target RNA into GAM107625 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4511 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4511 gene: GAM6924 target protein and GAM107625 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6924 and GAM107625

GR4512 BE537746 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4512(GR4512) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4512 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4512 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4512 gene encodes GR4512 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4512 precursor RNA folds spatially, forming GR4512 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4512 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4512 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4512 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM5863 precursor RNA, GAM229202 precursor RNA and GAM307324 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5863 RNA, GAM229202 RNA and GAM307324 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5863 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5863 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5863 target RNA into GAM5863 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM229202 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM229202 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM229202 target RNA into GAM229202 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM307324 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM307324 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM307324 target RNA into GAM307324 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4512 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4512 gene: GAM5863 target protein, GAM229202 target protein and GAM307324 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5863, GAM229202 and GAM307324

GR4513 AA233954 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4513(GR4513) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4513 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4513 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4513 gene encodes GR4513 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4513 precursor RNA folds spatially, forming GR4513 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4513 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4513 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4513 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2

separate GAM precursor RNAs, GAM93139 precursor RNA and GAM335251 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM93139 RNA and GAM335251 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM93139 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM93139 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM93139 target RNA into GAM93139 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM335251 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM335251 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM335251 target RNA into GAM335251 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4513 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4513 gene: GAM93139 target protein and GAM335251 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM93139 and GAM335251

GR4514 BF794785 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4514(GR4514) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4514 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4514 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4514 gene encodes GR4514 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR4514 precursor RNA folds spatially, forming GR4514 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4514 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4514 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4514 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3506 precursor RNA and GAM6812 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3506 RNA and GAM6812 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3506 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3506 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3506 target RNA into GAM3506 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6812 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6812 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6812 target RNA into GAM6812 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4514 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4514 gene: GAM3506 target protein and GAM6812 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3506 and GAM6812

GR4515 BG740672 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4515(GR4515) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4515 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4515 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4515 gene encodes GR4515 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4515 precursor RNA folds spatially, forming GR4515 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4515 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4515 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4515 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2668 precursor RNA, GAM13178 precursor RNA and GAM59973 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2668 RNA, GAM13178 RNA and GAM59973 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2668 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2668 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2668 target RNA into GAM2668 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM13178 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM13178 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM13178 target RNA into GAM13178 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM59973 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM59973 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM59973 target RNA into GAM59973 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4515 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4515 gene: GAM2668 target protein, GAM13178 target protein and GAM59973 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2668, GAM13178 and GAM59973

GR4516 AI765412 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4516(GR4516) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4516 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4516 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4516 gene encodes GR4516 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4516 precursor RNA folds spatially, forming GR4516 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4516 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4516 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4516 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM140863 precursor RNA and GAM239157 precursor

RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM140863 RNA and GAM239157 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM140863 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM140863 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM140863 target RNA into GAM140863 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM239157 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM239157 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM239157 target RNA into GAM239157 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4516 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4516 gene: GAM140863 target protein and GAM239157 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM140863 and GAM239157

GR4517 R53255 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4517(GR4517) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4517 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4517 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4517 gene encodes GR4517 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4517 precursor RNA folds spatially, forming GR4517 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4517 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4517 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4517 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM178035 precursor RNA and GAM231768 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM178035 RNA and GAM231768 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM178035 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM178035 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM178035 target RNA into GAM178035 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM231768 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM231768 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM231768 target RNA into GAM231768 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4517 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4517 gene: GAM178035 target protein and GAM231768 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM178035 and GAM231768

bioinformatically detected regulatory gene, referred to here as Genomic Record 4518(GR4518) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4518 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4518 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4518 gene encodes GR4518 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4518 precursor RNA folds spatially, forming GR4518 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4518 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4518 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4518 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6173 precursor RNA and GAM269118 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6173 RNA and GAM269118 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6173 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6173 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6173 target RNA into GAM6173 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM269118 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM269118 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM269118

target RNA into GAM269118 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4518 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4518 gene: GAM6173 target protein and GAM269118 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6173 and GAM269118

GR4519 AI203546 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4519(GR4519) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4519 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4519 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4519 gene encodes GR4519 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4519 precursor RNA folds spatially, forming GR4519 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4519 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4519 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4519 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6622 precursor RNA and GAM7868 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6622 RNA and GAM7868 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6622 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6622 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6622 target RNA into GAM6622 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7868 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7868 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7868 target RNA into GAM7868 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4519 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4519 gene: GAM6622 target protein and GAM7868 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6622 and GAM7868

GR4520 BF341852 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4520(GR4520) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4520 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4520 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4520 gene encodes GR4520 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4520 precursor RNA folds spatially, forming GR4520 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4520 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4520 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4520 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2806 precursor RNA, GAM6424 precursor RNA and GAM205075 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2806 RNA, GAM6424 RNA and GAM205075 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2806 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2806 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2806 target RNA into GAM2806 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6424 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6424 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6424 target RNA into GAM6424 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM205075 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM205075 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM205075 target RNA into GAM205075 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4520 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4520 gene: GAM2806 target protein, GAM6424 target protein and GAM205075 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2806, GAM6424 and GAM205075

4521(GR4521) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4521 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4521 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4521 gene encodes GR4521 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4521 precursor RNA folds spatially, forming GR4521 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4521 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4521 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4521 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM230 precursor RNA and GAM119541 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM230 RNA and GAM119541 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM230 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM230 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM230 target RNA into GAM230 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM119541 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM119541 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM119541 target RNA into GAM119541 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4521 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4521 gene: GAM230 target protein and GAM119541 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM230 and GAM119541

GR4522 BG324383 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4522(GR4522) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4522 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4522 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4522 gene encodes GR4522 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4522 precursor RNA folds spatially, forming GR4522 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4522 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4522 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4522 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM7033 precursor RNA, GAM46975 precursor RNA and GAM63355 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7033 RNA, GAM46975 RNA and GAM63355 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7033 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7033 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7033 target RNA into GAM7033 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM46975 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM46975 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM46975 target RNA into GAM46975 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM63355 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM63355 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM63355 target RNA into GAM63355 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4522 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4522 gene: GAM7033 target protein, GAM46975 target protein and GAM63355 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7033, GAM46975 and GAM63355

GR4523 AA486506 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4523(GR4523) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4523 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4523 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4523 gene encodes GR4523 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4523 precursor RNA folds spatially, forming GR4523 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4523 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4523 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4523 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM14773 precursor RNA, GAM26374 precursor RNA and GAM294641 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM14773 RNA, GAM26374 RNA and GAM294641 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM14773 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM14773 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM14773 target RNA into GAM14773 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM26374 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM26374 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM26374 target RNA into GAM26374 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM294641 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM294641 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM294641 target RNA into GAM294641 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4523 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR4523 gene: GAM14773 target protein, GAM26374 target protein and GAM294641 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM14773, GAM26374 and GAM294641

GR4524 BM977278 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4524(GR4524) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4524 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4524 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4524 gene encodes GR4524 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4524 precursor RNA folds spatially, forming GR4524 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4524 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4524 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4524 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2716 precursor RNA, GAM6258 precursor RNA and GAM27070 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2716 RNA, GAM6258 RNA and GAM27070 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2716 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2716 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig. 8, thereby inhibiting translation of GAM2716 target RNA into GAM2716 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6258 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6258 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6258 target RNA into GAM6258 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM27070 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM27070 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM27070 target RNA into GAM27070 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4524 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4524 gene: GAM2716 target protein, GAM6258 target protein and GAM27070 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2716, GAM6258 and GAM27070

GR4525 BG490432 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4525(GR4525) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4525 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4525 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4525 gene encodes GR4525 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4525 precursor RNA folds spatially, forming GR4525 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4525 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4525 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4525 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4802 precursor RNA, GAM64214 precursor RNA and GAM249096 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4802 RNA, GAM64214 RNA and GAM249096 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4802 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4802 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4802 target RNA into GAM4802 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM64214 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM64214 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM64214 target RNA into GAM64214 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM249096 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM249096 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM249096 target RNA into GAM249096 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4525 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4525 gene: GAM4802 target protein, GAM64214 target protein and GAM249096 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6,

hereby incorporated by reference, with references to GAM4802, GAM64214 and GAM249096

GR4526 BE407546 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4526(GR4526) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4526 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4526 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4526 gene encodes GR4526 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4526 precursor RNA folds spatially, forming GR4526 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4526 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4526 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4526 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM100275 precursor RNA, GAM113661 precursor RNA and GAM225587 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM100275 RNA, GAM113661 RNA and GAM225587 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM100275 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM100275 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM100275 target RNA into GAM100275 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM113661 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM113661 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM113661 target RNA into GAM113661 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM225587 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM225587 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM225587 target RNA into GAM225587 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4526 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4526 gene: GAM100275 target protein, GAM113661 target protein and GAM225587 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM100275, GAM113661 and GAM225587

GR4527 BM014822 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4527(GR4527) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4527 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4527 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4527 gene encodes GR4527 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4527 precursor RNA folds spatially, forming GR4527 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4527 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4527 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4527 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM70210 precursor RNA and GAM298999 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM70210 RNA and GAM298999 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM70210 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM70210 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM70210 target RNA into GAM70210 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM298999 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM298999 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM298999 target RNA into GAM298999 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4527 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4527 gene: GAM70210 target protein and GAM298999 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM70210 and GAM298999

GR4528 BE728468 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4528(GR4528) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4528 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4528 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4528 gene encodes GR4528 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4528 precursor RNA folds spatially, forming GR4528 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4528 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4528 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4528 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM176293 precursor RNA and GAM291360 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM176293 RNA and GAM291360 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM176293 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM176293 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM176293 target RNA into GAM176293 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM291360 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM291360 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM291360 target RNA into GAM291360 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4528 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4528 gene: GAM176293 target protein and GAM291360 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference,

with references to GAM176293 and GAM291360

GR4529 BG681094 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4529 (GR4529) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4529 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4529 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4529 gene encodes GR4529 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4529 precursor RNA folds spatially, forming GR4529 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4529 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4529 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4529 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8057 precursor RNA and GAM23277 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8057 RNA and GAM23277 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8057 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8057 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8057 target RNA into GAM8057 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM23277 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM23277 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM23277 target RNA into GAM23277 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4529 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4529 gene: GAM8057 target protein and GAM23277 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8057 and GAM23277

GR4530 BM797187 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4530(GR4530) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4530 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4530 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4530 gene encodes GR4530 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4530 precursor RNA folds spatially, forming GR4530 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4530 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4530 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4530 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6131 precursor RNA and GAM289833 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6131 RNA and GAM289833 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding

to GAM RNA of Fig. 8.

GAM6131 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6131 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6131 target RNA into GAM6131 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM289833 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM289833 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM289833 target RNA into GAM289833 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4530 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4530 gene: GAM6131 target protein and GAM289833 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6131 and GAM289833

GR4531 AA255935 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4531 (GR4531) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4531 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4531 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4531 gene encodes GR4531 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4531 precursor RNA folds spatially, forming GR4531 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4531 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4531 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR4531 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM986 precursor RNA and GAM6043 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM986 RNA and GAM6043 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM986 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM986 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM986 target RNA into GAM986 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6043 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6043 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6043 target RNA into GAM6043 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4531 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4531 gene: GAM986 target protein and GAM6043 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM986 and GAM6043

GR4532 BE467284 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4532(GR4532) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4532 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4532

gene was detected is described hereinabove with reference to Figs. 8-18.

GR4532 gene encodes GR4532 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4532 precursor RNA folds spatially, forming GR4532 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4532 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4532 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4532 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM13962 precursor RNA and GAM119551 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM13962 RNA and GAM119551 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM13962 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM13962 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM13962 target RNA into GAM13962 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM119551 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM119551 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM119551 target RNA into GAM119551 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4532 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4532 gene: GAM13962 target protein and GAM119551 target protein, herein schematically represented by GAM1

TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM13962 and GAM119551

GR4533 H50099 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4533(GR4533) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4533 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4533 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4533 gene encodes GR4533 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4533 precursor RNA folds spatially, forming GR4533 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4533 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4533 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4533 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM94627 precursor RNA and GAM209986 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM94627 RNA and GAM209986 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM94627 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM94627 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM94627 target RNA into GAM94627 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM209986 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM209986 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM209986 target RNA into GAM209986 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4533 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4533 gene: GAM94627 target protein and GAM209986 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM94627 and GAM209986

GR4534 AA505031 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4534(GR4534) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4534 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4534 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4534 gene encodes GR4534 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4534 precursor RNA folds spatially, forming GR4534 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4534 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4534 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4534 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5711 precursor RNA and GAM245263 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM5711 RNA and GAM245263 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5711 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5711 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5711 target RNA into GAM5711 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM245263 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM245263 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM245263 target RNA into GAM245263 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4534 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4534 gene: GAM5711 target protein and GAM245263 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5711 and GAM245263

GR4535 BF663067 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4535(GR4535) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4535 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4535 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4535 gene encodes GR4535 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4535 precursor RNA folds spatially, forming GR4535 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4535 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4535 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4535 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM5330 precursor RNA, GAM43697 precursor RNA and GAM264255 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5330 RNA, GAM43697 RNA and GAM264255 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5330 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5330 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5330 target RNA into GAM5330 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM43697 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM43697 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM43697 target RNA into GAM43697 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM264255 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM264255 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM264255 target RNA into GAM264255 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4535 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4535 gene: GAM5330 target protein, GAM43697 target protein and GAM264255 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6,

hereby incorporated by reference, with references to GAM5330, GAM43697 and GAM264255

GR4536 BM987500 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4536(GR4536) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4536 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4536 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4536 gene encodes GR4536 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4536 precursor RNA folds spatially, forming GR4536 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4536 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4536 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4536 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM188701 precursor RNA and GAM305880 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM188701 RNA and GAM305880 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM188701 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM188701 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM188701 target RNA into GAM188701 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM305880 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM305880 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM305880 target RNA into GAM305880 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4536 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4536 gene: GAM188701 target protein and GAM305880 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM188701 and GAM305880

GR4537 AI989869 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4537(GR4537) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4537 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4537 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4537 gene encodes GR4537 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4537 precursor RNA folds spatially, forming GR4537 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4537 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4537 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4537 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2527 precursor RNA, GAM4670 precursor RNA and GAM239691 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM2527 RNA, GAM4670 RNA and GAM239691 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2527 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2527 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2527 target RNA into GAM2527 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM4670 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4670 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4670 target RNA into GAM4670 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM239691 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM239691 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM239691 target RNA into GAM239691 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4537 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4537 gene: GAM2527 target protein, GAM4670 target protein and GAM239691 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2527, GAM4670 and GAM239691

GR4538 BE250091 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4538(GR4538) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4538 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4538 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4538 gene encodes GR4538 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4538 precursor RNA folds spatially, forming GR4538 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4538 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4538 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4538 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM11724 precursor RNA and GAM212043 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM11724 RNA and GAM212043 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM11724 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM11724 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM11724 target RNA into GAM11724 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM212043 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM212043 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM212043 target RNA into GAM212043 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4538 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4538 gene: GAM11724 target protein and GAM212043 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference,

with references to GAM11724 and GAM212043

GR4539 AW196262 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4539 (GR4539) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4539 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4539 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4539 gene encodes GR4539 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4539 precursor RNA folds spatially, forming GR4539 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4539 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4539 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4539 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM88292 precursor RNA and GAM141892 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM88292 RNA and GAM141892 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM88292 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM88292 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM88292 target RNA into GAM88292 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM141892 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM141892 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM141892 target RNA into GAM141892 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4539 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4539 gene: GAM88292 target protein and GAM141892 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM88292 and GAM141892

GR4540 AI174196 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4540(GR4540) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4540 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4540 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4540 gene encodes GR4540 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4540 precursor RNA folds spatially, forming GR4540 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4540 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4540 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4540 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3248 precursor RNA and GAM7429 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3248 RNA and GAM7429 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding

to GAM RNA of Fig. 8.

GAM3248 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3248 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3248 target RNA into GAM3248 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7429 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7429 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7429 target RNA into GAM7429 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4540 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4540 gene: GAM3248 target protein and GAM7429 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3248 and GAM7429

GR4541 BE535967 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4541 (GR4541) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4541 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4541 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4541 gene encodes GR4541 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4541 precursor RNA folds spatially, forming GR4541 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4541 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4541 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR4541 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM14600 precursor RNA, GAM40845 precursor RNA and GAM113301 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM14600 RNA, GAM40845 RNA and GAM113301 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM14600 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM14600 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM14600 target RNA into GAM14600 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM40845 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM40845 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM40845 target RNA into GAM40845 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM113301 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM113301 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM113301 target RNA into GAM113301 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4541 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4541 gene: GAM14600 target protein, GAM40845 target protein and GAM113301 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM14600, GAM40845 and GAM113301

GR4542 F32197 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4542(GR4542) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4542 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4542 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4542 gene encodes GR4542 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4542 precursor RNA folds spatially, forming GR4542 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4542 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4542 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4542 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4412 precursor RNA, GAM7387 precursor RNA and GAM273533 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4412 RNA, GAM7387 RNA and GAM273533 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4412 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4412 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4412 target RNA into GAM4412 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7387 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7387 target RNA, herein schematically represented by

GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7387 target RNA into GAM7387 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM273533 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM273533 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM273533 target RNA into GAM273533 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4542 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4542 gene: GAM4412 target protein, GAM7387 target protein and GAM273533 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4412, GAM7387 and GAM273533

GR4543 BI458410 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4543(GR4543) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4543 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4543 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4543 gene encodes GR4543 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4543 precursor RNA folds spatially, forming GR4543 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4543 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4543 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4543 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4

separate GAM precursor RNAs, GAM23433 precursor RNA, GAM156745 precursor RNA, GAM210182 precursor RNA and GAM303585 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM23433 RNA, GAM156745 RNA, GAM210182 RNA and GAM303585 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM23433 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM23433 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM23433 target RNA into GAM23433 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM156745 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM156745 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM156745 target RNA into GAM156745 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM210182 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM210182 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM210182 target RNA into GAM210182 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM303585 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM303585 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM303585 target RNA into GAM303585 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4543 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4543 gene: GAM23433 target protein, GAM156745 target protein, GAM210182 target protein and GAM303585

target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM23433, GAM156745, GAM210182 and GAM303585

GR4544 R64080 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4544(GR4544) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4544 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4544 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4544 gene encodes GR4544 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4544 precursor RNA folds spatially, forming GR4544 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4544 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4544 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4544 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM13959 precursor RNA and GAM46438 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM13959 RNA and GAM46438 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM13959 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM13959 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM13959 target RNA into GAM13959 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM46438 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM46438 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM46438 target RNA into GAM46438 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4544 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4544 gene: GAM13959 target protein and GAM46438 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM13959 and GAM46438

GR4545 BG257882 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4545(GR4545) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4545 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4545 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4545 gene encodes GR4545 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4545 precursor RNA folds spatially, forming GR4545 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4545 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4545 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4545 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM52539 precursor RNA and GAM102831 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM52539 RNA and GAM102831 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM52539 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM52539 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM52539 target RNA into GAM52539 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM102831 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM102831 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM102831 target RNA into GAM102831 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4545 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4545 gene: GAM52539 target protein and GAM102831 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM52539 and GAM102831

GR4546 H65024 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4546(GR4546) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4546 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4546 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4546 gene encodes GR4546 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4546 precursor RNA folds spatially, forming GR4546 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4546 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR4546 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4546 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM59589 precursor RNA and GAM120640 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM59589 RNA and GAM120640 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM59589 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM59589 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM59589 target RNA into GAM59589 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM120640 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM120640 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM120640 target RNA into GAM120640 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4546 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4546 gene: GAM59589 target protein and GAM120640 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM59589 and GAM120640

GR4547 W02939 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4547(GR4547) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4547 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4547 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4547 gene encodes GR4547 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4547 precursor RNA folds spatially, forming GR4547 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4547 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4547 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4547 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3802 precursor RNA, GAM100955 precursor RNA and GAM283692 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3802 RNA, GAM100955 RNA and GAM283692 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3802 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3802 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3802 target RNA into GAM3802 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM100955 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM100955 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM100955 target RNA into GAM100955 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM283692 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM283692 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM283692 target RNA into GAM283692 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4547 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4547 gene: GAM3802 target protein, GAM100955 target protein and GAM283692 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3802, GAM100955 and GAM283692

GR4548 AA731080 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4548(GR4548) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4548 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4548 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4548 gene encodes GR4548 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4548 precursor RNA folds spatially, forming GR4548 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4548 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4548 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4548 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM28479 precursor RNA and GAM125123 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM28479 RNA and GAM125123 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM28479 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM28479 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM28479 target RNA into GAM28479 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM125123 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM125123 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM125123 target RNA into GAM125123 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4548 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4548 gene: GAM28479 target protein and GAM125123 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM28479 and GAM125123

GR4549 BE972037 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4549(GR4549) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4549 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4549 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4549 gene encodes GR4549 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4549 precursor RNA folds spatially, forming GR4549 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4549 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4549 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4549 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM281391 precursor RNA and GAM335980 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM281391 RNA and GAM335980 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM281391 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM281391 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM281391 target RNA into GAM281391 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM335980 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM335980 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM335980 target RNA into GAM335980 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4549 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4549 gene: GAM281391 target protein and GAM335980 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM281391 and GAM335980

GR4550 BG697859 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4550(GR4550) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4550 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4550 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4550 gene encodes GR4550 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4550 precursor RNA folds spatially, forming GR4550 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4550 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4550 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4550 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM14155 precursor RNA, GAM128445 precursor RNA and GAM260678 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM14155 RNA, GAM128445 RNA and GAM260678 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM14155 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM14155 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM14155 target RNA into GAM14155 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM128445 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM128445 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM128445 target RNA into GAM128445 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM260678 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM260678 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM260678 target RNA into GAM260678 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4550 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4550 gene: GAM14155 target protein, GAM128445 target protein and GAM260678 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM14155, GAM128445 and GAM260678

GR4551 AI253797 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4551 (GR4551) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4551 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4551 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4551 gene encodes GR4551 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4551 precursor RNA folds spatially, forming GR4551 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4551 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4551 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4551 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3005 precursor RNA and GAM6914 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3005 RNA and GAM6914 RNA, herein schematically

represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3005 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3005 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3005 target RNA into GAM3005 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6914 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6914 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6914 target RNA into GAM6914 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4551 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4551 gene: GAM3005 target protein and GAM6914 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3005 and GAM6914

GR4552 AW953240 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4552(GR4552) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4552 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4552 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4552 gene encodes GR4552 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4552 precursor RNA folds spatially, forming GR4552 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4552 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4552 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4552 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3495 precursor RNA and GAM259676 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3495 RNA and GAM259676 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3495 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3495 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3495 target RNA into GAM3495 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM259676 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM259676 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM259676 target RNA into GAM259676 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4552 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4552 gene: GAM3495 target protein and GAM259676 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3495 and GAM259676

GR4553 AA911685 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4553(GR4553) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4553 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR4553 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4553 gene encodes GR4553 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4553 precursor RNA folds spatially, forming GR4553 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4553 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4553 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4553 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM211456 precursor RNA and GAM235658 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM211456 RNA and GAM235658 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM211456 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM211456 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM211456 target RNA into GAM211456 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM235658 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM235658 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM235658 target RNA into GAM235658 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4553 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4553 gene: GAM211456 target

protein and GAM235658 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM211456 and GAM235658

GR4554 AA985357 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4554(GR4554) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4554 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4554 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4554 gene encodes GR4554 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4554 precursor RNA folds spatially, forming GR4554 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4554 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4554 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4554 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8565 precursor RNA and GAM331731 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8565 RNA and GAM331731 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8565 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8565 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8565 target RNA into GAM8565 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM331731 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM331731 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM331731 target RNA into GAM331731 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4554 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4554 gene: GAM8565 target protein and GAM331731 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8565 and GAM331731

GR4555 BG745470 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4555(GR4555) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4555 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4555 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4555 gene encodes GR4555 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4555 precursor RNA folds spatially, forming GR4555 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4555 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4555 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4555 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM149345 precursor RNA, GAM217623 precursor RNA and GAM316588 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM149345 RNA, GAM217623 RNA and GAM316588 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM149345 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM149345 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM149345 target RNA into GAM149345 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM217623 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM217623 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM217623 target RNA into GAM217623 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM316588 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM316588 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM316588 target RNA into GAM316588 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4555 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4555 gene: GAM149345 target protein, GAM217623 target protein and GAM316588 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM149345, GAM217623 and GAM316588

GR4556 BG619137 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4556(GR4556) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4556 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4556

gene was detected is described hereinabove with reference to Figs. 8-18.

GR4556 gene encodes GR4556 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4556 precursor RNA folds spatially, forming GR4556 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4556 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4556 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4556 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM45232 precursor RNA and GAM141813 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM45232 RNA and GAM141813 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM45232 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM45232 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM45232 target RNA into GAM45232 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM141813 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM141813 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM141813 target RNA into GAM141813 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4556 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4556 gene: GAM45232 target protein and GAM141813 target protein, herein schematically represented by GAM1

TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM45232 and GAM141813

GR4557 AL547866 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4557(GR4557) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4557 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4557 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4557 gene encodes GR4557 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4557 precursor RNA folds spatially, forming GR4557 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4557 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4557 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4557 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2985 precursor RNA and GAM19411 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2985 RNA and GAM19411 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2985 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2985 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2985 target RNA into GAM2985 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM19411 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM19411 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM19411 target RNA into GAM19411 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4557 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4557 gene: GAM2985 target protein and GAM19411 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2985 and GAM19411

GR4558 BI256843 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4558(GR4558) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4558 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4558 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4558 gene encodes GR4558 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4558 precursor RNA folds spatially, forming GR4558 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4558 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4558 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4558 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM41083 precursor RNA, GAM199655 precursor RNA and GAM255663 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM41083 RNA, GAM199655 RNA and GAM255663 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM41083 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM41083 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM41083 target RNA into GAM41083 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM199655 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM199655 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM199655 target RNA into GAM199655 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM255663 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM255663 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM255663 target RNA into GAM255663 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4558 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4558 gene: GAM41083 target protein, GAM199655 target protein and GAM255663 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM41083, GAM199655 and GAM255663

GR4559 AI968210 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4559(GR4559) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4559 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4559 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4559 gene encodes GR4559 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4559 precursor RNA folds spatially, forming GR4559 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4559 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4559 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4559 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM3430 precursor RNA, GAM176523 precursor RNA, GAM252225 precursor RNA and GAM331753 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3430 RNA, GAM176523 RNA, GAM252225 RNA and GAM331753 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3430 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3430 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3430 target RNA into GAM3430 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM176523 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM176523 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM176523 target RNA into GAM176523 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM252225 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM252225 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM252225

target RNA into GAM252225 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM331753 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM331753 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM331753 target RNA into GAM331753 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4559 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4559 gene: GAM3430 target protein, GAM176523 target protein, GAM252225 target protein and GAM331753 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3430, GAM176523, GAM252225 and GAM331753

GR4560 AI590391 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4560(GR4560) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4560 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4560 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4560 gene encodes GR4560 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4560 precursor RNA folds spatially, forming GR4560 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4560 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4560 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4560 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM223038 precursor RNA and GAM230829 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin

shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM223038 RNA and GAM230829 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM223038 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM223038 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM223038 target RNA into GAM223038 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM230829 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM230829 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM230829 target RNA into GAM230829 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4560 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4560 gene: GAM223038 target protein and GAM230829 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM223038 and GAM230829

GR4561 BG122357 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4561(GR4561) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4561 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4561 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4561 gene encodes GR4561 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4561 precursor RNA folds spatially, forming GR4561 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4561 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4561 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4561 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM111457 precursor RNA and GAM133061 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM111457 RNA and GAM133061 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM111457 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM111457 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM111457 target RNA into GAM111457 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM133061 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM133061 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM133061 target RNA into GAM133061 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4561 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4561 gene: GAM111457 target protein and GAM133061 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM111457 and GAM133061

GR4562 BM010376 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4562(GR4562) gene, which encodes an `operon-like` cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4562 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4562 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4562 gene encodes GR4562 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4562 precursor RNA folds spatially, forming GR4562 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4562 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4562 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4562 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM118901 precursor RNA and GAM145379 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM118901 RNA and GAM145379 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM118901 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM118901 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM118901 target RNA into GAM118901 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM145379 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM145379 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM145379 target RNA into GAM145379 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4562 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4562 gene: GAM118901 target protein and GAM145379 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM118901 and GAM145379

GR4563 AI479433 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4563(GR4563) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4563 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4563 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4563 gene encodes GR4563 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4563 precursor RNA folds spatially, forming GR4563 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4563 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4563 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4563 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM61095 precursor RNA, GAM113737 precursor RNA and GAM175577 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM61095 RNA, GAM113737 RNA and GAM175577 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM61095 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM61095 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM61095 target RNA into GAM61095 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM113737 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM113737 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM113737 target RNA into GAM113737 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM175577 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM175577 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM175577 target RNA into GAM175577 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4563 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4563 gene: GAM61095 target protein, GAM113737 target protein and GAM175577 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM61095, GAM113737 and GAM175577

GR4564 BE762649 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4564(GR4564) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4564 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4564 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4564 gene encodes GR4564 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4564 precursor RNA folds spatially, forming GR4564 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated

that GR4564 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4564 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4564 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM17507 precursor RNA, GAM206158 precursor RNA and GAM230961 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM17507 RNA, GAM206158 RNA and GAM230961 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM17507 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM17507 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM17507 target RNA into GAM17507 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM206158 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM206158 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM206158 target RNA into GAM206158 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM230961 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM230961 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM230961 target RNA into GAM230961 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4564 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4564 gene: GAM17507 target

protein, GAM206158 target protein and GAM230961 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM17507, GAM206158 and GAM230961

GR4565 BF968928 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4565(GR4565) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4565 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4565 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4565 gene encodes GR4565 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4565 precursor RNA folds spatially, forming GR4565 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4565 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4565 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4565 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM203602 precursor RNA and GAM219489 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM203602 RNA and GAM219489 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM203602 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM203602 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM203602 target RNA into GAM203602 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM219489 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM219489 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM219489 target RNA into GAM219489 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4565 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4565 gene: GAM203602 target protein and GAM219489 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM203602 and GAM219489

GR4566 BM044240 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4566(GR4566) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4566 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4566 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4566 gene encodes GR4566 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4566 precursor RNA folds spatially, forming GR4566 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4566 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4566 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4566 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4114 precursor RNA, GAM62345 precursor RNA and GAM222484 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4114 RNA, GAM62345 RNA and GAM222484 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4114 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4114 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4114 target RNA into GAM4114 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM62345 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM62345 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM62345 target RNA into GAM62345 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM222484 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM222484 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM222484 target RNA into GAM222484 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4566 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4566 gene: GAM4114 target protein, GAM62345 target protein and GAM222484 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4114, GAM62345 and GAM222484

GR4567 BF380818 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4567(GR4567) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4567 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR4567 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4567 gene encodes GR4567 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4567 precursor RNA folds spatially, forming GR4567 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4567 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4567 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4567 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM7571 precursor RNA, GAM12847 precursor RNA and GAM33854 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7571 RNA, GAM12847 RNA and GAM33854 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7571 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7571 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7571 target RNA into GAM7571 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM12847 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM12847 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM12847 target RNA into GAM12847 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM33854 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM33854 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM33854 target RNA into GAM33854 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4567 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4567 gene: GAM7571 target protein, GAM12847 target protein and GAM33854 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7571, GAM12847 and GAM33854

GR4568 BG911727 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4568(GR4568) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4568 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4568 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4568 gene encodes GR4568 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4568 precursor RNA folds spatially, forming GR4568 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4568 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4568 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4568 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM203435 precursor RNA and GAM296263 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM203435 RNA and GAM296263 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding

to GAM RNA of Fig. 8.

GAM203435 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM203435 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM203435 target RNA into GAM203435 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM296263 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM296263 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM296263 target RNA into GAM296263 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4568 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4568 gene: GAM203435 target protein and GAM296263 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM203435 and GAM296263

GR4569 R23394 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4569(GR4569) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4569 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4569 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4569 gene encodes GR4569 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4569 precursor RNA folds spatially, forming GR4569 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4569 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4569 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR4569 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM40534 precursor RNA and GAM185083 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM40534 RNA and GAM185083 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM40534 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM40534 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM40534 target RNA into GAM40534 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM185083 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM185083 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM185083 target RNA into GAM185083 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4569 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4569 gene: GAM40534 target protein and GAM185083 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM40534 and GAM185083

GR4570 BF838304 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4570(GR4570) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4570 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4570

gene was detected is described hereinabove with reference to Figs. 8-18.

GR4570 gene encodes GR4570 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4570 precursor RNA folds spatially, forming GR4570 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4570 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4570 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4570 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2075 precursor RNA, GAM96319 precursor RNA and GAM219130 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2075 RNA, GAM96319 RNA and GAM219130 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2075 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2075 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2075 target RNA into GAM2075 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM96319 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM96319 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM96319 target RNA into GAM96319 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM219130 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM219130 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM219130 target RNA into GAM219130 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4570 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4570 gene: GAM2075 target protein, GAM96319 target protein and GAM219130 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2075, GAM96319 and GAM219130

GR4571 T85163 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4571 (GR4571) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4571 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4571 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4571 gene encodes GR4571 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4571 precursor RNA folds spatially, forming GR4571 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4571 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4571 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4571 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7576 precursor RNA and GAM226172 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7576 RNA and GAM226172 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7576 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7576 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7576 target RNA into GAM7576 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM226172 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM226172 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM226172 target RNA into GAM226172 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4571 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4571 gene: GAM7576 target protein and GAM226172 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7576 and GAM226172

GR4572 BI791942 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4572(GR4572) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4572 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4572 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4572 gene encodes GR4572 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4572 precursor RNA folds spatially, forming GR4572 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4572 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4572 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4572 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM169074 precursor RNA and GAM235861 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM169074 RNA and GAM235861 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM169074 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM169074 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM169074 target RNA into GAM169074 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM235861 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM235861 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM235861 target RNA into GAM235861 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4572 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4572 gene: GAM169074 target protein and GAM235861 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM169074 and GAM235861

GR4573 BF575078 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4573(GR4573) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4573 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4573 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4573 gene encodes GR4573 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4573 precursor RNA folds spatially, forming GR4573 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4573 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4573 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4573 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM6940 precursor RNA, GAM8193 precursor RNA and GAM243591 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6940 RNA, GAM8193 RNA and GAM243591 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6940 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6940 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6940 target RNA into GAM6940 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8193 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8193 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8193 target RNA into GAM8193 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM243591 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM243591 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM243591

target RNA into GAM243591 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4573 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4573 gene: GAM6940 target protein, GAM8193 target protein and GAM243591 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6940, GAM8193 and GAM243591

GR4574 BF677643 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4574(GR4574) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4574 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4574 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4574 gene encodes GR4574 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4574 precursor RNA folds spatially, forming GR4574 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4574 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4574 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4574 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM109894 precursor RNA, GAM170000 precursor RNA and GAM245729 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM109894 RNA, GAM170000 RNA and GAM245729 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM109894 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM109894 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM109894 target RNA into GAM109894 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM170000 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM170000 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM170000 target RNA into GAM170000 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM245729 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM245729 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM245729 target RNA into GAM245729 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4574 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4574 gene: GAM109894 target protein, GAM170000 target protein and GAM245729 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM109894, GAM170000 and GAM245729

GR4575 BG753683 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4575(GR4575) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4575 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4575 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4575 gene encodes GR4575 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4575 precursor RNA folds spatially, forming GR4575 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4575 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4575 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4575 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM25360 precursor RNA, GAM79778 precursor RNA and GAM217736 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM25360 RNA, GAM79778 RNA and GAM217736 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM25360 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM25360 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM25360 target RNA into GAM25360 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM79778 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM79778 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM79778 target RNA into GAM79778 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM217736 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM217736 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM217736 target RNA into GAM217736 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly

utilities, of GR4575 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4575 gene: GAM25360 target protein, GAM79778 target protein and GAM217736 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM25360, GAM79778 and GAM217736

GR4576 BM758378 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4576(GR4576) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4576 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4576 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4576 gene encodes GR4576 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4576 precursor RNA folds spatially, forming GR4576 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4576 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4576 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4576 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM82714 precursor RNA, GAM146474 precursor RNA and GAM274522 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM82714 RNA, GAM146474 RNA and GAM274522 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM82714 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM82714 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM82714 target RNA into GAM82714 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM146474 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM146474 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM146474 target RNA into GAM146474 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM274522 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM274522 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM274522 target RNA into GAM274522 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4576 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4576 gene: GAM82714 target protein, GAM146474 target protein and GAM274522 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM82714, GAM146474 and GAM274522

GR4577 R84921 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4577(GR4577) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4577 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4577 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4577 gene encodes GR4577 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4577 precursor RNA folds spatially, forming GR4577 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4577 folded precursor RNA comprises a plurality of what is known in the

art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4577 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4577 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM6965 precursor RNA, GAM153930 precursor RNA and GAM270183 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6965 RNA, GAM153930 RNA and GAM270183 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6965 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6965 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6965 target RNA into GAM6965 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM153930 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM153930 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM153930 target RNA into GAM153930 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM270183 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM270183 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM270183 target RNA into GAM270183 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4577 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4577 gene: GAM6965 target protein, GAM153930 target protein and GAM270183 target protein, herein

schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6965, GAM153930 and GAM270183

GR4578 BF760402 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4578(GR4578) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4578 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4578 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4578 gene encodes GR4578 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4578 precursor RNA folds spatially, forming GR4578 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4578 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4578 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4578 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM96583 precursor RNA, GAM104614 precursor RNA and GAM309408 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM96583 RNA, GAM104614 RNA and GAM309408 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM96583 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM96583 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM96583 target RNA into GAM96583 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM104614 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM104614 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM104614 target RNA into GAM104614 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM309408 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM309408 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM309408 target RNA into GAM309408 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4578 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4578 gene: GAM96583 target protein, GAM104614 target protein and GAM309408 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM96583, GAM104614 and GAM309408

GR4579 BF935736 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4579(GR4579) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4579 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4579 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4579 gene encodes GR4579 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4579 precursor RNA folds spatially, forming GR4579 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4579 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4579 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR4579 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2666 precursor RNA and GAM10649 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2666 RNA and GAM10649 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2666 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2666 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2666 target RNA into GAM2666 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM10649 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM10649 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM10649 target RNA into GAM10649 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4579 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4579 gene: GAM2666 target protein and GAM10649 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2666 and GAM10649

GR4580 AW104865 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4580 (GR4580) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4580 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4580

gene was detected is described hereinabove with reference to Figs. 8-18.

GR4580 gene encodes GR4580 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4580 precursor RNA folds spatially, forming GR4580 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4580 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4580 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4580 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1314 precursor RNA and GAM175382 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1314 RNA and GAM175382 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1314 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1314 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1314 target RNA into GAM1314 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM175382 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM175382 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM175382 target RNA into GAM175382 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4580 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4580 gene: GAM1314 target protein and GAM175382 target protein, herein schematically represented by GAM1

TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1314 and GAM175382

GR4581 AV758078 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4581 (GR4581) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4581 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4581 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4581 gene encodes GR4581 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4581 precursor RNA folds spatially, forming GR4581 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4581 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4581 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4581 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1957 precursor RNA and GAM99770 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1957 RNA and GAM99770 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1957 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1957 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1957 target RNA into GAM1957 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM99770 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM99770 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM99770 target RNA into GAM99770 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4581 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4581 gene: GAM1957 target protein and GAM99770 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1957 and GAM99770

GR4582 BM925320 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4582(GR4582) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4582 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4582 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4582 gene encodes GR4582 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4582 precursor RNA folds spatially, forming GR4582 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4582 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4582 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4582 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM73874 precursor RNA and GAM273006 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM73874 RNA and GAM273006 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM73874 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM73874 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM73874 target RNA into GAM73874 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM273006 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM273006 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM273006 target RNA into GAM273006 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4582 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4582 gene: GAM73874 target protein and GAM273006 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM73874 and GAM273006

GR4583 AW294807 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4583(GR4583) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4583 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4583 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4583 gene encodes GR4583 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4583 precursor RNA folds spatially, forming GR4583 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4583 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4583 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4583 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM191810 precursor RNA and GAM227964 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM191810 RNA and GAM227964 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM191810 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM191810 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM191810 target RNA into GAM191810 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM227964 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM227964 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM227964 target RNA into GAM227964 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4583 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4583 gene: GAM191810 target protein and GAM227964 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM191810 and GAM227964

GR4584 BG111996 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4584(GR4584) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4584 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4584 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4584 gene encodes GR4584 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4584 precursor RNA folds spatially, forming GR4584 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4584 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4584 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4584 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1129 precursor RNA and GAM7759 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1129 RNA and GAM7759 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1129 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1129 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1129 target RNA into GAM1129 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7759 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7759 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7759 target RNA into GAM7759 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4584 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR4584 gene: GAM1129 target protein and GAM7759 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1129 and GAM7759

GR4585 N28698 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4585(GR4585) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4585 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4585 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4585 gene encodes GR4585 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4585 precursor RNA folds spatially, forming GR4585 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4585 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4585 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4585 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM1729 precursor RNA, GAM2820 precursor RNA, GAM285079 precursor RNA and GAM303061 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1729 RNA, GAM2820 RNA, GAM285079 RNA and GAM303061 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1729 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1729 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1729 target RNA into

GAM1729 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM2820 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2820 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2820 target RNA into GAM2820 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM285079 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM285079 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM285079 target RNA into GAM285079 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM303061 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM303061 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM303061 target RNA into GAM303061 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4585 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4585 gene: GAM1729 target protein, GAM2820 target protein, GAM285079 target protein and GAM303061 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1729, GAM2820, GAM285079 and GAM303061

GR4586 BF998057 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4586(GR4586) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4586 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4586 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4586 gene encodes GR4586 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR4586 precursor RNA folds spatially, forming GR4586 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4586 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4586 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4586 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7508 precursor RNA and GAM159049 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7508 RNA and GAM159049 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7508 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7508 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7508 target RNA into GAM7508 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM159049 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM159049 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM159049 target RNA into GAM159049 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4586 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4586 gene: GAM7508 target protein and GAM159049 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7508 and GAM159049

GR4587 AA576896 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4587(GR4587) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4587 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4587 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4587 gene encodes GR4587 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4587 precursor RNA folds spatially, forming GR4587 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4587 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4587 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4587 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM316083 precursor RNA and GAM320197 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM316083 RNA and GAM320197 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM316083 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM316083 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM316083 target RNA into GAM316083 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM320197 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM320197 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM320197 target RNA into GAM320197 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4587 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4587 gene: GAM316083 target protein and GAM320197 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM316083 and GAM320197

GR4588 BI601729 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4588(GR4588) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4588 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4588 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4588 gene encodes GR4588 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4588 precursor RNA folds spatially, forming GR4588 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4588 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4588 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4588 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM254499 precursor RNA and GAM255394 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM254499 RNA and GAM255394 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM254499 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM254499 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM254499 target RNA into GAM254499 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM255394 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM255394 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM255394 target RNA into GAM255394 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4588 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4588 gene: GAM254499 target protein and GAM255394 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM254499 and GAM255394

GR4589 BI918151 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4589(GR4589) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4589 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4589 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4589 gene encodes GR4589 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4589 precursor RNA folds spatially, forming GR4589 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4589 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4589 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4589 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM141755 precursor RNA and GAM311344 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM141755 RNA and GAM311344 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM141755 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM141755 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM141755 target RNA into GAM141755 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM311344 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM311344 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM311344 target RNA into GAM311344 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4589 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4589 gene: GAM141755 target protein and GAM311344 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM141755 and GAM311344

GR4590 AV697661 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4590(GR4590) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4590 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4590 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4590 gene encodes GR4590 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4590 precursor RNA folds spatially, forming GR4590 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4590 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4590 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4590 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM306473 precursor RNA and GAM324635 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM306473 RNA and GAM324635 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM306473 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM306473 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM306473 target RNA into GAM306473 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM324635 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM324635 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM324635 target RNA into GAM324635 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4590 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4590 gene: GAM306473 target protein and GAM324635 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference,

with references to GAM306473 and GAM324635

GR4591 AW149528 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4591 (GR4591) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4591 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4591 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4591 gene encodes GR4591 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4591 precursor RNA folds spatially, forming GR4591 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4591 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4591 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4591 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2731 precursor RNA and GAM3800 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2731 RNA and GAM3800 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2731 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2731 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2731 target RNA into GAM2731 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM3800 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3800 target RNA, herein schematically represented by

GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3800 target RNA into GAM3800 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4591 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4591 gene: GAM2731 target protein and GAM3800 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2731 and GAM3800

GR4592 BF849818 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4592(GR4592) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4592 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4592 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4592 gene encodes GR4592 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4592 precursor RNA folds spatially, forming GR4592 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4592 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4592 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4592 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7020 precursor RNA and GAM176949 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7020 RNA and GAM176949 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding

to GAM RNA of Fig. 8.

GAM7020 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7020 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7020 target RNA into GAM7020 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM176949 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM176949 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM176949 target RNA into GAM176949 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4592 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4592 gene: GAM7020 target protein and GAM176949 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7020 and GAM176949

GR4593 BM822876 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4593(GR4593) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4593 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4593 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4593 gene encodes GR4593 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4593 precursor RNA folds spatially, forming GR4593 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4593 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4593 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR4593 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM15496 precursor RNA and GAM87782 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM15496 RNA and GAM87782 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM15496 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM15496 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM15496 target RNA into GAM15496 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM87782 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM87782 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM87782 target RNA into GAM87782 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4593 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4593 gene: GAM15496 target protein and GAM87782 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM15496 and GAM87782

GR4594 BF953530 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4594(GR4594) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4594 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4594

gene was detected is described hereinabove with reference to Figs. 8-18.

GR4594 gene encodes GR4594 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4594 precursor RNA folds spatially, forming GR4594 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4594 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4594 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4594 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM63913 precursor RNA, GAM142748 precursor RNA and GAM186538 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM63913 RNA, GAM142748 RNA and GAM186538 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM63913 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM63913 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM63913 target RNA into GAM63913 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM142748 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM142748 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM142748 target RNA into GAM142748 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM186538 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM186538 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM186538 target RNA into GAM186538 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4594 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4594 gene: GAM63913 target protein, GAM142748 target protein and GAM186538 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM63913, GAM142748 and GAM186538

GR4595 AA039353 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4595(GR4595) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4595 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4595 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4595 gene encodes GR4595 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4595 precursor RNA folds spatially, forming GR4595 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4595 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4595 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4595 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4805 precursor RNA, GAM156716 precursor RNA and GAM208533 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4805 RNA, GAM156716 RNA and GAM208533 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs

corresponding to GAM RNA of Fig. 8.

GAM4805 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4805 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4805 target RNA into GAM4805 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM156716 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM156716 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM156716 target RNA into GAM156716 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM208533 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM208533 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM208533 target RNA into GAM208533 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4595 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4595 gene: GAM4805 target protein, GAM156716 target protein and GAM208533 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4805, GAM156716 and GAM208533

GR4596 BM696378 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4596(GR4596) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4596 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4596 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4596 gene encodes GR4596 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR4596 precursor RNA folds spatially, forming GR4596 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4596 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4596 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4596 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7818 precursor RNA and GAM271704 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7818 RNA and GAM271704 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7818 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7818 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7818 target RNA into GAM7818 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM271704 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM271704 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM271704 target RNA into GAM271704 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4596 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4596 gene: GAM7818 target protein and GAM271704 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7818 and GAM271704

GR4597 AL048126 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4597(GR4597) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4597 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4597 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4597 gene encodes GR4597 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4597 precursor RNA folds spatially, forming GR4597 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4597 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4597 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4597 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM6709 precursor RNA, GAM163521 precursor RNA and GAM227026 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6709 RNA, GAM163521 RNA and GAM227026 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6709 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6709 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6709 target RNA into GAM6709 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM163521 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM163521 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM163521 target RNA into GAM163521 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM227026 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM227026 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM227026 target RNA into GAM227026 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4597 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4597 gene: GAM6709 target protein, GAM163521 target protein and GAM227026 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6709, GAM163521 and GAM227026

GR4598 BG117420 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4598(GR4598) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4598 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4598 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4598 gene encodes GR4598 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4598 precursor RNA folds spatially, forming GR4598 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4598 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4598 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4598 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM9937 precursor RNA, GAM21414 precursor RNA and

GAM63378 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM9937 RNA, GAM21414 RNA and GAM63378 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM9937 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM9937 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM9937 target RNA into GAM9937 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM21414 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM21414 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM21414 target RNA into GAM21414 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM63378 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM63378 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM63378 target RNA into GAM63378 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4598 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4598 gene: GAM9937 target protein, GAM21414 target protein and GAM63378 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM9937, GAM21414 and GAM63378

GR4599 BI491766 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4599(GR4599) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR4599 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4599 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4599 gene encodes GR4599 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4599 precursor RNA folds spatially, forming GR4599 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4599 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4599 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4599 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1639 precursor RNA, GAM224823 precursor RNA and GAM277686 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1639 RNA, GAM224823 RNA and GAM277686 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1639 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1639 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1639 target RNA into GAM1639 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM224823 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM224823 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM224823 target RNA into GAM224823 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM277686 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM277686 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM277686 target RNA into GAM277686 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4599 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4599 gene: GAM1639 target protein, GAM224823 target protein and GAM277686 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1639, GAM224823 and GAM277686

GR4600 AU118397 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4600(GR4600) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4600 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4600 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4600 gene encodes GR4600 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4600 precursor RNA folds spatially, forming GR4600 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4600 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4600 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4600 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2721 precursor RNA and GAM138962 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2721 RNA and GAM138962 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2721 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2721 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2721 target RNA into GAM2721 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM138962 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM138962 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM138962 target RNA into GAM138962 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4600 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4600 gene: GAM2721 target protein and GAM138962 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2721 and GAM138962

GR4601 BQ082285 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4601(GR4601) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4601 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4601 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4601 gene encodes GR4601 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4601 precursor RNA folds spatially, forming GR4601 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4601 folded precursor RNA comprises a plurality of what is known in the

art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4601 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4601 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM87772 precursor RNA and GAM290271 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM87772 RNA and GAM290271 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM87772 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM87772 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM87772 target RNA into GAM87772 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM290271 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM290271 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM290271 target RNA into GAM290271 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4601 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4601 gene: GAM87772 target protein and GAM290271 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM87772 and GAM290271

GR4602 BE206242 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4602(GR4602) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR4602 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4602 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4602 gene encodes GR4602 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4602 precursor RNA folds spatially, forming GR4602 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4602 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4602 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4602 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM8605 precursor RNA, GAM73152 precursor RNA and GAM150042 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8605 RNA, GAM73152 RNA and GAM150042 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8605 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8605 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8605 target RNA into GAM8605 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM73152 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM73152 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM73152 target RNA into GAM73152 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM150042 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM150042 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM150042 target RNA into GAM150042 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4602 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4602 gene: GAM8605 target protein, GAM73152 target protein and GAM150042 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8605, GAM73152 and GAM150042

GR4603 AW750057 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4603(GR4603) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4603 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4603 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4603 gene encodes GR4603 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4603 precursor RNA folds spatially, forming GR4603 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4603 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4603 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4603 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3977 precursor RNA, GAM147832 precursor RNA and GAM148098 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3977 RNA, GAM147832 RNA and GAM148098 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3977 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3977 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3977 target RNA into GAM3977 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM147832 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM147832 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM147832 target RNA into GAM147832 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM148098 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM148098 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM148098 target RNA into GAM148098 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4603 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4603 gene: GAM3977 target protein, GAM147832 target protein and GAM148098 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3977, GAM147832 and GAM148098

GR4604 BM969267 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4604(GR4604) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4604 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4604

gene was detected is described hereinabove with reference to Figs. 8-18.

GR4604 gene encodes GR4604 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4604 precursor RNA folds spatially, forming GR4604 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4604 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4604 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4604 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM222611 precursor RNA and GAM336067 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM222611 RNA and GAM336067 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM222611 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM222611 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM222611 target RNA into GAM222611 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336067 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336067 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336067 target RNA into GAM336067 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4604 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4604 gene: GAM222611 target protein and GAM336067 target protein, herein schematically represented by GAM1

TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM222611 and GAM336067

GR4605 AA476397 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4605(GR4605) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4605 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4605 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4605 gene encodes GR4605 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4605 precursor RNA folds spatially, forming GR4605 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4605 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4605 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4605 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6501 precursor RNA and GAM329444 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6501 RNA and GAM329444 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6501 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6501 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6501 target RNA into GAM6501 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM329444 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM329444 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM329444 target RNA into GAM329444 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4605 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4605 gene: GAM6501 target protein and GAM329444 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6501 and GAM329444

GR4606 AA932808 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4606(GR4606) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4606 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4606 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4606 gene encodes GR4606 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4606 precursor RNA folds spatially, forming GR4606 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4606 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4606 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4606 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM35904 precursor RNA and GAM325143 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM35904 RNA and GAM325143 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM35904 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM35904 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM35904 target RNA into GAM35904 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM325143 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM325143 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM325143 target RNA into GAM325143 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4606 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4606 gene: GAM35904 target protein and GAM325143 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM35904 and GAM325143

GR4607 BF217070 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4607(GR4607) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4607 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4607 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4607 gene encodes GR4607 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4607 precursor RNA folds spatially, forming GR4607 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4607 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4607 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4607 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3895 precursor RNA, GAM90222 precursor RNA and GAM139478 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3895 RNA, GAM90222 RNA and GAM139478 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3895 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3895 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3895 target RNA into GAM3895 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM90222 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM90222 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM90222 target RNA into GAM90222 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM139478 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM139478 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM139478 target RNA into GAM139478 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4607 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4607 gene: GAM3895 target protein, GAM90222 target protein and GAM139478 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6,

hereby incorporated by reference, with references to GAM3895, GAM90222 and GAM139478

GR4608 BG481848 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4608(GR4608) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4608 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4608 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4608 gene encodes GR4608 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4608 precursor RNA folds spatially, forming GR4608 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4608 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4608 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4608 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM91755 precursor RNA and GAM117051 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM91755 RNA and GAM117051 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM91755 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM91755 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM91755 target RNA into GAM91755 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM117051 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM117051 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM117051 target RNA into GAM117051 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4608 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4608 gene: GAM91755 target protein and GAM117051 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM91755 and GAM117051

GR4609 AW997696 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4609(GR4609) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4609 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4609 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4609 gene encodes GR4609 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4609 precursor RNA folds spatially, forming GR4609 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4609 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4609 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4609 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM75139 precursor RNA and GAM317854 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM75139 RNA and GAM317854 RNA, herein schematically

represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM75139 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM75139 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM75139 target RNA into GAM75139 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM317854 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM317854 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM317854 target RNA into GAM317854 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4609 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4609 gene: GAM75139 target protein and GAM317854 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM75139 and GAM317854

GR4610 AW897219 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4610(GR4610) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4610 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4610 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4610 gene encodes GR4610 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4610 precursor RNA folds spatially, forming GR4610 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4610 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4610 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4610 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8440 precursor RNA and GAM188179 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8440 RNA and GAM188179 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8440 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8440 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8440 target RNA into GAM8440 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM188179 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM188179 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM188179 target RNA into GAM188179 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4610 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4610 gene: GAM8440 target protein and GAM188179 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8440 and GAM188179

GR4611 BF437559 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4611 (GR4611) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4611 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR4611 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4611 gene encodes GR4611 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4611 precursor RNA folds spatially, forming GR4611 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4611 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4611 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4611 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM6403 precursor RNA, GAM8287 precursor RNA and GAM179352 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6403 RNA, GAM8287 RNA and GAM179352 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6403 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6403 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6403 target RNA into GAM6403 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8287 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8287 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8287 target RNA into GAM8287 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM179352 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM179352 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM179352 target RNA into GAM179352 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4611 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4611 gene: GAM6403 target protein, GAM8287 target protein and GAM179352 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6403, GAM8287 and GAM179352

GR4612 BG654913 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4612(GR4612) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4612 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4612 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4612 gene encodes GR4612 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4612 precursor RNA folds spatially, forming GR4612 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4612 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4612 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4612 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM627 precursor RNA and GAM163009 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM627 RNA and GAM163009 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding

to GAM RNA of Fig. 8.

GAM627 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM627 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM627 target RNA into GAM627 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM163009 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM163009 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM163009 target RNA into GAM163009 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4612 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4612 gene: GAM627 target protein and GAM163009 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM627 and GAM163009

GR4613 AW474312 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4613(GR4613) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4613 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4613 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4613 gene encodes GR4613 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4613 precursor RNA folds spatially, forming GR4613 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4613 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4613 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR4613 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM10112 precursor RNA and GAM51920 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM10112 RNA and GAM51920 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM10112 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM10112 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM10112 target RNA into GAM10112 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM51920 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM51920 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM51920 target RNA into GAM51920 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4613 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4613 gene: GAM10112 target protein and GAM51920 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM10112 and GAM51920

GR4614 BF185225 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4614(GR4614) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4614 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4614

gene was detected is described hereinabove with reference to Figs. 8-18.

GR4614 gene encodes GR4614 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4614 precursor RNA folds spatially, forming GR4614 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4614 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4614 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4614 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM45567 precursor RNA and GAM311092 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM45567 RNA and GAM311092 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM45567 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM45567 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM45567 target RNA into GAM45567 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM311092 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM311092 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM311092 target RNA into GAM311092 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4614 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4614 gene: GAM45567 target protein and GAM311092 target protein, herein schematically represented by GAM1

TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM45567 and GAM311092

GR4615 BE277877 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4615(GR4615) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4615 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4615 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4615 gene encodes GR4615 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4615 precursor RNA folds spatially, forming GR4615 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4615 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4615 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4615 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3088 precursor RNA and GAM8385 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3088 RNA and GAM8385 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3088 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3088 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3088 target RNA into GAM3088 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8385 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8385 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8385 target RNA into GAM8385 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4615 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4615 gene: GAM3088 target protein and GAM8385 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3088 and GAM8385

GR4616 BG413499 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4616(GR4616) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4616 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4616 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4616 gene encodes GR4616 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4616 precursor RNA folds spatially, forming GR4616 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4616 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4616 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4616 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM81682 precursor RNA and GAM165698 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM81682 RNA and GAM165698 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM81682 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM81682 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM81682 target RNA into GAM81682 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM165698 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM165698 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM165698 target RNA into GAM165698 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4616 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4616 gene: GAM81682 target protein and GAM165698 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM81682 and GAM165698

GR4617 BE842327 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4617(GR4617) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4617 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4617 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4617 gene encodes GR4617 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4617 precursor RNA folds spatially, forming GR4617 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4617 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4617 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4617 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6392 precursor RNA and GAM274634 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6392 RNA and GAM274634 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6392 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6392 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6392 target RNA into GAM6392 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM274634 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM274634 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM274634 target RNA into GAM274634 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4617 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4617 gene: GAM6392 target protein and GAM274634 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6392 and GAM274634

GR4618 BE876680 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4618(GR4618) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4618 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4618 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4618 gene encodes GR4618 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4618 precursor RNA folds spatially, forming GR4618 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4618 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4618 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4618 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3874 precursor RNA and GAM57818 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3874 RNA and GAM57818 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3874 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3874 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3874 target RNA into GAM3874 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM57818 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM57818 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM57818 target RNA into GAM57818 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4618 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR4618 gene: GAM3874 target protein and GAM57818 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3874 and GAM57818

GR4619 BG207133 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4619(GR4619) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4619 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4619 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4619 gene encodes GR4619 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4619 precursor RNA folds spatially, forming GR4619 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4619 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4619 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4619 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2181 precursor RNA, GAM4430 precursor RNA and GAM8477 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2181 RNA, GAM4430 RNA and GAM8477 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2181 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2181 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2181 target RNA into

GAM2181 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM4430 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4430 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4430 target RNA into GAM4430 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8477 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8477 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8477 target RNA into GAM8477 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4619 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4619 gene: GAM2181 target protein, GAM4430 target protein and GAM8477 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2181, GAM4430 and GAM8477

GR4620 T40984 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4620(GR4620) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4620 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4620 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4620 gene encodes GR4620 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4620 precursor RNA folds spatially, forming GR4620 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4620 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4620 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4620 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM8152 precursor RNA, GAM11814 precursor RNA and GAM227499 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8152 RNA, GAM11814 RNA and GAM227499 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8152 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8152 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8152 target RNA into GAM8152 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM11814 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM11814 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM11814 target RNA into GAM11814 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM227499 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM227499 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM227499 target RNA into GAM227499 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4620 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4620 gene: GAM8152 target protein, GAM11814 target protein and GAM227499 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8152, GAM11814 and

GR4621 AL712036 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4621 (GR4621) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4621 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4621 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4621 gene encodes GR4621 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4621 precursor RNA folds spatially, forming GR4621 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4621 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4621 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4621 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1078 precursor RNA, GAM8487 precursor RNA and GAM153370 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1078 RNA, GAM8487 RNA and GAM153370 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1078 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1078 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1078 target RNA into GAM1078 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8487 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM8487 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8487 target RNA into GAM8487 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM153370 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM153370 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM153370 target RNA into GAM153370 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4621 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4621 gene: GAM1078 target protein, GAM8487 target protein and GAM153370 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1078, GAM8487 and GAM153370

GR4622 BF692741 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4622(GR4622) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4622 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4622 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4622 gene encodes GR4622 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4622 precursor RNA folds spatially, forming GR4622 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4622 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4622 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4622 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM226985 precursor RNA and GAM316311 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM226985 RNA and GAM316311 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM226985 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM226985 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM226985 target RNA into GAM226985 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM316311 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM316311 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM316311 target RNA into GAM316311 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4622 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4622 gene: GAM226985 target protein and GAM316311 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM226985 and GAM316311

GR4623 BF525404 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4623(GR4623) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4623 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4623 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4623 gene encodes GR4623 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4623 precursor RNA folds spatially, forming GR4623 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4623 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4623 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4623 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM63120 precursor RNA, GAM219755 precursor RNA and GAM319861 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM63120 RNA, GAM219755 RNA and GAM319861 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM63120 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM63120 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM63120 target RNA into GAM63120 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM219755 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM219755 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM219755 target RNA into GAM219755 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM319861 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM319861 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM319861 target RNA into GAM319861 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4623 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4623 gene: GAM63120 target protein, GAM219755 target protein and GAM319861 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM63120, GAM219755 and GAM319861

GR4624 BF885242 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4624(GR4624) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4624 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4624 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4624 gene encodes GR4624 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4624 precursor RNA folds spatially, forming GR4624 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4624 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4624 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4624 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3481 precursor RNA and GAM113937 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3481 RNA and GAM113937 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3481 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM3481 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3481 target RNA into GAM3481 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM113937 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM113937 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM113937 target RNA into GAM113937 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4624 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4624 gene: GAM3481 target protein and GAM113937 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3481 and GAM113937

GR4625 BM832054 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4625(GR4625) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4625 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4625 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4625 gene encodes GR4625 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4625 precursor RNA folds spatially, forming GR4625 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4625 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4625 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4625 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2

separate GAM precursor RNAs, GAM223736 precursor RNA and GAM260890 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM223736 RNA and GAM260890 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM223736 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM223736 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM223736 target RNA into GAM223736 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM260890 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM260890 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM260890 target RNA into GAM260890 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4625 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4625 gene: GAM223736 target protein and GAM260890 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM223736 and GAM260890

GR4626 BM263167 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4626(GR4626) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4626 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4626 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4626 gene encodes GR4626 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR4626 precursor RNA folds spatially, forming GR4626 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4626 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4626 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4626 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM131866 precursor RNA and GAM223641 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM131866 RNA and GAM223641 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM131866 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM131866 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM131866 target RNA into GAM131866 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM223641 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM223641 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM223641 target RNA into GAM223641 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4626 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4626 gene: GAM131866 target protein and GAM223641 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM131866 and GAM223641

GR4627 BI086801 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4627(GR4627) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4627 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4627 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4627 gene encodes GR4627 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4627 precursor RNA folds spatially, forming GR4627 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4627 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4627 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4627 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1449 precursor RNA and GAM8517 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1449 RNA and GAM8517 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1449 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1449 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1449 target RNA into GAM1449 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8517 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8517 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig. 8, thereby inhibiting translation of GAM8517 target RNA into GAM8517 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4627 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4627 gene: GAM1449 target protein and GAM8517 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1449 and GAM8517

GR4628 AA598517 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4628(GR4628) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4628 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4628 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4628 gene encodes GR4628 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4628 precursor RNA folds spatially, forming GR4628 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4628 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4628 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4628 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM99795 precursor RNA and GAM111528 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM99795 RNA and GAM111528 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM99795 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM99795 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM99795 target RNA into GAM99795 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM111528 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM111528 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM111528 target RNA into GAM111528 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4628 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4628 gene: GAM99795 target protein and GAM111528 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM99795 and GAM111528

GR4629 AI373793 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4629(GR4629) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4629 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4629 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4629 gene encodes GR4629 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4629 precursor RNA folds spatially, forming GR4629 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4629 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4629 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4629 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1303 precursor RNA, GAM316614 precursor RNA and GAM317187 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1303 RNA, GAM316614 RNA and GAM317187 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1303 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1303 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1303 target RNA into GAM1303 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM316614 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM316614 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM316614 target RNA into GAM316614 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM317187 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM317187 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM317187 target RNA into GAM317187 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4629 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4629 gene: GAM1303 target protein, GAM316614 target protein and GAM317187 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1303, GAM316614 and GAM317187

bioinformatically detected regulatory gene, referred to here as Genomic Record 4630 (GR4630) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4630 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4630 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4630 gene encodes GR4630 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4630 precursor RNA folds spatially, forming GR4630 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4630 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4630 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4630 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3391 precursor RNA and GAM276065 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3391 RNA and GAM276065 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3391 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3391 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3391 target RNA into GAM3391 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM276065 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM276065 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM276065

target RNA into GAM276065 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4630 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4630 gene: GAM3391 target protein and GAM276065 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3391 and GAM276065

GR4631 AA071078 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4631(GR4631) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4631 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4631 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4631 gene encodes GR4631 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4631 precursor RNA folds spatially, forming GR4631 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4631 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4631 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4631 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM47237 precursor RNA and GAM205017 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM47237 RNA and GAM205017 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM47237 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM47237 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM47237 target RNA into GAM47237 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM205017 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM205017 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM205017 target RNA into GAM205017 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4631 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4631 gene: GAM47237 target protein and GAM205017 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM47237 and GAM205017

GR4632 BF182813 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4632(GR4632) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4632 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4632 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4632 gene encodes GR4632 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4632 precursor RNA folds spatially, forming GR4632 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4632 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4632 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4632 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM57635 precursor RNA, GAM86446 precursor RNA and GAM319335 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM57635 RNA, GAM86446 RNA and GAM319335 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM57635 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM57635 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM57635 target RNA into GAM57635 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM86446 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM86446 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM86446 target RNA into GAM86446 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM319335 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM319335 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM319335 target RNA into GAM319335 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4632 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4632 gene: GAM57635 target protein, GAM86446 target protein and GAM319335 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM57635, GAM86446 and GAM319335

4633(GR4633) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4633 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4633 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4633 gene encodes GR4633 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4633 precursor RNA folds spatially, forming GR4633 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4633 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4633 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4633 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4823 precursor RNA, GAM123530 precursor RNA and GAM223804 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4823 RNA, GAM123530 RNA and GAM223804 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4823 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4823 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4823 target RNA into GAM4823 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM123530 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM123530 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM123530

target RNA into GAM123530 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM223804 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM223804 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM223804 target RNA into GAM223804 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4633 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4633 gene: GAM4823 target protein, GAM123530 target protein and GAM223804 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4823, GAM123530 and GAM223804

GR4634 BM716381 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4634(GR4634) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4634 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4634 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4634 gene encodes GR4634 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4634 precursor RNA folds spatially, forming GR4634 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4634 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4634 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4634 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2105 precursor RNA and GAM230067 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin

shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2105 RNA and GAM230067 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2105 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2105 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2105 target RNA into GAM2105 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM230067 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM230067 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM230067 target RNA into GAM230067 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4634 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4634 gene: GAM2105 target protein and GAM230067 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2105 and GAM230067

GR4635 BI114371 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4635(GR4635) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4635 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4635 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4635 gene encodes GR4635 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4635 precursor RNA folds spatially, forming GR4635 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4635 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4635 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4635 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM6651 precursor RNA, GAM75228 precursor RNA and GAM227933 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6651 RNA, GAM75228 RNA and GAM227933 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6651 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6651 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6651 target RNA into GAM6651 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM75228 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM75228 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM75228 target RNA into GAM75228 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM227933 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM227933 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM227933 target RNA into GAM227933 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4635 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR4635 gene: GAM6651 target protein, GAM75228 target protein and GAM227933 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6651, GAM75228 and GAM227933

GR4636 BG213509 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4636(GR4636) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4636 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4636 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4636 gene encodes GR4636 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4636 precursor RNA folds spatially, forming GR4636 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4636 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4636 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4636 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM138241 precursor RNA, GAM243010 precursor RNA and GAM333390 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM138241 RNA, GAM243010 RNA and GAM333390 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM138241 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM138241 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM138241 target RNA into GAM138241 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM243010 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM243010 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM243010 target RNA into GAM243010 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM333390 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM333390 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM333390 target RNA into GAM333390 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4636 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4636 gene: GAM138241 target protein, GAM243010 target protein and GAM333390 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM138241, GAM243010 and GAM333390

GR4637 AI057015 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4637(GR4637) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4637 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4637 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4637 gene encodes GR4637 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4637 precursor RNA folds spatially, forming GR4637 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4637 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4637 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4637 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM28872 precursor RNA and GAM325368 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM28872 RNA and GAM325368 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM28872 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM28872 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM28872 target RNA into GAM28872 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM325368 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM325368 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM325368 target RNA into GAM325368 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4637 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4637 gene: GAM28872 target protein and GAM325368 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM28872 and GAM325368

GR4638 BF688448 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4638(GR4638) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4638 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4638 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4638 gene encodes GR4638 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4638 precursor RNA folds spatially, forming GR4638 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4638 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4638 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4638 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7360 precursor RNA and GAM220531 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7360 RNA and GAM220531 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7360 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7360 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7360 target RNA into GAM7360 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM220531 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM220531 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM220531 target RNA into GAM220531 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4638 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR4638 gene: GAM7360 target protein and GAM220531 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7360 and GAM220531

GR4639 AW002211 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4639(GR4639) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4639 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4639 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4639 gene encodes GR4639 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4639 precursor RNA folds spatially, forming GR4639 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4639 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4639 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4639 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM121900 precursor RNA and GAM260564 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM121900 RNA and GAM260564 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM121900 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM121900 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM121900 target RNA into GAM121900 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM260564 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM260564 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM260564 target RNA into GAM260564 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4639 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4639 gene: GAM121900 target protein and GAM260564 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM121900 and GAM260564

GR4640 BM723244 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4640(GR4640) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4640 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4640 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4640 gene encodes GR4640 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4640 precursor RNA folds spatially, forming GR4640 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4640 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4640 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4640 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM16511 precursor RNA and GAM59854 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM16511 RNA and GAM59854 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM16511 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM16511 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM16511 target RNA into GAM16511 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM59854 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM59854 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM59854 target RNA into GAM59854 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4640 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4640 gene: GAM16511 target protein and GAM59854 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM16511 and GAM59854

GR4641 N80478 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4641(GR4641) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4641 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4641 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4641 gene encodes GR4641 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4641 precursor RNA folds spatially, forming GR4641 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4641 folded precursor RNA comprises a plurality of what is known in the

art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4641 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4641 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2195 precursor RNA and GAM112168 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2195 RNA and GAM112168 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2195 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2195 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2195 target RNA into GAM2195 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM112168 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM112168 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM112168 target RNA into GAM112168 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4641 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4641 gene: GAM2195 target protein and GAM112168 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2195 and GAM112168

GR4642 BE560420 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4642(GR4642) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR4642 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4642 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4642 gene encodes GR4642 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4642 precursor RNA folds spatially, forming GR4642 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4642 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4642 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4642 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM32667 precursor RNA and GAM224338 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM32667 RNA and GAM224338 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM32667 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM32667 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM32667 target RNA into GAM32667 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM224338 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM224338 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM224338 target RNA into GAM224338 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly

utilities, of GR4642 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4642 gene: GAM32667 target protein and GAM224338 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM32667 and GAM224338

GR4643 BG775218 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4643(GR4643) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4643 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4643 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4643 gene encodes GR4643 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4643 precursor RNA folds spatially, forming GR4643 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4643 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4643 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4643 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1680 precursor RNA, GAM8444 precursor RNA and GAM60400 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1680 RNA, GAM8444 RNA and GAM60400 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1680 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1680 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds

to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1680 target RNA into GAM1680 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8444 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8444 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8444 target RNA into GAM8444 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM60400 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM60400 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM60400 target RNA into GAM60400 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4643 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4643 gene: GAM1680 target protein, GAM8444 target protein and GAM60400 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1680, GAM8444 and GAM60400

GR4644 BG016008 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4644(GR4644) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4644 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4644 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4644 gene encodes GR4644 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4644 precursor RNA folds spatially, forming GR4644 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4644 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR4644 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4644 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM102863 precursor RNA and GAM109222 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM102863 RNA and GAM109222 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM102863 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM102863 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM102863 target RNA into GAM102863 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM109222 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM109222 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM109222 target RNA into GAM109222 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4644 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4644 gene: GAM102863 target protein and GAM109222 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM102863 and GAM109222

GR4645 AA773250 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4645(GR4645) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4645 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4645 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4645 gene encodes GR4645 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4645 precursor RNA folds spatially, forming GR4645 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4645 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4645 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4645 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM153139 precursor RNA and GAM225169 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM153139 RNA and GAM225169 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM153139 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM153139 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM153139 target RNA into GAM153139 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM225169 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM225169 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM225169 target RNA into GAM225169 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4645 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4645 gene: GAM153139 target protein and GAM225169 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM153139 and GAM225169

GR4646 BG531736 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4646(GR4646) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4646 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4646 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4646 gene encodes GR4646 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4646 precursor RNA folds spatially, forming GR4646 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4646 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4646 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4646 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM65167 precursor RNA and GAM152604 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM65167 RNA and GAM152604 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM65167 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM65167 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM65167

target RNA into GAM65167 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM152604 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM152604 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM152604 target RNA into GAM152604 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4646 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4646 gene: GAM65167 target protein and GAM152604 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM65167 and GAM152604

GR4647 AW769753 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4647(GR4647) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4647 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4647 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4647 gene encodes GR4647 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4647 precursor RNA folds spatially, forming GR4647 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4647 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4647 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4647 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4630 precursor RNA and GAM137193 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4630 RNA and GAM137193 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4630 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4630 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4630 target RNA into GAM4630 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM137193 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM137193 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM137193 target RNA into GAM137193 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4647 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4647 gene: GAM4630 target protein and GAM137193 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4630 and GAM137193

GR4648 BF892722 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4648(GR4648) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4648 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4648 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4648 gene encodes GR4648 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4648 precursor RNA folds spatially, forming GR4648 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated

that GR4648 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4648 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4648 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6319 precursor RNA and GAM186457 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6319 RNA and GAM186457 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6319 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6319 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6319 target RNA into GAM6319 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM186457 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM186457 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM186457 target RNA into GAM186457 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4648 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4648 gene: GAM6319 target protein and GAM186457 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6319 and GAM186457

GR4649 BM145531 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4649(GR4649) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR4649 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4649 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4649 gene encodes GR4649 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4649 precursor RNA folds spatially, forming GR4649 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4649 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4649 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4649 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM43351 precursor RNA, GAM166432 precursor RNA and GAM171303 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM43351 RNA, GAM166432 RNA and GAM171303 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM43351 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM43351 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM43351 target RNA into GAM43351 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM166432 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM166432 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM166432 target RNA into GAM166432 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM171303 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM171303 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM171303 target RNA into GAM171303 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4649 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4649 gene: GAM43351 target protein, GAM166432 target protein and GAM171303 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM43351, GAM166432 and GAM171303

GR4650 BQ018325 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4650(GR4650) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4650 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4650 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4650 gene encodes GR4650 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4650 precursor RNA folds spatially, forming GR4650 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4650 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4650 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4650 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM104262 precursor RNA and GAM104765 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM104262 RNA and GAM104765 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM104262 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM104262 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM104262 target RNA into GAM104262 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM104765 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM104765 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM104765 target RNA into GAM104765 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4650 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4650 gene: GAM104262 target protein and GAM104765 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM104262 and GAM104765

GR4651 AI683635 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4651(GR4651) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4651 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4651 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4651 gene encodes GR4651 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4651 precursor RNA folds spatially, forming GR4651 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4651 folded precursor RNA comprises a plurality of what is known in the

art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4651 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4651 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1362 precursor RNA and GAM22263 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1362 RNA and GAM22263 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1362 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1362 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1362 target RNA into GAM1362 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM22263 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM22263 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM22263 target RNA into GAM22263 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4651 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4651 gene: GAM1362 target protein and GAM22263 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1362 and GAM22263

GR4652 BG770878 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4652(GR4652) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR4652 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4652 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4652 gene encodes GR4652 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4652 precursor RNA folds spatially, forming GR4652 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4652 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4652 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4652 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM124 precursor RNA, GAM2910 precursor RNA and GAM3762 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM124 RNA, GAM2910 RNA and GAM3762 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM124 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM124 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM124 target RNA into GAM124 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM2910 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2910 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2910 target RNA into GAM2910 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM3762 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3762 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3762 target RNA into GAM3762 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4652 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4652 gene: GAM124 target protein, GAM2910 target protein and GAM3762 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM124, GAM2910 and GAM3762

GR4653 AI393130 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4653(GR4653) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4653 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4653 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4653 gene encodes GR4653 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4653 precursor RNA folds spatially, forming GR4653 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4653 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4653 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4653 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM61924 precursor RNA and GAM257885 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM61924 RNA and GAM257885 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM61924 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM61924 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM61924 target RNA into GAM61924 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM257885 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM257885 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM257885 target RNA into GAM257885 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4653 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4653 gene: GAM61924 target protein and GAM257885 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM61924 and GAM257885

GR4654 BE270266 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4654(GR4654) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4654 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4654 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4654 gene encodes GR4654 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4654 precursor RNA folds spatially, forming GR4654 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4654 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR4654 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4654 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2255 precursor RNA and GAM3945 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2255 RNA and GAM3945 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2255 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2255 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2255 target RNA into GAM2255 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM3945 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3945 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3945 target RNA into GAM3945 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4654 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4654 gene: GAM2255 target protein and GAM3945 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2255 and GAM3945

GR4655 BI519749 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4655(GR4655) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4655 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4655 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4655 gene encodes GR4655 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4655 precursor RNA folds spatially, forming GR4655 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4655 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4655 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4655 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1709 precursor RNA and GAM206268 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1709 RNA and GAM206268 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1709 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1709 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1709 target RNA into GAM1709 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM206268 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM206268 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM206268 target RNA into GAM206268 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4655 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4655 gene: GAM1709 target protein and GAM206268 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1709 and GAM206268

GR4656 BG506641 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4656(GR4656) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4656 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4656 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4656 gene encodes GR4656 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4656 precursor RNA folds spatially, forming GR4656 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4656 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4656 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4656 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM8681 precursor RNA, GAM61055 precursor RNA and GAM239577 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8681 RNA, GAM61055 RNA and GAM239577 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8681 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8681 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig. 8, thereby inhibiting translation of GAM8681 target RNA into GAM8681 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM61055 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM61055 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM61055 target RNA into GAM61055 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM239577 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM239577 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM239577 target RNA into GAM239577 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4656 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4656 gene: GAM8681 target protein, GAM61055 target protein and GAM239577 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8681, GAM61055 and GAM239577

GR4657 AI921016 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4657(GR4657) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4657 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4657 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4657 gene encodes GR4657 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4657 precursor RNA folds spatially, forming GR4657 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4657 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4657 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4657 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM124974 precursor RNA, GAM139523 precursor RNA and GAM193473 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM124974 RNA, GAM139523 RNA and GAM193473 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM124974 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM124974 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM124974 target RNA into GAM124974 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM139523 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM139523 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM139523 target RNA into GAM139523 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM193473 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM193473 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM193473 target RNA into GAM193473 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4657 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4657 gene: GAM124974 target protein, GAM139523 target protein and GAM193473 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6,

hereby incorporated by reference, with references to GAM124974, GAM139523 and GAM193473

GR4658 AI659280 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4658(GR4658) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4658 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4658 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4658 gene encodes GR4658 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4658 precursor RNA folds spatially, forming GR4658 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4658 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4658 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4658 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1844 precursor RNA, GAM280612 precursor RNA and GAM316987 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1844 RNA, GAM280612 RNA and GAM316987 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1844 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1844 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1844 target RNA into GAM1844 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM280612 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM280612 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM280612 target RNA into GAM280612 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM316987 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM316987 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM316987 target RNA into GAM316987 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4658 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4658 gene: GAM1844 target protein, GAM280612 target protein and GAM316987 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1844, GAM280612 and GAM316987

GR4659 BI550777 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4659(GR4659) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4659 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4659 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4659 gene encodes GR4659 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4659 precursor RNA folds spatially, forming GR4659 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4659 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4659 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4659 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1815 precursor RNA and GAM272058 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1815 RNA and GAM272058 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1815 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1815 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1815 target RNA into GAM1815 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM272058 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM272058 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM272058 target RNA into GAM272058 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4659 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4659 gene: GAM1815 target protein and GAM272058 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1815 and GAM272058

GR4660 BG028147 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4660(GR4660) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4660 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4660 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4660 gene encodes GR4660 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4660 precursor RNA folds spatially, forming GR4660 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4660 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4660 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4660 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1853 precursor RNA, GAM188360 precursor RNA and GAM299764 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1853 RNA, GAM188360 RNA and GAM299764 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1853 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1853 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1853 target RNA into GAM1853 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM188360 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM188360 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM188360 target RNA into GAM188360 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM299764 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM299764 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM299764 target RNA into GAM299764 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4660 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4660 gene: GAM1853 target protein, GAM188360 target protein and GAM299764 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1853, GAM188360 and GAM299764

GR4661 H24393 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4661 (GR4661) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4661 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4661 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4661 gene encodes GR4661 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4661 precursor RNA folds spatially, forming GR4661 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4661 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4661 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4661 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM38047 precursor RNA, GAM112141 precursor RNA and GAM330609 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM38047 RNA, GAM112141 RNA and GAM330609 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM38047 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM38047 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM38047 target RNA into GAM38047 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM112141 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM112141 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM112141 target RNA into GAM112141 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM330609 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM330609 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM330609 target RNA into GAM330609 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4661 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4661 gene: GAM38047 target protein, GAM112141 target protein and GAM330609 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM38047, GAM112141 and GAM330609

GR4662 BE044498 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4662(GR4662) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4662 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4662 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4662 gene encodes GR4662 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4662 precursor RNA folds spatially, forming GR4662 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4662 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4662 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4662 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM104229 precursor RNA and GAM165666 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM104229 RNA and GAM165666 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM104229 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM104229 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM104229 target RNA into GAM104229 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM165666 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM165666 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM165666 target RNA into GAM165666 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4662 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4662 gene: GAM104229 target protein and GAM165666 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM104229 and GAM165666

4663(GR4663) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4663 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4663 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4663 gene encodes GR4663 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4663 precursor RNA folds spatially, forming GR4663 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4663 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4663 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4663 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1551 precursor RNA and GAM38840 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1551 RNA and GAM38840 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1551 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1551 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1551 target RNA into GAM1551 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM38840 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM38840 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM38840 target RNA into GAM38840 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4663 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4663 gene: GAM1551 target protein and GAM38840 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1551 and GAM38840

GR4664 BQ024192 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4664(GR4664) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4664 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4664 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4664 gene encodes GR4664 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4664 precursor RNA folds spatially, forming GR4664 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4664 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4664 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4664 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4056 precursor RNA, GAM8613 precursor RNA and GAM292958 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4056 RNA, GAM8613 RNA and GAM292958 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4056 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4056 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4056 target RNA into GAM4056 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8613 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8613 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8613 target RNA into GAM8613 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM292958 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM292958 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM292958 target RNA into GAM292958 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4664 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4664 gene: GAM4056 target protein, GAM8613 target protein and GAM292958 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4056, GAM8613 and GAM292958

GR4665 BI835000 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4665(GR4665) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4665 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4665 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4665 gene encodes GR4665 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4665 precursor RNA folds spatially, forming GR4665 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4665 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4665 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4665 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM5423 precursor RNA, GAM219816 precursor RNA, GAM232023 precursor RNA and GAM254522 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5423 RNA, GAM219816 RNA, GAM232023 RNA and GAM254522 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5423 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5423 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5423 target RNA into GAM5423 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM219816 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM219816 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM219816 target RNA into GAM219816 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM232023 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM232023 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM232023 target RNA into GAM232023 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM254522 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM254522 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM254522 target RNA into GAM254522 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4665 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4665 gene: GAM5423 target protein, GAM219816 target protein, GAM232023 target protein and GAM254522 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5423, GAM219816, GAM232023 and GAM254522

GR4666 AA570209 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4666(GR4666) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4666 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4666 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4666 gene encodes GR4666 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4666 precursor RNA folds spatially, forming GR4666 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4666 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4666 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4666 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4279 precursor RNA, GAM120515 precursor RNA and GAM121402 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4279 RNA, GAM120515 RNA and GAM121402 RNA, herein

schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4279 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4279 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4279 target RNA into GAM4279 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM120515 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM120515 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM120515 target RNA into GAM120515 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM121402 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM121402 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM121402 target RNA into GAM121402 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4666 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4666 gene: GAM4279 target protein, GAM120515 target protein and GAM121402 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4279, GAM120515 and GAM121402

GR4667 AI869949 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4667(GR4667) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4667 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4667 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4667 gene encodes GR4667 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4667 precursor RNA folds spatially, forming GR4667 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4667 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4667 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4667 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6295 precursor RNA and GAM177023 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6295 RNA and GAM177023 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6295 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6295 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6295 target RNA into GAM6295 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM177023 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM177023 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM177023 target RNA into GAM177023 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4667 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4667 gene: GAM6295 target protein and GAM177023 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6295 and GAM177023

GR4668 AW808167 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4668 (GR4668) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4668 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4668 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4668 gene encodes GR4668 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4668 precursor RNA folds spatially, forming GR4668 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4668 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4668 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4668 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM175101 precursor RNA and GAM254437 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM175101 RNA and GAM254437 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM175101 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM175101 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM175101 target RNA into GAM175101 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM254437 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM254437 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM254437 target RNA into GAM254437 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4668 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4668 gene: GAM175101 target protein and GAM254437 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM175101 and GAM254437

GR4669 BF571093 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4669(GR4669) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4669 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4669 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4669 gene encodes GR4669 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4669 precursor RNA folds spatially, forming GR4669 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4669 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4669 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4669 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1119 precursor RNA and GAM316106 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1119 RNA and GAM316106 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1119 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1119 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1119 target RNA into GAM1119 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM316106 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM316106 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM316106 target RNA into GAM316106 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4669 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4669 gene: GAM1119 target protein and GAM316106 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1119 and GAM316106

GR4670 BE819667 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4670(GR4670) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4670 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4670 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4670 gene encodes GR4670 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4670 precursor RNA folds spatially, forming GR4670 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4670 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4670 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4670 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM93806 precursor RNA, GAM97146 precursor RNA and GAM293923 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM93806 RNA, GAM97146 RNA and GAM293923 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM93806 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM93806 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM93806 target RNA into GAM93806 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM97146 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM97146 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM97146 target RNA into GAM97146 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM293923 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM293923 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM293923 target RNA into GAM293923 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4670 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4670 gene: GAM93806 target protein, GAM97146 target protein and GAM293923 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM93806, GAM97146 and GAM293923

GR4671 BG425822 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4671 (GR4671) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4671 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4671 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4671 gene encodes GR4671 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4671 precursor RNA folds spatially, forming GR4671 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4671 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4671 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4671 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM295 precursor RNA and GAM2987 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM295 RNA and GAM2987 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM295 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM295 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM295 target RNA into GAM295 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM2987 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2987 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig. 8, thereby inhibiting translation of GAM2987 target RNA into GAM2987 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4671 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4671 gene: GAM295 target protein and GAM2987 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM295 and GAM2987

GR4672 AW367242 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4672(GR4672) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4672 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4672 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4672 gene encodes GR4672 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4672 precursor RNA folds spatially, forming GR4672 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4672 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4672 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4672 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2979 precursor RNA and GAM38224 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2979 RNA and GAM38224 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2979 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2979 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2979 target RNA into GAM2979 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM38224 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM38224 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM38224 target RNA into GAM38224 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4672 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4672 gene: GAM2979 target protein and GAM38224 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2979 and GAM38224

GR4673 BG830094 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4673(GR4673) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4673 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4673 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4673 gene encodes GR4673 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4673 precursor RNA folds spatially, forming GR4673 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4673 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4673 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4673 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM172390 precursor RNA and GAM322473 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM172390 RNA and GAM322473 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM172390 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM172390 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM172390 target RNA into GAM172390 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM322473 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM322473 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM322473 target RNA into GAM322473 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4673 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4673 gene: GAM172390 target protein and GAM322473 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM172390 and GAM322473

GR4674 BM686484 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4674(GR4674) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4674 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4674 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4674 gene encodes GR4674 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4674 precursor RNA folds spatially, forming GR4674 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4674 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4674 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4674 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM281154 precursor RNA and GAM318777 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM281154 RNA and GAM318777 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM281154 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM281154 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM281154 target RNA into GAM281154 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM318777 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM318777 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM318777 target RNA into GAM318777 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4674 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4674 gene: GAM281154 target protein and GAM318777 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference,

with references to GAM281154 and GAM318777

GR4675 BE311813 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4675(GR4675) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4675 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4675 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4675 gene encodes GR4675 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4675 precursor RNA folds spatially, forming GR4675 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4675 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4675 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4675 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM72266 precursor RNA and GAM252327 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM72266 RNA and GAM252327 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM72266 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM72266 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM72266 target RNA into GAM72266 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM252327 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM252327 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM252327 target RNA into GAM252327 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4675 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4675 gene: GAM72266 target protein and GAM252327 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM72266 and GAM252327

GR4676 BG717530 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4676(GR4676) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4676 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4676 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4676 gene encodes GR4676 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4676 precursor RNA folds spatially, forming GR4676 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4676 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4676 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4676 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6815 precursor RNA and GAM257335 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6815 RNA and GAM257335 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding

to GAM RNA of Fig. 8.

GAM6815 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6815 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6815 target RNA into GAM6815 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM257335 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM257335 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM257335 target RNA into GAM257335 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4676 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4676 gene: GAM6815 target protein and GAM257335 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6815 and GAM257335

GR4677 BM843439 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4677(GR4677) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4677 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4677 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4677 gene encodes GR4677 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4677 precursor RNA folds spatially, forming GR4677 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4677 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4677 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR4677 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM37928 precursor RNA and GAM73773 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM37928 RNA and GAM73773 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM37928 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM37928 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM37928 target RNA into GAM37928 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM73773 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM73773 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM73773 target RNA into GAM73773 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4677 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4677 gene: GAM37928 target protein and GAM73773 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM37928 and GAM73773

GR4678 BF511462 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4678(GR4678) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4678 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4678

gene was detected is described hereinabove with reference to Figs. 8-18.

GR4678 gene encodes GR4678 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4678 precursor RNA folds spatially, forming GR4678 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4678 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4678 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4678 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1146 precursor RNA and GAM147677 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1146 RNA and GAM147677 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1146 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1146 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1146 target RNA into GAM1146 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM147677 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM147677 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM147677 target RNA into GAM147677 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4678 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4678 gene: GAM1146 target protein and GAM147677 target protein, herein schematically represented by GAM1

TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1146 and GAM147677

GR4679 BF112119 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4679(GR4679) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4679 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4679 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4679 gene encodes GR4679 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4679 precursor RNA folds spatially, forming GR4679 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4679 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4679 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4679 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2497 precursor RNA and GAM299401 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2497 RNA and GAM299401 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2497 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2497 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2497 target RNA into GAM2497 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM299401 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM299401 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM299401 target RNA into GAM299401 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4679 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4679 gene: GAM2497 target protein and GAM299401 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2497 and GAM299401

GR4680 BG104911 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4680(GR4680) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4680 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4680 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4680 gene encodes GR4680 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4680 precursor RNA folds spatially, forming GR4680 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4680 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4680 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4680 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2755 precursor RNA and GAM290135 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM2755 RNA and GAM290135 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2755 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2755 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2755 target RNA into GAM2755 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM290135 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM290135 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM290135 target RNA into GAM290135 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4680 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4680 gene: GAM2755 target protein and GAM290135 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2755 and GAM290135

GR4681 BG708268 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4681(GR4681) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4681 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4681 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4681 gene encodes GR4681 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4681 precursor RNA folds spatially, forming GR4681 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4681 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4681 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4681 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1797 precursor RNA and GAM14443 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1797 RNA and GAM14443 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1797 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1797 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1797 target RNA into GAM1797 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM14443 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM14443 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM14443 target RNA into GAM14443 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4681 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4681 gene: GAM1797 target protein and GAM14443 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1797 and GAM14443

GR4682 BQ058000 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4682(GR4682) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4682 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4682 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4682 gene encodes GR4682 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4682 precursor RNA folds spatially, forming GR4682 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4682 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4682 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4682 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM231132 precursor RNA and GAM276327 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM231132 RNA and GAM276327 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM231132 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM231132 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM231132 target RNA into GAM231132 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM276327 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM276327 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM276327 target RNA into GAM276327 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4682 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR4682 gene: GAM231132 target protein and GAM276327 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM231132 and GAM276327

GR4683 AA447984 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4683(GR4683) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4683 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4683 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4683 gene encodes GR4683 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4683 precursor RNA folds spatially, forming GR4683 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4683 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4683 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4683 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4337 precursor RNA, GAM7115 precursor RNA and GAM137849 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4337 RNA, GAM7115 RNA and GAM137849 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4337 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4337 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4337 target RNA into

GAM4337 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7115 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7115 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7115 target RNA into GAM7115 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM137849 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM137849 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM137849 target RNA into GAM137849 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4683 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4683 gene: GAM4337 target protein, GAM7115 target protein and GAM137849 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4337, GAM7115 and GAM137849

GR4684 AI638348 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4684(GR4684) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4684 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4684 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4684 gene encodes GR4684 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4684 precursor RNA folds spatially, forming GR4684 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4684 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4684 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4684 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM78426 precursor RNA and GAM294160 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM78426 RNA and GAM294160 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM78426 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM78426 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM78426 target RNA into GAM78426 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM294160 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM294160 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM294160 target RNA into GAM294160 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4684 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4684 gene: GAM78426 target protein and GAM294160 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM78426 and GAM294160

GR4685 BF921350 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4685(GR4685) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4685 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR4685 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4685 gene encodes GR4685 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4685 precursor RNA folds spatially, forming GR4685 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4685 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4685 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4685 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM110108 precursor RNA and GAM138722 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM110108 RNA and GAM138722 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM110108 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM110108 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM110108 target RNA into GAM110108 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM138722 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM138722 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM138722 target RNA into GAM138722 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4685 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4685 gene: GAM110108 target

protein and GAM138722 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM110108 and GAM138722

GR4686 AI280138 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4686(GR4686) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4686 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4686 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4686 gene encodes GR4686 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4686 precursor RNA folds spatially, forming GR4686 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4686 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4686 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4686 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1267 precursor RNA, GAM6262 precursor RNA and GAM25341 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1267 RNA, GAM6262 RNA and GAM25341 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1267 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1267 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1267 target RNA into GAM1267 target protein, herein schematically represented by GAM1 TARGET

PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6262 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6262 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6262 target RNA into GAM6262 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM25341 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM25341 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM25341 target RNA into GAM25341 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4686 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4686 gene: GAM1267 target protein, GAM6262 target protein and GAM25341 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1267, GAM6262 and GAM25341

GR4687 BE387260 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4687 (GR4687) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4687 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4687 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4687 gene encodes GR4687 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4687 precursor RNA folds spatially, forming GR4687 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4687 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4687 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR4687 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1827 precursor RNA and GAM6463 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1827 RNA and GAM6463 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1827 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1827 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1827 target RNA into GAM1827 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6463 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6463 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6463 target RNA into GAM6463 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4687 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4687 gene: GAM1827 target protein and GAM6463 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1827 and GAM6463

GR4688 BG435862 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4688(GR4688) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4688 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4688

gene was detected is described hereinabove with reference to Figs. 8-18.

GR4688 gene encodes GR4688 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4688 precursor RNA folds spatially, forming GR4688 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4688 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4688 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4688 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM113431 precursor RNA, GAM255307 precursor RNA and GAM280169 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM113431 RNA, GAM255307 RNA and GAM280169 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM113431 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM113431 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM113431 target RNA into GAM113431 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM255307 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM255307 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM255307 target RNA into GAM255307 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM280169 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM280169 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM280169 target RNA into GAM280169 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4688 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4688 gene: GAM113431 target protein, GAM255307 target protein and GAM280169 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM113431, GAM255307 and GAM280169

GR4689 AI126795 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4689(GR4689) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4689 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4689 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4689 gene encodes GR4689 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4689 precursor RNA folds spatially, forming GR4689 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4689 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4689 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4689 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4007 precursor RNA and GAM5834 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4007 RNA and GAM5834 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4007 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4007 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4007 target RNA into GAM4007 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5834 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5834 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5834 target RNA into GAM5834 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4689 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4689 gene: GAM4007 target protein and GAM5834 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4007 and GAM5834

GR4690 BF732795 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4690(GR4690) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4690 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4690 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4690 gene encodes GR4690 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4690 precursor RNA folds spatially, forming GR4690 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4690 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4690 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4690 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM233797 precursor RNA and GAM301673 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM233797 RNA and GAM301673 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM233797 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM233797 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM233797 target RNA into GAM233797 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM301673 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM301673 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM301673 target RNA into GAM301673 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4690 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4690 gene: GAM233797 target protein and GAM301673 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM233797 and GAM301673

GR4691 H14857 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4691(GR4691) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4691 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4691 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4691 gene encodes GR4691 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4691 precursor RNA folds spatially, forming GR4691 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4691 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4691 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4691 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3446 precursor RNA and GAM227919 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3446 RNA and GAM227919 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3446 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3446 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3446 target RNA into GAM3446 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM227919 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM227919 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM227919 target RNA into GAM227919 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4691 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4691 gene: GAM3446 target protein and GAM227919 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes

is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3446 and GAM227919

GR4692 AI695149 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4692(GR4692) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4692 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4692 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4692 gene encodes GR4692 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4692 precursor RNA folds spatially, forming GR4692 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4692 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4692 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4692 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2287 precursor RNA, GAM8495 precursor RNA and GAM35861 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2287 RNA, GAM8495 RNA and GAM35861 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2287 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2287 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2287 target RNA into GAM2287 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8495 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8495 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8495 target RNA into GAM8495 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM35861 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM35861 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM35861 target RNA into GAM35861 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4692 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4692 gene: GAM2287 target protein, GAM8495 target protein and GAM35861 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2287, GAM8495 and GAM35861

GR4693 BE959492 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4693(GR4693) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4693 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4693 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4693 gene encodes GR4693 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4693 precursor RNA folds spatially, forming GR4693 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4693 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4693 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4693 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM3508 precursor RNA, GAM6586 precursor RNA, GAM8603 precursor RNA and GAM223448 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3508 RNA, GAM6586 RNA, GAM8603 RNA and GAM223448 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3508 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3508 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3508 target RNA into GAM3508 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6586 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6586 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6586 target RNA into GAM6586 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8603 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8603 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8603 target RNA into GAM8603 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM223448 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM223448 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM223448 target RNA into GAM223448 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4693 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR4693 gene: GAM3508 target protein, GAM6586 target protein, GAM8603 target protein and GAM223448 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3508, GAM6586, GAM8603 and GAM223448

GR4694 BE780865 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4694(GR4694) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4694 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4694 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4694 gene encodes GR4694 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4694 precursor RNA folds spatially, forming GR4694 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4694 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4694 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4694 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM13388 precursor RNA, GAM112912 precursor RNA and GAM270016 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM13388 RNA, GAM112912 RNA and GAM270016 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM13388 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM13388 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM13388 target RNA into GAM13388 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM112912 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM112912 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM112912 target RNA into GAM112912 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM270016 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM270016 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM270016 target RNA into GAM270016 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4694 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4694 gene: GAM13388 target protein, GAM112912 target protein and GAM270016 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM13388, GAM112912 and GAM270016

GR4695 BG251196 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4695(GR4695) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4695 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4695 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4695 gene encodes GR4695 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4695 precursor RNA folds spatially, forming GR4695 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4695 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4695 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4695 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM575 precursor RNA, GAM60371 precursor RNA and GAM232966 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM575 RNA, GAM60371 RNA and GAM232966 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM575 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM575 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM575 target RNA into GAM575 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM60371 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM60371 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM60371 target RNA into GAM60371 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM232966 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM232966 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM232966 target RNA into GAM232966 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4695 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4695 gene: GAM575 target protein, GAM60371 target protein and GAM232966 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6,

hereby incorporated by reference, with references to GAM575, GAM60371 and GAM232966

GR4696 AI823839 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4696(GR4696) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4696 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4696 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4696 gene encodes GR4696 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4696 precursor RNA folds spatially, forming GR4696 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4696 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4696 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4696 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM12848 precursor RNA, GAM43346 precursor RNA, GAM120953 precursor RNA and GAM188174 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM12848 RNA, GAM43346 RNA, GAM120953 RNA and GAM188174 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM12848 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM12848 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM12848 target RNA into GAM12848 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM43346 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM43346 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM43346 target RNA into GAM43346 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM120953 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM120953 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM120953 target RNA into GAM120953 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM188174 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM188174 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM188174 target RNA into GAM188174 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4696 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4696 gene: GAM12848 target protein, GAM43346 target protein, GAM120953 target protein and GAM188174 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM12848, GAM43346, GAM120953 and GAM188174

GR4697 AA759158 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4697(GR4697) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4697 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4697 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4697 gene encodes GR4697 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4697 precursor RNA folds spatially, forming GR4697 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4697 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4697 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4697 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM63406 precursor RNA and GAM125328 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM63406 RNA and GAM125328 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM63406 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM63406 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM63406 target RNA into GAM63406 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM125328 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM125328 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM125328 target RNA into GAM125328 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4697 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4697 gene: GAM63406 target protein and GAM125328 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM63406 and GAM125328

GR4698 AI021982 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4698(GR4698) gene, which encodes an `operon-like` cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4698 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4698 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4698 gene encodes GR4698 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4698 precursor RNA folds spatially, forming GR4698 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4698 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4698 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4698 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1042 precursor RNA and GAM85409 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1042 RNA and GAM85409 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1042 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1042 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1042 target RNA into GAM1042 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM85409 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM85409 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM85409 target RNA into GAM85409 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4698 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4698 gene: GAM1042 target protein and GAM85409 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1042 and GAM85409

GR4699 AW967849 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4699(GR4699) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4699 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4699 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4699 gene encodes GR4699 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4699 precursor RNA folds spatially, forming GR4699 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4699 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4699 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4699 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2117 precursor RNA and GAM3120 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2117 RNA and GAM3120 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2117 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2117 target RNA, herein schematically represented by

GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2117 target RNA into GAM2117 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM3120 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3120 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3120 target RNA into GAM3120 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4699 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4699 gene: GAM2117 target protein and GAM3120 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2117 and GAM3120

GR4700 BF822229 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4700(GR4700) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4700 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4700 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4700 gene encodes GR4700 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4700 precursor RNA folds spatially, forming GR4700 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4700 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4700 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4700 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM255699 precursor RNA and GAM306547 precursor

RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM255699 RNA and GAM306547 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM255699 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM255699 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM255699 target RNA into GAM255699 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM306547 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM306547 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM306547 target RNA into GAM306547 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4700 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4700 gene: GAM255699 target protein and GAM306547 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM255699 and GAM306547

GR4701 BG431814 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4701 (GR4701) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4701 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4701 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4701 gene encodes GR4701 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4701 precursor RNA folds spatially, forming GR4701 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4701 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4701 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4701 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM39476 precursor RNA and GAM231961 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM39476 RNA and GAM231961 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM39476 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM39476 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM39476 target RNA into GAM39476 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM231961 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM231961 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM231961 target RNA into GAM231961 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4701 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4701 gene: GAM39476 target protein and GAM231961 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM39476 and GAM231961

bioinformatically detected regulatory gene, referred to here as Genomic Record 4702(GR4702) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4702 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4702 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4702 gene encodes GR4702 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4702 precursor RNA folds spatially, forming GR4702 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4702 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4702 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4702 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 5 separate GAM precursor RNAs, GAM2372 precursor RNA, GAM154655 precursor RNA, GAM209948 precursor RNA, GAM227260 precursor RNA and GAM308535 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2372 RNA, GAM154655 RNA, GAM209948 RNA, GAM227260 RNA and GAM308535 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2372 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2372 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2372 target RNA into GAM2372 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM154655 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM154655 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM154655 target RNA into GAM154655 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM209948 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM209948 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM209948 target RNA into GAM209948 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM227260 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM227260 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM227260 target RNA into GAM227260 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM308535 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM308535 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM308535 target RNA into GAM308535 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4702 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4702 gene: GAM2372 target protein, GAM154655 target protein, GAM209948 target protein, GAM227260 target protein and GAM308535 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2372, GAM154655, GAM209948, GAM227260 and GAM308535

GR4703 BE791648 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4703(GR4703) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4703 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4703 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4703 gene encodes GR4703 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4703 precursor RNA folds spatially, forming GR4703 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4703 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4703 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4703 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3369 precursor RNA and GAM46135 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3369 RNA and GAM46135 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3369 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3369 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3369 target RNA into GAM3369 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM46135 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM46135 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM46135 target RNA into GAM46135 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4703 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4703 gene: GAM3369 target protein and GAM46135 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference,

with references to GAM3369 and GAM46135

GR4704 BE262400 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4704(GR4704) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4704 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4704 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4704 gene encodes GR4704 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4704 precursor RNA folds spatially, forming GR4704 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4704 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4704 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4704 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM60734 precursor RNA, GAM178185 precursor RNA and GAM215296 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM60734 RNA, GAM178185 RNA and GAM215296 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM60734 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM60734 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM60734 target RNA into GAM60734 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM178185 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM178185 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM178185 target RNA into GAM178185 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM215296 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM215296 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM215296 target RNA into GAM215296 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4704 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4704 gene: GAM60734 target protein, GAM178185 target protein and GAM215296 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM60734, GAM178185 and GAM215296

GR4705 AA541802 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4705(GR4705) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4705 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4705 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4705 gene encodes GR4705 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4705 precursor RNA folds spatially, forming GR4705 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4705 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4705 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4705 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5478 precursor RNA and GAM119796 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5478 RNA and GAM119796 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5478 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5478 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5478 target RNA into GAM5478 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM119796 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM119796 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM119796 target RNA into GAM119796 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4705 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4705 gene: GAM5478 target protein and GAM119796 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5478 and GAM119796

GR4706 AI453143 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4706(GR4706) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4706 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4706 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4706 gene encodes GR4706 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4706 precursor RNA folds spatially, forming GR4706 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4706 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4706 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4706 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM642 precursor RNA and GAM3752 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM642 RNA and GAM3752 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM642 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM642 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM642 target RNA into GAM642 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM3752 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3752 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3752 target RNA into GAM3752 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4706 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4706 gene: GAM642 target protein and GAM3752 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM642 and GAM3752

GR4707 BM679857 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4707(GR4707) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4707 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4707 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4707 gene encodes GR4707 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4707 precursor RNA folds spatially, forming GR4707 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4707 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4707 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4707 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM132929 precursor RNA and GAM182778 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM132929 RNA and GAM182778 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM132929 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM132929 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM132929 target RNA into GAM132929 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM182778 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM182778 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM182778 target RNA into GAM182778 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4707 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4707 gene: GAM132929 target protein and GAM182778 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM132929 and GAM182778

GR4708 BF986853 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4708(GR4708) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4708 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4708 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4708 gene encodes GR4708 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4708 precursor RNA folds spatially, forming GR4708 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4708 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4708 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4708 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM137598 precursor RNA, GAM149866 precursor RNA and GAM333250 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM137598 RNA, GAM149866 RNA and GAM333250 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs

corresponding to GAM RNA of Fig. 8.

GAM137598 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM137598 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM137598 target RNA into GAM137598 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM149866 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM149866 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM149866 target RNA into GAM149866 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM333250 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM333250 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM333250 target RNA into GAM333250 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4708 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4708 gene: GAM137598 target protein, GAM149866 target protein and GAM333250 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM137598, GAM149866 and GAM333250

GR4709 AW388638 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4709(GR4709) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4709 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4709 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4709 gene encodes GR4709 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR4709 precursor RNA folds spatially, forming GR4709 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4709 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4709 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4709 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM220491 precursor RNA and GAM299709 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM220491 RNA and GAM299709 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM220491 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM220491 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM220491 target RNA into GAM220491 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM299709 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM299709 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM299709 target RNA into GAM299709 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4709 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4709 gene: GAM220491 target protein and GAM299709 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM220491 and GAM299709

GR4710 AI433260 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4710(GR4710) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4710 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4710 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4710 gene encodes GR4710 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4710 precursor RNA folds spatially, forming GR4710 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4710 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4710 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4710 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1058 precursor RNA and GAM149677 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1058 RNA and GAM149677 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1058 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1058 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1058 target RNA into GAM1058 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM149677 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM149677 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM149677 target RNA into GAM149677 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4710 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4710 gene: GAM1058 target protein and GAM149677 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1058 and GAM149677

GR4711 BG495306 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4711 (GR4711) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4711 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4711 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4711 gene encodes GR4711 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4711 precursor RNA folds spatially, forming GR4711 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4711 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4711 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4711 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM11720 precursor RNA, GAM196465 precursor RNA, GAM296704 precursor RNA and GAM309825 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM11720 RNA, GAM196465 RNA, GAM296704 RNA and GAM309825 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM11720 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM11720 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM11720 target RNA into GAM11720 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM196465 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM196465 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM196465 target RNA into GAM196465 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM296704 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM296704 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM296704 target RNA into GAM296704 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM309825 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM309825 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM309825 target RNA into GAM309825 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4711 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4711 gene: GAM11720 target protein, GAM196465 target protein, GAM296704 target protein and GAM309825 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM11720, GAM196465, GAM296704 and GAM309825

GR4712 BG612063 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4712(GR4712) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4712 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4712 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4712 gene encodes GR4712 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4712 precursor RNA folds spatially, forming GR4712 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4712 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4712 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4712 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM190441 precursor RNA and GAM304449 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM190441 RNA and GAM304449 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM190441 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM190441 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM190441 target RNA into GAM190441 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM304449 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM304449 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM304449 target RNA into GAM304449 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4712 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4712 gene: GAM190441 target protein and GAM304449 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM190441 and GAM304449

GR4713 AF150352 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4713(GR4713) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4713 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4713 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4713 gene encodes GR4713 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4713 precursor RNA folds spatially, forming GR4713 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4713 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4713 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4713 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM7507 precursor RNA, GAM53004 precursor RNA and GAM109438 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7507 RNA, GAM53004 RNA and GAM109438 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7507 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7507 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig. 8, thereby inhibiting translation of GAM7507 target RNA into GAM7507 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM53004 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM53004 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM53004 target RNA into GAM53004 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM109438 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM109438 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM109438 target RNA into GAM109438 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4713 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4713 gene: GAM7507 target protein, GAM53004 target protein and GAM109438 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7507, GAM53004 and GAM109438

GR4714 AW852379 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4714(GR4714) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4714 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4714 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4714 gene encodes GR4714 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4714 precursor RNA folds spatially, forming GR4714 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4714 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4714 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4714 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM303 precursor RNA and GAM16125 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM303 RNA and GAM16125 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM303 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM303 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM303 target RNA into GAM303 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM16125 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM16125 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM16125 target RNA into GAM16125 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4714 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4714 gene: GAM303 target protein and GAM16125 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM303 and GAM16125

GR4715 BE063132 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4715(GR4715) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4715 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4715 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4715 gene encodes GR4715 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4715 precursor RNA folds spatially, forming GR4715 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4715 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4715 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4715 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM35151 precursor RNA, GAM142314 precursor RNA and GAM241496 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM35151 RNA, GAM142314 RNA and GAM241496 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM35151 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM35151 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM35151 target RNA into GAM35151 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM142314 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM142314 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM142314 target RNA into GAM142314 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM241496 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM241496 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM241496 target RNA into GAM241496 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4715 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4715 gene: GAM35151 target protein, GAM142314 target protein and GAM241496 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM35151, GAM142314 and GAM241496

GR4716 BE906032 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4716(GR4716) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4716 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4716 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4716 gene encodes GR4716 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4716 precursor RNA folds spatially, forming GR4716 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4716 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4716 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4716 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2296 precursor RNA and GAM5715 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2296 RNA and GAM5715 RNA, herein schematically

represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2296 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2296 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2296 target RNA into GAM2296 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5715 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5715 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5715 target RNA into GAM5715 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4716 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4716 gene: GAM2296 target protein and GAM5715 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2296 and GAM5715

GR4717 AA884740 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4717(GR4717) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4717 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4717 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4717 gene encodes GR4717 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4717 precursor RNA folds spatially, forming GR4717 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4717 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4717 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4717 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1787 precursor RNA, GAM3407 precursor RNA and GAM5993 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1787 RNA, GAM3407 RNA and GAM5993 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1787 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1787 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1787 target RNA into GAM1787 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM3407 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3407 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3407 target RNA into GAM3407 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5993 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5993 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5993 target RNA into GAM5993 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4717 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4717 gene: GAM1787 target protein, GAM3407 target protein and GAM5993 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1787, GAM3407 and

GR4718 BI766141 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4718(GR4718) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4718 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4718 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4718 gene encodes GR4718 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4718 precursor RNA folds spatially, forming GR4718 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4718 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4718 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4718 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4684 precursor RNA and GAM99224 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4684 RNA and GAM99224 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4684 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4684 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4684 target RNA into GAM4684 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM99224 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM99224 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM99224 target RNA into GAM99224 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4718 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4718 gene: GAM4684 target protein and GAM99224 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4684 and GAM99224

GR4719 BM807539 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4719(GR4719) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4719 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4719 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4719 gene encodes GR4719 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4719 precursor RNA folds spatially, forming GR4719 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4719 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4719 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4719 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1153 precursor RNA and GAM223233 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1153 RNA and GAM223233 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding

to GAM RNA of Fig. 8.

GAM1153 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1153 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1153 target RNA into GAM1153 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM223233 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM223233 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM223233 target RNA into GAM223233 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4719 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4719 gene: GAM1153 target protein and GAM223233 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1153 and GAM223233

GR4720 AW377262 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4720(GR4720) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4720 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4720 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4720 gene encodes GR4720 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4720 precursor RNA folds spatially, forming GR4720 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4720 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4720 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR4720 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5014 precursor RNA and GAM146730 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5014 RNA and GAM146730 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5014 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5014 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5014 target RNA into GAM5014 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM146730 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM146730 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM146730 target RNA into GAM146730 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4720 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4720 gene: GAM5014 target protein and GAM146730 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5014 and GAM146730

GR4721 BF697940 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4721(GR4721) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4721 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4721

gene was detected is described hereinabove with reference to Figs. 8-18.

GR4721 gene encodes GR4721 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4721 precursor RNA folds spatially, forming GR4721 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4721 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4721 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4721 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM40333 precursor RNA, GAM295658 precursor RNA and GAM326262 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM40333 RNA, GAM295658 RNA and GAM326262 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM40333 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM40333 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM40333 target RNA into GAM40333 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM295658 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM295658 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM295658 target RNA into GAM295658 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM326262 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM326262 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM326262 target RNA into GAM326262 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4721 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4721 gene: GAM40333 target protein, GAM295658 target protein and GAM326262 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM40333, GAM295658 and GAM326262

GR4722 BG167607 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4722(GR4722) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4722 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4722 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4722 gene encodes GR4722 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4722 precursor RNA folds spatially, forming GR4722 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4722 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4722 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4722 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM107009 precursor RNA, GAM129413 precursor RNA and GAM273870 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM107009 RNA, GAM129413 RNA and GAM273870 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs

corresponding to GAM RNA of Fig. 8.

GAM107009 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM107009 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM107009 target RNA into GAM107009 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM129413 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM129413 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM129413 target RNA into GAM129413 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM273870 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM273870 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM273870 target RNA into GAM273870 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4722 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4722 gene: GAM107009 target protein, GAM129413 target protein and GAM273870 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM107009, GAM129413 and GAM273870

GR4723 AI858475 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4723(GR4723) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4723 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4723 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4723 gene encodes GR4723 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR4723 precursor RNA folds spatially, forming GR4723 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4723 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4723 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4723 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3234 precursor RNA and GAM280373 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3234 RNA and GAM280373 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3234 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3234 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3234 target RNA into GAM3234 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM280373 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM280373 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM280373 target RNA into GAM280373 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4723 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4723 gene: GAM3234 target protein and GAM280373 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3234 and GAM280373

GR4724 AW834819 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4724(GR4724) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4724 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4724 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4724 gene encodes GR4724 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4724 precursor RNA folds spatially, forming GR4724 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4724 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4724 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4724 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM7730 precursor RNA, GAM58589 precursor RNA and GAM67859 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7730 RNA, GAM58589 RNA and GAM67859 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7730 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7730 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7730 target RNA into GAM7730 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM58589 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM58589 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM58589 target RNA into GAM58589 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM67859 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM67859 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM67859 target RNA into GAM67859 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4724 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4724 gene: GAM7730 target protein, GAM58589 target protein and GAM67859 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7730, GAM58589 and GAM67859

GR4725 BF540738 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4725(GR4725) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4725 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4725 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4725 gene encodes GR4725 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4725 precursor RNA folds spatially, forming GR4725 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4725 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4725 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4725 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM18179 precursor RNA, GAM181276 precursor RNA,

GAM295983 precursor RNA and GAM304097 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM18179 RNA, GAM181276 RNA, GAM295983 RNA and GAM304097 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM18179 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM18179 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM18179 target RNA into GAM18179 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM181276 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM181276 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM181276 target RNA into GAM181276 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM295983 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM295983 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM295983 target RNA into GAM295983 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM304097 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM304097 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM304097 target RNA into GAM304097 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4725 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4725 gene: GAM18179 target protein, GAM181276 target protein, GAM295983 target protein and GAM304097 target protein, herein schematically represented by GAM1 TARGET PROTEIN

through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM18179, GAM181276, GAM295983 and GAM304097

GR4726 BM313724 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4726(GR4726) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4726 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4726 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4726 gene encodes GR4726 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4726 precursor RNA folds spatially, forming GR4726 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4726 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4726 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4726 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM5095 precursor RNA, GAM142548 precursor RNA and GAM206284 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5095 RNA, GAM142548 RNA and GAM206284 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5095 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5095 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5095 target RNA into GAM5095 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM142548 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM142548 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM142548 target RNA into GAM142548 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM206284 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM206284 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM206284 target RNA into GAM206284 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4726 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4726 gene: GAM5095 target protein, GAM142548 target protein and GAM206284 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5095, GAM142548 and GAM206284

GR4727 BG033435 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4727(GR4727) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4727 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4727 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4727 gene encodes GR4727 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4727 precursor RNA folds spatially, forming GR4727 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4727 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4727 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4727 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM60917 precursor RNA, GAM218146 precursor RNA and GAM266264 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM60917 RNA, GAM218146 RNA and GAM266264 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM60917 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM60917 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM60917 target RNA into GAM60917 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM218146 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM218146 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM218146 target RNA into GAM218146 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM266264 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM266264 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM266264 target RNA into GAM266264 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4727 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4727 gene: GAM60917 target protein, GAM218146 target protein and GAM266264 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM60917, GAM218146 and GAM266264

GR4728 BF805533 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4728(GR4728) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4728 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4728 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4728 gene encodes GR4728 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4728 precursor RNA folds spatially, forming GR4728 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4728 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4728 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4728 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM1470 precursor RNA, GAM89031 precursor RNA, GAM151415 precursor RNA and GAM286381 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1470 RNA, GAM89031 RNA, GAM151415 RNA and GAM286381 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1470 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1470 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1470 target RNA into GAM1470 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM89031 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM89031 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM89031 target RNA into GAM89031 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM151415 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM151415 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM151415 target RNA into GAM151415 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM286381 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM286381 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM286381 target RNA into GAM286381 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4728 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4728 gene: GAM1470 target protein, GAM89031 target protein, GAM151415 target protein and GAM286381 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1470, GAM89031, GAM151415 and GAM286381

GR4729 BF904658 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4729(GR4729) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4729 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4729 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4729 gene encodes GR4729 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4729 precursor RNA folds spatially, forming GR4729 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4729 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR4729 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4729 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM291421 precursor RNA and GAM292050 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM291421 RNA and GAM292050 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM291421 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM291421 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM291421 target RNA into GAM291421 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM292050 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM292050 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM292050 target RNA into GAM292050 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4729 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4729 gene: GAM291421 target protein and GAM292050 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM291421 and GAM292050

GR4730 AW242010 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4730(GR4730) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4730 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4730 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4730 gene encodes GR4730 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4730 precursor RNA folds spatially, forming GR4730 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4730 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4730 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4730 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM697 precursor RNA, GAM10933 precursor RNA and GAM132153 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM697 RNA, GAM10933 RNA and GAM132153 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM697 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM697 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM697 target RNA into GAM697 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM10933 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM10933 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM10933 target RNA into GAM10933 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM132153 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM132153 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM132153 target RNA into GAM132153 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4730 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4730 gene: GAM697 target protein, GAM10933 target protein and GAM132153 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM697, GAM10933 and GAM132153

GR4731 BI869938 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4731(GR4731) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4731 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4731 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4731 gene encodes GR4731 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4731 precursor RNA folds spatially, forming GR4731 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4731 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4731 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4731 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM7494 precursor RNA, GAM27049 precursor RNA and GAM99563 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7494 RNA, GAM27049 RNA and GAM99563 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7494 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7494 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7494 target RNA into GAM7494 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM27049 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM27049 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM27049 target RNA into GAM27049 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM99563 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM99563 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM99563 target RNA into GAM99563 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4731 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4731 gene: GAM7494 target protein, GAM27049 target protein and GAM99563 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7494, GAM27049 and GAM99563

GR4732 AI719052 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4732(GR4732) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4732 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4732 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4732 gene encodes GR4732 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4732 precursor RNA folds spatially, forming GR4732 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4732 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4732 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4732 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM167108 precursor RNA, GAM261996 precursor RNA and GAM296958 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM167108 RNA, GAM261996 RNA and GAM296958 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM167108 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM167108 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM167108 target RNA into GAM167108 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM261996 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM261996 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM261996 target RNA into GAM261996 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM296958 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM296958 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM296958

target RNA into GAM296958 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4732 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4732 gene: GAM167108 target protein, GAM261996 target protein and GAM296958 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM167108, GAM261996 and GAM296958

GR4733 BF673270 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4733(GR4733) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4733 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4733 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4733 gene encodes GR4733 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4733 precursor RNA folds spatially, forming GR4733 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4733 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4733 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4733 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5412 precursor RNA and GAM275547 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5412 RNA and GAM275547 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5412 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5412 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5412 target RNA into GAM5412 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM275547 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM275547 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM275547 target RNA into GAM275547 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4733 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4733 gene: GAM5412 target protein and GAM275547 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5412 and GAM275547

GR4734 BG572034 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4734(GR4734) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4734 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4734 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4734 gene encodes GR4734 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4734 precursor RNA folds spatially, forming GR4734 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4734 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4734 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4734 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM197556 precursor RNA and GAM233675 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM197556 RNA and GAM233675 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM197556 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM197556 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM197556 target RNA into GAM197556 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM233675 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM233675 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM233675 target RNA into GAM233675 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4734 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4734 gene: GAM197556 target protein and GAM233675 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM197556 and GAM233675

GR4735 AI949657 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4735(GR4735) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4735 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4735 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4735 gene encodes GR4735 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4735 precursor RNA folds spatially, forming GR4735 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4735 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4735 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4735 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM61383 precursor RNA and GAM84864 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM61383 RNA and GAM84864 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM61383 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM61383 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM61383 target RNA into GAM61383 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM84864 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM84864 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM84864 target RNA into GAM84864 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4735 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4735 gene: GAM61383 target protein and GAM84864 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference,

with references to GAM61383 and GAM84864

GR4736 BE258967 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4736(GR4736) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4736 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4736 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4736 gene encodes GR4736 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4736 precursor RNA folds spatially, forming GR4736 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4736 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4736 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4736 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM319 precursor RNA, GAM190451 precursor RNA and GAM190699 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM319 RNA, GAM190451 RNA and GAM190699 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM319 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM319 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM319 target RNA into GAM319 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM190451 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM190451 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM190451 target RNA into GAM190451 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM190699 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM190699 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM190699 target RNA into GAM190699 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4736 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4736 gene: GAM319 target protein, GAM190451 target protein and GAM190699 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM319, GAM190451 and GAM190699

GR4737 AW590040 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4737(GR4737) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4737 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4737 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4737 gene encodes GR4737 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4737 precursor RNA folds spatially, forming GR4737 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4737 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4737 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4737 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM77526 precursor RNA, GAM130878 precursor RNA and GAM210509 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM77526 RNA, GAM130878 RNA and GAM210509 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM77526 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM77526 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM77526 target RNA into GAM77526 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM130878 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM130878 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM130878 target RNA into GAM130878 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM210509 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM210509 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM210509 target RNA into GAM210509 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4737 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4737 gene: GAM77526 target protein, GAM130878 target protein and GAM210509 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM77526, GAM130878 and GAM210509

4738(GR4738) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4738 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4738 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4738 gene encodes GR4738 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4738 precursor RNA folds spatially, forming GR4738 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4738 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4738 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4738 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM8116 precursor RNA, GAM19975 precursor RNA, GAM220551 precursor RNA and GAM240209 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8116 RNA, GAM19975 RNA, GAM220551 RNA and GAM240209 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8116 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8116 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8116 target RNA into GAM8116 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM19975 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM19975 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM19975

target RNA into GAM19975 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM220551 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM220551 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM220551 target RNA into GAM220551 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM240209 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM240209 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM240209 target RNA into GAM240209 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4738 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4738 gene: GAM8116 target protein, GAM19975 target protein, GAM220551 target protein and GAM240209 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8116, GAM19975, GAM220551 and GAM240209

GR4739 BQ049157 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4739(GR4739) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4739 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4739 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4739 gene encodes GR4739 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4739 precursor RNA folds spatially, forming GR4739 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4739 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4739 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4739 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1629 precursor RNA and GAM241478 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1629 RNA and GAM241478 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1629 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1629 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1629 target RNA into GAM1629 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM241478 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM241478 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM241478 target RNA into GAM241478 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4739 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4739 gene: GAM1629 target protein and GAM241478 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1629 and GAM241478

GR4740 BE542485 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4740(GR4740) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4740 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR4740 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4740 gene encodes GR4740 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4740 precursor RNA folds spatially, forming GR4740 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4740 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4740 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4740 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM191415 precursor RNA, GAM268878 precursor RNA and GAM328110 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM191415 RNA, GAM268878 RNA and GAM328110 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM191415 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM191415 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM191415 target RNA into GAM191415 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM268878 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM268878 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM268878 target RNA into GAM268878 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM328110 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM328110 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM328110 target RNA into GAM328110 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4740 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4740 gene: GAM191415 target protein, GAM268878 target protein and GAM328110 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM191415, GAM268878 and GAM328110

GR4741 N62122 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4741(GR4741) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4741 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4741 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4741 gene encodes GR4741 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4741 precursor RNA folds spatially, forming GR4741 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4741 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4741 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4741 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM167387 precursor RNA, GAM209074 precursor RNA and GAM226943 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM167387 RNA, GAM209074 RNA and GAM226943 RNA, herein

schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM167387 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM167387 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM167387 target RNA into GAM167387 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM209074 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM209074 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM209074 target RNA into GAM209074 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM226943 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM226943 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM226943 target RNA into GAM226943 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4741 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4741 gene: GAM167387 target protein, GAM209074 target protein and GAM226943 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM167387, GAM209074 and GAM226943

GR4742 AW051687 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4742(GR4742) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4742 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4742 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4742 gene encodes GR4742 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4742 precursor RNA folds spatially, forming GR4742 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4742 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4742 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4742 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM20341 precursor RNA and GAM134096 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM20341 RNA and GAM134096 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM20341 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM20341 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM20341 target RNA into GAM20341 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM134096 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM134096 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM134096 target RNA into GAM134096 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4742 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4742 gene: GAM20341 target protein and GAM134096 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM20341 and GAM134096

GR4743 AA430291 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4743(GR4743) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4743 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4743 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4743 gene encodes GR4743 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4743 precursor RNA folds spatially, forming GR4743 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4743 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4743 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4743 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM110882 precursor RNA and GAM268479 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM110882 RNA and GAM268479 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM110882 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM110882 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM110882 target RNA into GAM110882 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM268479 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM268479 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM268479 target RNA into GAM268479 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4743 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4743 gene: GAM110882 target protein and GAM268479 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM110882 and GAM268479

GR4744 BG977700 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4744(GR4744) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4744 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4744 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4744 gene encodes GR4744 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4744 precursor RNA folds spatially, forming GR4744 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4744 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4744 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4744 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM5801 precursor RNA, GAM8704 precursor RNA and GAM81069 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5801 RNA, GAM8704 RNA and GAM81069 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs

corresponding to GAM RNA of Fig. 8.

GAM5801 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5801 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5801 target RNA into GAM5801 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8704 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8704 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8704 target RNA into GAM8704 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM81069 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM81069 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM81069 target RNA into GAM81069 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4744 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4744 gene: GAM5801 target protein, GAM8704 target protein and GAM81069 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5801, GAM8704 and GAM81069

GR4745 BM017552 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4745(GR4745) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4745 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4745 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4745 gene encodes GR4745 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR4745 precursor RNA folds spatially, forming GR4745 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4745 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4745 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4745 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2933 precursor RNA, GAM3817 precursor RNA and GAM269278 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2933 RNA, GAM3817 RNA and GAM269278 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2933 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2933 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2933 target RNA into GAM2933 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM3817 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3817 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3817 target RNA into GAM3817 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM269278 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM269278 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM269278 target RNA into GAM269278 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4745 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4745 gene: GAM2933 target protein, GAM3817 target protein and GAM269278 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2933, GAM3817 and GAM269278

GR4746 BE621282 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4746(GR4746) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4746 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4746 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4746 gene encodes GR4746 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4746 precursor RNA folds spatially, forming GR4746 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4746 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4746 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4746 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM228526 precursor RNA and GAM269218 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM228526 RNA and GAM269218 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM228526 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM228526 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM228526 target RNA into GAM228526 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM269218 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM269218 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM269218 target RNA into GAM269218 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4746 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4746 gene: GAM228526 target protein and GAM269218 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM228526 and GAM269218

GR4747 AI798225 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4747(GR4747) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4747 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4747 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4747 gene encodes GR4747 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4747 precursor RNA folds spatially, forming GR4747 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4747 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4747 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4747 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM156741 precursor RNA and GAM229411 precursor

RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM156741 RNA and GAM229411 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM156741 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM156741 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM156741 target RNA into GAM156741 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM229411 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM229411 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM229411 target RNA into GAM229411 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4747 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4747 gene: GAM156741 target protein and GAM229411 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM156741 and GAM229411

GR4748 BF801932 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4748(GR4748) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4748 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4748 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4748 gene encodes GR4748 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4748 precursor RNA folds spatially, forming GR4748 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4748 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4748 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4748 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM108723 precursor RNA and GAM242429 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM108723 RNA and GAM242429 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM108723 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM108723 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM108723 target RNA into GAM108723 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM242429 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM242429 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM242429 target RNA into GAM242429 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4748 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4748 gene: GAM108723 target protein and GAM242429 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM108723 and GAM242429

bioinformatically detected regulatory gene, referred to here as Genomic Record 4749(GR4749) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4749 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4749 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4749 gene encodes GR4749 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4749 precursor RNA folds spatially, forming GR4749 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4749 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4749 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4749 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8091 precursor RNA and GAM274616 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8091 RNA and GAM274616 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8091 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8091 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8091 target RNA into GAM8091 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM274616 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM274616 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM274616

target RNA into GAM274616 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4749 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4749 gene: GAM8091 target protein and GAM274616 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8091 and GAM274616

GR4750 BM562569 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4750(GR4750) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4750 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4750 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4750 gene encodes GR4750 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4750 precursor RNA folds spatially, forming GR4750 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4750 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4750 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4750 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM19891 precursor RNA, GAM94907 precursor RNA and GAM256689 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM19891 RNA, GAM94907 RNA and GAM256689 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM19891 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM19891 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM19891 target RNA into GAM19891 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM94907 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM94907 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM94907 target RNA into GAM94907 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM256689 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM256689 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM256689 target RNA into GAM256689 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4750 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4750 gene: GAM19891 target protein, GAM94907 target protein and GAM256689 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM19891, GAM94907 and GAM256689

GR4751 BF664089 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4751 (GR4751) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4751 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4751 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4751 gene encodes GR4751 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4751 precursor RNA folds spatially, forming GR4751 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4751 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4751 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4751 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM107942 precursor RNA, GAM243666 precursor RNA and GAM247583 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM107942 RNA, GAM243666 RNA and GAM247583 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM107942 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM107942 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM107942 target RNA into GAM107942 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM243666 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM243666 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM243666 target RNA into GAM243666 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM247583 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM247583 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM247583 target RNA into GAM247583 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4751 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4751 gene: GAM107942 target protein, GAM243666 target protein and GAM247583 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM107942, GAM243666 and GAM247583

GR4752 AW952424 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4752(GR4752) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4752 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4752 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4752 gene encodes GR4752 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4752 precursor RNA folds spatially, forming GR4752 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4752 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4752 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4752 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3070 precursor RNA and GAM35478 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3070 RNA and GAM35478 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3070 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3070 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig. 8, thereby inhibiting translation of GAM3070 target RNA into GAM3070 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM35478 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM35478 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM35478 target RNA into GAM35478 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4752 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4752 gene: GAM3070 target protein and GAM35478 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3070 and GAM35478

GR4753 BG118811 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4753(GR4753) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4753 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4753 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4753 gene encodes GR4753 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4753 precursor RNA folds spatially, forming GR4753 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4753 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4753 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4753 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5348 precursor RNA and GAM8431 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin

shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5348 RNA and GAM8431 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5348 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5348 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5348 target RNA into GAM5348 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8431 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8431 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8431 target RNA into GAM8431 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4753 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4753 gene: GAM5348 target protein and GAM8431 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5348 and GAM8431

GR4754 BF059145 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4754(GR4754) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4754 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4754 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4754 gene encodes GR4754 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4754 precursor RNA folds spatially, forming GR4754 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4754 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4754 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4754 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM62295 precursor RNA, GAM129650 precursor RNA and GAM292037 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM62295 RNA, GAM129650 RNA and GAM292037 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM62295 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM62295 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM62295 target RNA into GAM62295 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM129650 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM129650 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM129650 target RNA into GAM129650 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM292037 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM292037 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM292037 target RNA into GAM292037 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4754 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR4754 gene: GAM62295 target protein, GAM129650 target protein and GAM292037 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM62295, GAM129650 and GAM292037

GR4755 BM013325 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4755(GR4755) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4755 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4755 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4755 gene encodes GR4755 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4755 precursor RNA folds spatially, forming GR4755 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4755 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4755 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4755 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM80683 precursor RNA, GAM123377 precursor RNA and GAM227224 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM80683 RNA, GAM123377 RNA and GAM227224 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM80683 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM80683 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM80683 target RNA into GAM80683 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM123377 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM123377 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM123377 target RNA into GAM123377 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM227224 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM227224 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM227224 target RNA into GAM227224 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4755 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4755 gene: GAM80683 target protein, GAM123377 target protein and GAM227224 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM80683, GAM123377 and GAM227224

GR4756 BF975738 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4756(GR4756) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4756 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4756 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4756 gene encodes GR4756 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4756 precursor RNA folds spatially, forming GR4756 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4756 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4756 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4756 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM158562 precursor RNA and GAM270021 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM158562 RNA and GAM270021 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM158562 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM158562 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM158562 target RNA into GAM158562 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM270021 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM270021 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM270021 target RNA into GAM270021 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4756 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4756 gene: GAM158562 target protein and GAM270021 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM158562 and GAM270021

GR4757 BG678970 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4757(GR4757) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4757 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4757 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4757 gene encodes GR4757 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4757 precursor RNA folds spatially, forming GR4757 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4757 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4757 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4757 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM35515 precursor RNA, GAM41497 precursor RNA and GAM231309 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM35515 RNA, GAM41497 RNA and GAM231309 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM35515 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM35515 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM35515 target RNA into GAM35515 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM41497 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM41497 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM41497 target RNA into GAM41497 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM231309 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM231309 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM231309 target RNA into GAM231309 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4757 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4757 gene: GAM35515 target protein, GAM41497 target protein and GAM231309 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM35515, GAM41497 and GAM231309

GR4758 AL045610 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4758(GR4758) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4758 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4758 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4758 gene encodes GR4758 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4758 precursor RNA folds spatially, forming GR4758 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4758 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4758 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4758 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM32196 precursor RNA and GAM312271 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM32196 RNA and GAM312271 RNA, herein schematically

represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM32196 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM32196 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM32196 target RNA into GAM32196 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM312271 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM312271 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM312271 target RNA into GAM312271 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4758 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4758 gene: GAM32196 target protein and GAM312271 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM32196 and GAM312271

GR4759 BE208652 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4759(GR4759) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4759 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4759 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4759 gene encodes GR4759 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4759 precursor RNA folds spatially, forming GR4759 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4759 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4759 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4759 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3685 precursor RNA and GAM7646 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3685 RNA and GAM7646 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3685 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3685 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3685 target RNA into GAM3685 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7646 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7646 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7646 target RNA into GAM7646 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4759 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4759 gene: GAM3685 target protein and GAM7646 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3685 and GAM7646

GR4760 BG944110 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4760(GR4760) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4760 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR4760 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4760 gene encodes GR4760 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4760 precursor RNA folds spatially, forming GR4760 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4760 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4760 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4760 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM47046 precursor RNA and GAM207746 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM47046 RNA and GAM207746 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM47046 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM47046 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM47046 target RNA into GAM47046 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM207746 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM207746 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM207746 target RNA into GAM207746 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4760 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4760 gene: GAM47046 target

protein and GAM207746 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM47046 and GAM207746

GR4761 AI207560 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4761 (GR4761) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4761 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4761 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4761 gene encodes GR4761 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4761 precursor RNA folds spatially, forming GR4761 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4761 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4761 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4761 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3103 precursor RNA and GAM271856 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3103 RNA and GAM271856 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3103 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3103 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3103 target RNA into GAM3103 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM271856 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM271856 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM271856 target RNA into GAM271856 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4761 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4761 gene: GAM3103 target protein and GAM271856 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3103 and GAM271856

GR4762 AA713777 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4762(GR4762) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4762 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4762 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4762 gene encodes GR4762 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4762 precursor RNA folds spatially, forming GR4762 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4762 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4762 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4762 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM136432 precursor RNA and GAM141470 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM136432 RNA and GAM141470 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM136432 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM136432 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM136432 target RNA into GAM136432 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM141470 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM141470 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM141470 target RNA into GAM141470 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4762 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4762 gene: GAM136432 target protein and GAM141470 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM136432 and GAM141470

GR4763 BE394725 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4763(GR4763) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4763 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4763 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4763 gene encodes GR4763 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4763 precursor RNA folds spatially, forming GR4763 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4763 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR4763 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4763 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM191260 precursor RNA and GAM267250 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM191260 RNA and GAM267250 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM191260 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM191260 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM191260 target RNA into GAM191260 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM267250 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM267250 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM267250 target RNA into GAM267250 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4763 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4763 gene: GAM191260 target protein and GAM267250 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM191260 and GAM267250

GR4764 BF088450 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4764(GR4764) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4764 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4764 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4764 gene encodes GR4764 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4764 precursor RNA folds spatially, forming GR4764 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4764 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4764 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4764 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2330 precursor RNA, GAM3856 precursor RNA and GAM109360 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2330 RNA, GAM3856 RNA and GAM109360 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2330 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2330 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2330 target RNA into GAM2330 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM3856 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3856 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3856 target RNA into GAM3856 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM109360 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM109360 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM109360 target RNA into GAM109360 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4764 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4764 gene: GAM2330 target protein, GAM3856 target protein and GAM109360 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2330, GAM3856 and GAM109360

GR4765 R34642 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4765(GR4765) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4765 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4765 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4765 gene encodes GR4765 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4765 precursor RNA folds spatially, forming GR4765 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4765 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4765 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4765 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5930 precursor RNA and GAM105956 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM5930 RNA and GAM105956 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5930 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5930 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5930 target RNA into GAM5930 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM105956 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM105956 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM105956 target RNA into GAM105956 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4765 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4765 gene: GAM5930 target protein and GAM105956 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5930 and GAM105956

GR4766 BE163359 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4766(GR4766) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4766 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4766 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4766 gene encodes GR4766 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4766 precursor RNA folds spatially, forming GR4766 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4766 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4766 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4766 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2788 precursor RNA and GAM103327 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2788 RNA and GAM103327 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2788 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2788 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2788 target RNA into GAM2788 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM103327 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM103327 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM103327 target RNA into GAM103327 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4766 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4766 gene: GAM2788 target protein and GAM103327 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2788 and GAM103327

GR4767 BF668133 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4767(GR4767) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4767 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4767 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4767 gene encodes GR4767 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4767 precursor RNA folds spatially, forming GR4767 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4767 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4767 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4767 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2091 precursor RNA and GAM173386 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2091 RNA and GAM173386 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2091 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2091 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2091 target RNA into GAM2091 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM173386 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM173386 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM173386 target RNA into GAM173386 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4767 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR4767 gene: GAM2091 target protein and GAM173386 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2091 and GAM173386

GR4768 BI754338 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4768(GR4768) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4768 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4768 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4768 gene encodes GR4768 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4768 precursor RNA folds spatially, forming GR4768 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4768 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4768 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4768 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM64921 precursor RNA and GAM243990 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM64921 RNA and GAM243990 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM64921 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM64921 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM64921 target RNA into GAM64921 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM243990 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM243990 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM243990 target RNA into GAM243990 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4768 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4768 gene: GAM64921 target protein and GAM243990 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM64921 and GAM243990

GR4769 AV700343 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4769(GR4769) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4769 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4769 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4769 gene encodes GR4769 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4769 precursor RNA folds spatially, forming GR4769 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4769 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4769 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4769 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM5870 precursor RNA, GAM96397 precursor RNA, GAM180150 precursor RNA and GAM211368 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5870 RNA, GAM96397 RNA, GAM180150 RNA and GAM211368 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5870 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5870 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5870 target RNA into GAM5870 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM96397 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM96397 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM96397 target RNA into GAM96397 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM180150 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM180150 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM180150 target RNA into GAM180150 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM211368 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM211368 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM211368 target RNA into GAM211368 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4769 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4769 gene: GAM5870 target protein, GAM96397 target protein, GAM180150 target protein and GAM211368 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5870, GAM96397, GAM180150 and GAM211368

GR4770 BE747266 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4770(GR4770) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4770 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4770 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4770 gene encodes GR4770 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4770 precursor RNA folds spatially, forming GR4770 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4770 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4770 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4770 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4906 precursor RNA and GAM149779 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4906 RNA and GAM149779 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4906 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4906 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4906 target RNA into GAM4906 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM149779 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM149779 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM149779 target RNA into GAM149779 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4770 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4770 gene: GAM4906 target protein and GAM149779 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4906 and GAM149779

GR4771 BI259532 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4771 (GR4771) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4771 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4771 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4771 gene encodes GR4771 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4771 precursor RNA folds spatially, forming GR4771 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4771 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4771 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4771 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM52560 precursor RNA and GAM198472 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM52560 RNA and GAM198472 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM52560 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM52560 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM52560 target RNA into GAM52560 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM198472 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM198472 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM198472 target RNA into GAM198472 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4771 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4771 gene: GAM52560 target protein and GAM198472 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM52560 and GAM198472

GR4772 AW157423 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4772(GR4772) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4772 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4772 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4772 gene encodes GR4772 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4772 precursor RNA folds spatially, forming GR4772 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4772 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4772 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4772 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM76 precursor RNA, GAM3939 precursor RNA and GAM74221 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM76 RNA, GAM3939 RNA and GAM74221 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM76 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM76 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM76 target RNA into GAM76 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM3939 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3939 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3939 target RNA into GAM3939 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM74221 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM74221 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM74221 target RNA into GAM74221 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4772 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4772 gene: GAM76 target protein, GAM3939 target protein and GAM74221 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM76, GAM3939 and GAM74221

bioinformatically detected regulatory gene, referred to here as Genomic Record 4773(GR4773) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4773 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4773 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4773 gene encodes GR4773 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4773 precursor RNA folds spatially, forming GR4773 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4773 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4773 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4773 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM864 precursor RNA, GAM6806 precursor RNA and GAM252422 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM864 RNA, GAM6806 RNA and GAM252422 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM864 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM864 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM864 target RNA into GAM864 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6806 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6806 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig. 8, thereby inhibiting translation of GAM6806 target RNA into GAM6806 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM252422 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM252422 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM252422 target RNA into GAM252422 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4773 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4773 gene: GAM864 target protein, GAM6806 target protein and GAM252422 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM864, GAM6806 and GAM252422

GR4774 AI809777 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4774(GR4774) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4774 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4774 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4774 gene encodes GR4774 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4774 precursor RNA folds spatially, forming GR4774 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4774 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4774 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4774 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2089 precursor RNA and GAM200473 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3

FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2089 RNA and GAM200473 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2089 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2089 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2089 target RNA into GAM2089 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM200473 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM200473 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM200473 target RNA into GAM200473 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4774 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4774 gene: GAM2089 target protein and GAM200473 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2089 and GAM200473

GR4775 AI494407 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4775(GR4775) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4775 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4775 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4775 gene encodes GR4775 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4775 precursor RNA folds spatially, forming GR4775 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4775 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4775 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4775 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM165868 precursor RNA and GAM290063 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM165868 RNA and GAM290063 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM165868 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM165868 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM165868 target RNA into GAM165868 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM290063 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM290063 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM290063 target RNA into GAM290063 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4775 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4775 gene: GAM165868 target protein and GAM290063 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM165868 and GAM290063

4776(GR4776) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4776 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4776 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4776 gene encodes GR4776 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4776 precursor RNA folds spatially, forming GR4776 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4776 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4776 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4776 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM54681 precursor RNA and GAM253704 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM54681 RNA and GAM253704 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM54681 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM54681 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM54681 target RNA into GAM54681 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM253704 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM253704 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM253704 target RNA into GAM253704 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4776 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4776 gene: GAM54681 target protein and GAM253704 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM54681 and GAM253704

GR4777 BG288082 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4777(GR4777) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4777 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4777 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4777 gene encodes GR4777 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4777 precursor RNA folds spatially, forming GR4777 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4777 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4777 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4777 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM147144 precursor RNA, GAM157801 precursor RNA and GAM246404 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM147144 RNA, GAM157801 RNA and GAM246404 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM147144 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM147144 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM147144 target RNA into GAM147144 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM157801 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM157801 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM157801 target RNA into GAM157801 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM246404 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM246404 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM246404 target RNA into GAM246404 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4777 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4777 gene: GAM147144 target protein, GAM157801 target protein and GAM246404 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM147144, GAM157801 and GAM246404.

GR4778 AL526187 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4778(GR4778) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4778 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4778 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4778 gene encodes GR4778 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4778 precursor RNA folds spatially, forming GR4778 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4778 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4778 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4778 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM6785 precursor RNA, GAM81021 precursor RNA, GAM108994 precursor RNA and GAM237182 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6785 RNA, GAM81021 RNA, GAM108994 RNA and GAM237182 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6785 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6785 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6785 target RNA into GAM6785 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM81021 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM81021 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM81021 target RNA into GAM81021 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM108994 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM108994 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM108994 target RNA into GAM108994 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM237182 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM237182 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM237182 target RNA into GAM237182 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4778 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4778 gene: GAM6785 target protein, GAM81021 target protein, GAM108994 target protein and GAM237182 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6785, GAM81021, GAM108994 and GAM237182

GR4779 BG122893 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4779(GR4779) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4779 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4779 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4779 gene encodes GR4779 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4779 precursor RNA folds spatially, forming GR4779 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4779 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4779 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4779 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM7640 precursor RNA, GAM24342 precursor RNA and GAM255422 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7640 RNA, GAM24342 RNA and GAM255422 RNA, herein

schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7640 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7640 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7640 target RNA into GAM7640 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM24342 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM24342 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM24342 target RNA into GAM24342 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM255422 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM255422 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM255422 target RNA into GAM255422 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4779 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4779 gene: GAM7640 target protein, GAM24342 target protein and GAM255422 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7640, GAM24342 and GAM255422

GR4780 R54333 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4780(GR4780) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4780 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4780 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4780 gene encodes GR4780 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4780 precursor RNA folds spatially, forming GR4780 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4780 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4780 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4780 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM95149 precursor RNA, GAM247291 precursor RNA and GAM253340 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM95149 RNA, GAM247291 RNA and GAM253340 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM95149 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM95149 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM95149 target RNA into GAM95149 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM247291 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM247291 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM247291 target RNA into GAM247291 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM253340 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM253340 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM253340 target RNA into GAM253340 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4780 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4780 gene: GAM95149 target protein, GAM247291 target protein and GAM253340 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM95149, GAM247291 and GAM253340

GR4781 BI667317 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4781(GR4781) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4781 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4781 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4781 gene encodes GR4781 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4781 precursor RNA folds spatially, forming GR4781 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4781 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4781 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4781 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1724 precursor RNA and GAM175511 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1724 RNA and GAM175511 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1724 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM1724 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1724 target RNA into GAM1724 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM175511 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM175511 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM175511 target RNA into GAM175511 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4781 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4781 gene: GAM1724 target protein and GAM175511 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1724 and GAM175511

GR4782 BM007851 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4782(GR4782) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4782 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4782 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4782 gene encodes GR4782 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4782 precursor RNA folds spatially, forming GR4782 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4782 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4782 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4782 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3

separate GAM precursor RNAs, GAM4956 precursor RNA, GAM7858 precursor RNA and GAM231030 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4956 RNA, GAM7858 RNA and GAM231030 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4956 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4956 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4956 target RNA into GAM4956 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7858 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7858 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7858 target RNA into GAM7858 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM231030 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM231030 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM231030 target RNA into GAM231030 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4782 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4782 gene: GAM4956 target protein, GAM7858 target protein and GAM231030 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4956, GAM7858 and GAM231030

GR4783 BF030004 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4783(GR4783) gene, which encodes an `operon-like` cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4783 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4783 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4783 gene encodes GR4783 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4783 precursor RNA folds spatially, forming GR4783 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4783 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4783 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4783 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2035 precursor RNA and GAM76849 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2035 RNA and GAM76849 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2035 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2035 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2035 target RNA into GAM2035 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM76849 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM76849 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM76849 target RNA into GAM76849 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4783 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4783 gene: GAM2035 target protein and GAM76849 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2035 and GAM76849

GR4784 BE502408 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4784(GR4784) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4784 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4784 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4784 gene encodes GR4784 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4784 precursor RNA folds spatially, forming GR4784 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4784 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4784 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4784 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8228 precursor RNA and GAM241971 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8228 RNA and GAM241971 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8228 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8228 target RNA, herein schematically represented by

GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8228 target RNA into GAM8228 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM241971 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM241971 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM241971 target RNA into GAM241971 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4784 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4784 gene: GAM8228 target protein and GAM241971 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8228 and GAM241971

GR4785 T89989 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4785(GR4785) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4785 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4785 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4785 gene encodes GR4785 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4785 precursor RNA folds spatially, forming GR4785 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4785 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4785 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4785 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM31860 precursor RNA and GAM295448 precursor

RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM31860 RNA and GAM295448 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM31860 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM31860 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM31860 target RNA into GAM31860 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM295448 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM295448 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM295448 target RNA into GAM295448 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4785 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4785 gene: GAM31860 target protein and GAM295448 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM31860 and GAM295448

GR4786 BF793453 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4786(GR4786) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4786 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4786 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4786 gene encodes GR4786 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4786 precursor RNA folds spatially, forming GR4786 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4786 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4786 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4786 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM155526 precursor RNA and GAM241986 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM155526 RNA and GAM241986 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM155526 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM155526 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM155526 target RNA into GAM155526 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM241986 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM241986 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM241986 target RNA into GAM241986 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4786 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4786 gene: GAM155526 target protein and GAM241986 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM155526 and GAM241986

bioinformatically detected regulatory gene, referred to here as Genomic Record 4787(GR4787) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4787 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4787 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4787 gene encodes GR4787 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4787 precursor RNA folds spatially, forming GR4787 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4787 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4787 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4787 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM97484 precursor RNA, GAM101339 precursor RNA and GAM295029 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM97484 RNA, GAM101339 RNA and GAM295029 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM97484 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM97484 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM97484 target RNA into GAM97484 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM101339 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM101339 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM101339 target RNA into GAM101339 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM295029 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM295029 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM295029 target RNA into GAM295029 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4787 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4787 gene: GAM97484 target protein, GAM101339 target protein and GAM295029 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM97484, GAM101339 and GAM295029

GR4788 AA235667 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4788(GR4788) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4788 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4788 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4788 gene encodes GR4788 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4788 precursor RNA folds spatially, forming GR4788 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4788 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4788 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4788 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3335 precursor RNA, GAM113409 precursor RNA and GAM291742 precursor RNA, herein schematically represented by GAM1 FOLDED

PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3335 RNA, GAM113409 RNA and GAM291742 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3335 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3335 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3335 target RNA into GAM3335 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM113409 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM113409 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM113409 target RNA into GAM113409 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM291742 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM291742 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM291742 target RNA into GAM291742 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4788 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4788 gene: GAM3335 target protein, GAM113409 target protein and GAM291742 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3335, GAM113409 and GAM291742

GR4789 BE387922 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4789(GR4789) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR4789 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4789 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4789 gene encodes GR4789 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4789 precursor RNA folds spatially, forming GR4789 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4789 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4789 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4789 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM6977 precursor RNA, GAM59135 precursor RNA and GAM319674 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6977 RNA, GAM59135 RNA and GAM319674 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6977 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6977 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6977 target RNA into GAM6977 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM59135 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM59135 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM59135 target RNA into GAM59135 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM319674 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM319674 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM319674 target RNA into GAM319674 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4789 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4789 gene: GAM6977 target protein, GAM59135 target protein and GAM319674 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6977, GAM59135 and GAM319674

GR4790 AA489858 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4790(GR4790) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4790 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4790 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4790 gene encodes GR4790 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4790 precursor RNA folds spatially, forming GR4790 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4790 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4790 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4790 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM13935 precursor RNA and GAM199386 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM13935 RNA and GAM199386 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM13935 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM13935 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM13935 target RNA into GAM13935 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM199386 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM199386 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM199386 target RNA into GAM199386 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4790 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4790 gene: GAM13935 target protein and GAM199386 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM13935 and GAM199386

GR4791 Z19096 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4791(GR4791) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4791 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4791 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4791 gene encodes GR4791 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4791 precursor RNA folds spatially, forming GR4791 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4791 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR4791 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4791 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM977 precursor RNA, GAM2125 precursor RNA and GAM4935 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM977 RNA, GAM2125 RNA and GAM4935 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM977 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM977 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM977 target RNA into GAM977 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM2125 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2125 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2125 target RNA into GAM2125 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM4935 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4935 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4935 target RNA into GAM4935 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4791 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4791 gene: GAM977 target protein, GAM2125 target protein and GAM4935 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN.

The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM977, GAM2125 and GAM4935

GR4792 BE717341 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4792(GR4792) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4792 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4792 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4792 gene encodes GR4792 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4792 precursor RNA folds spatially, forming GR4792 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4792 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4792 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4792 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM171499 precursor RNA and GAM317621 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM171499 RNA and GAM317621 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM171499 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM171499 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM171499 target RNA into GAM171499 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM317621 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM317621 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM317621 target RNA into GAM317621 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4792 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4792 gene: GAM171499 target protein and GAM317621 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM171499 and GAM317621

GR4793 BI772182 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4793(GR4793) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4793 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4793 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4793 gene encodes GR4793 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4793 precursor RNA folds spatially, forming GR4793 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4793 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4793 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4793 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM470 precursor RNA and GAM31657 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM470 RNA and GAM31657 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM470 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM470 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM470 target RNA into GAM470 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM31657 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM31657 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM31657 target RNA into GAM31657 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4793 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4793 gene: GAM470 target protein and GAM31657 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM470 and GAM31657

GR4794 AA157899 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4794(GR4794) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4794 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4794 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4794 gene encodes GR4794 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4794 precursor RNA folds spatially, forming GR4794 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4794 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4794 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4794 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM114570 precursor RNA and GAM286056 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM114570 RNA and GAM286056 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM114570 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM114570 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM114570 target RNA into GAM114570 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM286056 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM286056 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM286056 target RNA into GAM286056 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4794 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4794 gene: GAM114570 target protein and GAM286056 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM114570 and GAM286056

GR4795 BG746692 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4795(GR4795) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4795 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4795 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4795 gene encodes GR4795 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4795 precursor RNA folds spatially, forming GR4795 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4795 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4795 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4795 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM6117 precursor RNA, GAM25205 precursor RNA and GAM227621 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6117 RNA, GAM25205 RNA and GAM227621 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6117 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6117 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6117 target RNA into GAM6117 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM25205 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM25205 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM25205 target RNA into GAM25205 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM227621 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM227621 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM227621 target RNA into GAM227621 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4795 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4795 gene: GAM6117 target protein, GAM25205 target protein and GAM227621 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6117, GAM25205 and GAM227621

GR4796 AI984807 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4796(GR4796) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4796 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4796 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4796 gene encodes GR4796 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4796 precursor RNA folds spatially, forming GR4796 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4796 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4796 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4796 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM71761 precursor RNA and GAM254677 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM71761 RNA and GAM254677 RNA, herein schematically

represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM71761 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM71761 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM71761 target RNA into GAM71761 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM254677 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM254677 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM254677 target RNA into GAM254677 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4796 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4796 gene: GAM71761 target protein and GAM254677 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM71761 and GAM254677

GR4797 BI003062 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4797(GR4797) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4797 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4797 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4797 gene encodes GR4797 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4797 precursor RNA folds spatially, forming GR4797 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4797 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4797 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4797 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM725 precursor RNA, GAM7490 precursor RNA, GAM48942 precursor RNA and GAM240617 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM725 RNA, GAM7490 RNA, GAM48942 RNA and GAM240617 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM725 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM725 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM725 target RNA into GAM725 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7490 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7490 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7490 target RNA into GAM7490 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM48942 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM48942 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM48942 target RNA into GAM48942 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM240617 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM240617 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM240617 target RNA into GAM240617 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4797 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4797 gene: GAM725 target protein, GAM7490 target protein, GAM48942 target protein and GAM240617 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM725, GAM7490, GAM48942 and GAM240617

GR4798 AA448490 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4798(GR4798) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4798 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4798 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4798 gene encodes GR4798 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4798 precursor RNA folds spatially, forming GR4798 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4798 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4798 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4798 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM712 precursor RNA, GAM4931 precursor RNA and GAM124475 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM712 RNA, GAM4931 RNA and GAM124475 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM712 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM712 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM712 target RNA into GAM712 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM4931 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4931 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4931 target RNA into GAM4931 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM124475 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM124475 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM124475 target RNA into GAM124475 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4798 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4798 gene: GAM712 target protein, GAM4931 target protein and GAM124475 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM712, GAM4931 and GAM124475

GR4799 BG617170 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4799(GR4799) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4799 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4799 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4799 gene encodes GR4799 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4799 precursor RNA folds spatially, forming GR4799 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated

that GR4799 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4799 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4799 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM202130 precursor RNA, GAM284130 precursor RNA and GAM297704 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM202130 RNA, GAM284130 RNA and GAM297704 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM202130 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM202130 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM202130 target RNA into GAM202130 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM284130 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM284130 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM284130 target RNA into GAM284130 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM297704 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM297704 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM297704 target RNA into GAM297704 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4799 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4799 gene: GAM202130 target

protein, GAM284130 target protein and GAM297704 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM202130, GAM284130 and GAM297704

GR4800 AA984394 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4800(GR4800) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4800 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4800 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4800 gene encodes GR4800 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4800 precursor RNA folds spatially, forming GR4800 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4800 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4800 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4800 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2725 precursor RNA, GAM6612 precursor RNA and GAM83245 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2725 RNA, GAM6612 RNA and GAM83245 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2725 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2725 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2725 target RNA into

GAM2725 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6612 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6612 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6612 target RNA into GAM6612 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM83245 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM83245 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM83245 target RNA into GAM83245 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4800 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4800 gene: GAM2725 target protein, GAM6612 target protein and GAM83245 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2725, GAM6612 and GAM83245

GR4801 AW084816 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4801(GR4801) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4801 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4801 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4801 gene encodes GR4801 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4801 precursor RNA folds spatially, forming GR4801 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4801 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4801 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4801 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM110149 precursor RNA, GAM304239 precursor RNA and GAM304748 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM110149 RNA, GAM304239 RNA and GAM304748 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM110149 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM110149 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM110149 target RNA into GAM110149 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM304239 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM304239 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM304239 target RNA into GAM304239 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM304748 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM304748 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM304748 target RNA into GAM304748 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4801 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4801 gene: GAM110149 target protein, GAM304239 target protein and GAM304748 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM110149, GAM304239 and

GR4802 BE141380 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4802(GR4802) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4802 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4802 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4802 gene encodes GR4802 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4802 precursor RNA folds spatially, forming GR4802 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4802 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4802 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4802 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM53280 precursor RNA, GAM272251 precursor RNA and GAM315500 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM53280 RNA, GAM272251 RNA and GAM315500 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM53280 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM53280 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM53280 target RNA into GAM53280 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM272251 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM272251 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM272251 target RNA into GAM272251 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM315500 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM315500 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM315500 target RNA into GAM315500 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4802 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4802 gene: GAM53280 target protein, GAM272251 target protein and GAM315500 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM53280, GAM272251 and GAM315500

GR4803 BG474477 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4803(GR4803) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4803 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4803 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4803 gene encodes GR4803 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4803 precursor RNA folds spatially, forming GR4803 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4803 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4803 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4803 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM64510 precursor RNA, GAM233701 precursor RNA and GAM241465 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM64510 RNA, GAM233701 RNA and GAM241465 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM64510 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM64510 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM64510 target RNA into GAM64510 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM233701 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM233701 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM233701 target RNA into GAM233701 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM241465 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM241465 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM241465 target RNA into GAM241465 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4803 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4803 gene: GAM64510 target protein, GAM233701 target protein and GAM241465 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM64510, GAM233701 and GAM241465

4804(GR4804) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4804 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4804 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4804 gene encodes GR4804 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4804 precursor RNA folds spatially, forming GR4804 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4804 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4804 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4804 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM55878 precursor RNA and GAM79246 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM55878 RNA and GAM79246 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM55878 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM55878 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM55878 target RNA into GAM55878 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM79246 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM79246 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM79246 target RNA into GAM79246 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4804 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4804 gene: GAM55878 target protein and GAM79246 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM55878 and GAM79246

GR4805 AA729530 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4805(GR4805) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4805 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4805 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4805 gene encodes GR4805 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4805 precursor RNA folds spatially, forming GR4805 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4805 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4805 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4805 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5985 precursor RNA and GAM14474 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5985 RNA and GAM14474 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5985 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM5985 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5985 target RNA into GAM5985 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM14474 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM14474 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM14474 target RNA into GAM14474 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4805 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4805 gene: GAM5985 target protein and GAM14474 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5985 and GAM14474

GR4806 BG928616 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4806(GR4806) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4806 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4806 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4806 gene encodes GR4806 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4806 precursor RNA folds spatially, forming GR4806 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4806 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4806 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4806 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2

separate GAM precursor RNAs, GAM5406 precursor RNA and GAM35375 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5406 RNA and GAM35375 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5406 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5406 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5406 target RNA into GAM5406 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM35375 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM35375 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM35375 target RNA into GAM35375 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4806 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4806 gene: GAM5406 target protein and GAM35375 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5406 and GAM35375

GR4807 R18886 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4807(GR4807) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4807 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4807 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4807 gene encodes GR4807 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR4807 precursor RNA folds spatially, forming GR4807 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4807 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4807 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4807 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM142870 precursor RNA and GAM214711 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM142870 RNA and GAM214711 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM142870 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM142870 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM142870 target RNA into GAM142870 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM214711 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM214711 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM214711 target RNA into GAM214711 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4807 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4807 gene: GAM142870 target protein and GAM214711 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM142870 and GAM214711

GR4808 BF932798 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4808(GR4808) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4808 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4808 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4808 gene encodes GR4808 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4808 precursor RNA folds spatially, forming GR4808 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4808 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4808 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4808 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM162453 precursor RNA and GAM316315 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM162453 RNA and GAM316315 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM162453 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM162453 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM162453 target RNA into GAM162453 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM316315 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM316315 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM316315 target RNA into GAM316315 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4808 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4808 gene: GAM162453 target protein and GAM316315 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM162453 and GAM316315

GR4809 BI194328 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4809(GR4809) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4809 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4809 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4809 gene encodes GR4809 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4809 precursor RNA folds spatially, forming GR4809 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4809 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4809 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4809 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM116034 precursor RNA and GAM266053 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM116034 RNA and GAM266053 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM116034 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM116034 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM116034 target RNA into GAM116034 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM266053 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM266053 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM266053 target RNA into GAM266053 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4809 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4809 gene: GAM116034 target protein and GAM266053 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM116034 and GAM266053

GR4810 T74968 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4810(GR4810) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4810 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4810 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4810 gene encodes GR4810 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4810 precursor RNA folds spatially, forming GR4810 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4810 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4810 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4810 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM13774 precursor RNA and GAM122699 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM13774 RNA and GAM122699 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM13774 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM13774 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM13774 target RNA into GAM13774 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM122699 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM122699 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM122699 target RNA into GAM122699 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4810 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4810 gene: GAM13774 target protein and GAM122699 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM13774 and GAM122699

GR4811 AW291190 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4811(GR4811) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4811 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4811 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4811 gene encodes GR4811 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4811 precursor RNA folds spatially, forming GR4811 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4811 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4811 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4811 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM8039 precursor RNA, GAM75002 precursor RNA, GAM95470 precursor RNA and GAM200404 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8039 RNA, GAM75002 RNA, GAM95470 RNA and GAM200404 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8039 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8039 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8039 target RNA into GAM8039 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM75002 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM75002 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM75002 target RNA into GAM75002 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM95470 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM95470 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM95470 target RNA into GAM95470 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM200404 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM200404 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM200404 target RNA into GAM200404 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4811 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4811 gene: GAM8039 target protein, GAM75002 target protein, GAM95470 target protein and GAM200404 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8039, GAM75002, GAM95470 and GAM200404

GR4812 BG896282 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4812(GR4812) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4812 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4812 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4812 gene encodes GR4812 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4812 precursor RNA folds spatially, forming GR4812 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4812 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4812 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4812 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM85086 precursor RNA and GAM291667 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM85086 RNA and GAM291667 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM85086 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM85086 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM85086 target RNA into GAM85086 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM291667 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM291667 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM291667 target RNA into GAM291667 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4812 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4812 gene: GAM85086 target protein and GAM291667 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM85086 and GAM291667

GR4813 BM820685 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4813(GR4813) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4813 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4813 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4813 gene encodes GR4813 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4813 precursor RNA folds spatially, forming GR4813 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated

that GR4813 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4813 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4813 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM120358 precursor RNA, GAM148840 precursor RNA and GAM259035 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM120358 RNA, GAM148840 RNA and GAM259035 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM120358 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM120358 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM120358 target RNA into GAM120358 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM148840 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM148840 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM148840 target RNA into GAM148840 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM259035 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM259035 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM259035 target RNA into GAM259035 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4813 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4813 gene: GAM120358 target

protein, GAM148840 target protein and GAM259035 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM120358, GAM148840 and GAM259035

GR4814 BF204406 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4814(GR4814) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4814 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4814 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4814 gene encodes GR4814 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4814 precursor RNA folds spatially, forming GR4814 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4814 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4814 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4814 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM6345 precursor RNA, GAM210283 precursor RNA and GAM308439 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6345 RNA, GAM210283 RNA and GAM308439 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6345 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6345 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6345 target RNA into

GAM6345 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM210283 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM210283 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM210283 target RNA into GAM210283 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM308439 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM308439 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM308439 target RNA into GAM308439 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4814 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4814 gene: GAM6345 target protein, GAM210283 target protein and GAM308439 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6345, GAM210283 and GAM308439

GR4815 BI015164 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4815(GR4815) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4815 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4815 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4815 gene encodes GR4815 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4815 precursor RNA folds spatially, forming GR4815 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4815 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4815 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4815 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM10854 precursor RNA and GAM68070 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM10854 RNA and GAM68070 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM10854 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM10854 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM10854 target RNA into GAM10854 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM68070 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM68070 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM68070 target RNA into GAM68070 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4815 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4815 gene: GAM10854 target protein and GAM68070 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM10854 and GAM68070

GR4816 BI913118 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4816(GR4816) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4816 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR4816 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4816 gene encodes GR4816 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4816 precursor RNA folds spatially, forming GR4816 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4816 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4816 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4816 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM31673 precursor RNA and GAM257511 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM31673 RNA and GAM257511 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM31673 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM31673 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM31673 target RNA into GAM31673 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM257511 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM257511 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM257511 target RNA into GAM257511 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4816 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4816 gene: GAM31673 target

protein and GAM257511 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM31673 and GAM257511

GR4817 BM480016 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4817(GR4817) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4817 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4817 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4817 gene encodes GR4817 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4817 precursor RNA folds spatially, forming GR4817 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4817 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4817 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4817 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM166744 precursor RNA and GAM290791 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM166744 RNA and GAM290791 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM166744 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM166744 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM166744 target RNA into GAM166744 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM290791 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM290791 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM290791 target RNA into GAM290791 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4817 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4817 gene: GAM166744 target protein and GAM290791 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM166744 and GAM290791

GR4818 AV657538 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4818(GR4818) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4818 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4818 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4818 gene encodes GR4818 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4818 precursor RNA folds spatially, forming GR4818 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4818 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4818 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4818 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3255 precursor RNA and GAM214043 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3255 RNA and GAM214043 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3255 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3255 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3255 target RNA into GAM3255 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM214043 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM214043 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM214043 target RNA into GAM214043 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4818 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4818 gene: GAM3255 target protein and GAM214043 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3255 and GAM214043

GR4819 H95282 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4819(GR4819) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4819 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4819 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4819 gene encodes GR4819 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4819 precursor RNA folds spatially, forming GR4819 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4819 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR4819 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4819 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM39390 precursor RNA, GAM90283 precursor RNA and GAM138963 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM39390 RNA, GAM90283 RNA and GAM138963 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM39390 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM39390 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM39390 target RNA into GAM39390 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM90283 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM90283 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM90283 target RNA into GAM90283 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM138963 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM138963 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM138963 target RNA into GAM138963 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4819 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4819 gene: GAM39390 target protein, GAM90283 target protein and GAM138963 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN.

The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM39390, GAM90283 and GAM138963

GR4820 AW471133 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4820(GR4820) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4820 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4820 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4820 gene encodes GR4820 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4820 precursor RNA folds spatially, forming GR4820 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4820 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4820 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4820 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM176 precursor RNA and GAM3398 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM176 RNA and GAM3398 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM176 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM176 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM176 target RNA into GAM176 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM3398 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3398 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3398 target RNA into GAM3398 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4820 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4820 gene: GAM176 target protein and GAM3398 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM176 and GAM3398

GR4821 AV745641 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4821(GR4821) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4821 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4821 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4821 gene encodes GR4821 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4821 precursor RNA folds spatially, forming GR4821 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4821 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4821 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4821 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2099 precursor RNA and GAM288373 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM2099 RNA and GAM288373 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2099 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2099 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2099 target RNA into GAM2099 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM288373 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM288373 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM288373 target RNA into GAM288373 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4821 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4821 gene: GAM2099 target protein and GAM288373 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2099 and GAM288373

GR4822 BM931560 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4822(GR4822) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4822 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4822 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4822 gene encodes GR4822 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4822 precursor RNA folds spatially, forming GR4822 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4822 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4822 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4822 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7304 precursor RNA and GAM147183 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7304 RNA and GAM147183 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7304 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7304 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7304 target RNA into GAM7304 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM147183 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM147183 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM147183 target RNA into GAM147183 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4822 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4822 gene: GAM7304 target protein and GAM147183 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7304 and GAM147183

GR4823 BF311820 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4823(GR4823) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4823 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4823 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4823 gene encodes GR4823 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4823 precursor RNA folds spatially, forming GR4823 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4823 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4823 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4823 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM844 precursor RNA and GAM218762 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM844 RNA and GAM218762 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM844 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM844 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM844 target RNA into GAM844 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM218762 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM218762 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM218762 target RNA into GAM218762 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4823 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR4823 gene: GAM844 target protein and GAM218762 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM844 and GAM218762

GR4824 BM045185 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4824(GR4824) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4824 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4824 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4824 gene encodes GR4824 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4824 precursor RNA folds spatially, forming GR4824 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4824 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4824 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4824 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 5 separate GAM precursor RNAs, GAM215 precursor RNA, GAM57922 precursor RNA, GAM72104 precursor RNA, GAM114172 precursor RNA and GAM229238 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM215 RNA, GAM57922 RNA, GAM72104 RNA, GAM114172 RNA and GAM229238 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM215 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM215 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM215 target RNA into

GAM215 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM57922 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM57922 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM57922 target RNA into GAM57922 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM72104 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM72104 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM72104 target RNA into GAM72104 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM114172 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM114172 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM114172 target RNA into GAM114172 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM229238 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM229238 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM229238 target RNA into GAM229238 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4824 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4824 gene: GAM215 target protein, GAM57922 target protein, GAM72104 target protein, GAM114172 target protein and GAM229238 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM215, GAM57922, GAM72104, GAM114172 and GAM229238

GR4825 BM688885 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4825(GR4825) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR4825 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4825 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4825 gene encodes GR4825 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4825 precursor RNA folds spatially, forming GR4825 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4825 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4825 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4825 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3100 precursor RNA and GAM210576 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3100 RNA and GAM210576 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3100 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3100 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3100 target RNA into GAM3100 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM210576 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM210576 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM210576 target RNA into GAM210576 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly

utilities, of GR4825 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4825 gene: GAM3100 target protein and GAM210576 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3100 and GAM210576

GR4826 AA693781 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4826(GR4826) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4826 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4826 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4826 gene encodes GR4826 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4826 precursor RNA folds spatially, forming GR4826 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4826 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4826 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4826 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM92885 precursor RNA and GAM153156 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM92885 RNA and GAM153156 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM92885 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM92885 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM92885 target RNA into GAM92885 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM153156 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM153156 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM153156 target RNA into GAM153156 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4826 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4826 gene: GAM92885 target protein and GAM153156 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM92885 and GAM153156

GR4827 BQ073134 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4827(GR4827) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4827 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4827 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4827 gene encodes GR4827 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4827 precursor RNA folds spatially, forming GR4827 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4827 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4827 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4827 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2616 precursor RNA, GAM5740 precursor RNA and GAM55442 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded

precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2616 RNA, GAM5740 RNA and GAM55442 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2616 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2616 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2616 target RNA into GAM2616 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5740 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5740 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5740 target RNA into GAM5740 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM55442 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM55442 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM55442 target RNA into GAM55442 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4827 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4827 gene: GAM2616 target protein, GAM5740 target protein and GAM55442 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2616, GAM5740 and GAM55442

GR4828 BF847244 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4828(GR4828) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4828 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4828 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4828 gene encodes GR4828 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4828 precursor RNA folds spatially, forming GR4828 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4828 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4828 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4828 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM736 precursor RNA, GAM7172 precursor RNA, GAM8445 precursor RNA and GAM120557 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM736 RNA, GAM7172 RNA, GAM8445 RNA and GAM120557 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM736 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM736 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM736 target RNA into GAM736 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7172 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7172 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7172 target RNA into GAM7172 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8445 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM8445 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8445 target RNA into GAM8445 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM120557 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM120557 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM120557 target RNA into GAM120557 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4828 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4828 gene: GAM736 target protein, GAM7172 target protein, GAM8445 target protein and GAM120557 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM736, GAM7172, GAM8445 and GAM120557

GR4829 BF572024 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4829(GR4829) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4829 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4829 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4829 gene encodes GR4829 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4829 precursor RNA folds spatially, forming GR4829 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4829 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4829 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4829 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2572 precursor RNA, GAM8075 precursor RNA and GAM245582 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2572 RNA, GAM8075 RNA and GAM245582 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2572 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2572 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2572 target RNA into GAM2572 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8075 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8075 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8075 target RNA into GAM8075 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM245582 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM245582 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM245582 target RNA into GAM245582 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4829 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4829 gene: GAM2572 target protein, GAM8075 target protein and GAM245582 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2572, GAM8075 and GAM245582

4830(GR4830) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4830 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4830 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4830 gene encodes GR4830 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4830 precursor RNA folds spatially, forming GR4830 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4830 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4830 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4830 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM175833 precursor RNA, GAM232414 precursor RNA and GAM260220 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM175833 RNA, GAM232414 RNA and GAM260220 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM175833 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM175833 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM175833 target RNA into GAM175833 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM232414 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM232414 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM232414

target RNA into GAM232414 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM260220 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM260220 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM260220 target RNA into GAM260220 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4830 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4830 gene: GAM175833 target protein, GAM232414 target protein and GAM260220 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM175833, GAM232414 and GAM260220

GR4831 AA927547 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4831(GR4831) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4831 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4831 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4831 gene encodes GR4831 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4831 precursor RNA folds spatially, forming GR4831 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4831 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4831 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4831 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM222391 precursor RNA and GAM245211 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin

shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM222391 RNA and GAM245211 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM222391 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM222391 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM222391 target RNA into GAM222391 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM245211 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM245211 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM245211 target RNA into GAM245211 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4831 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4831 gene: GAM222391 target protein and GAM245211 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM222391 and GAM245211

GR4832 BI822427 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4832(GR4832) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4832 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4832 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4832 gene encodes GR4832 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4832 precursor RNA folds spatially, forming GR4832 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4832 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4832 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4832 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2110 precursor RNA, GAM14895 precursor RNA and GAM206975 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2110 RNA, GAM14895 RNA and GAM206975 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2110 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2110 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2110 target RNA into GAM2110 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM14895 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM14895 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM14895 target RNA into GAM14895 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM206975 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM206975 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM206975 target RNA into GAM206975 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4832 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR4832 gene: GAM2110 target protein, GAM14895 target protein and GAM206975 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2110, GAM14895 and GAM206975

GR4833 AW893867 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4833(GR4833) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4833 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4833 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4833 gene encodes GR4833 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4833 precursor RNA folds spatially, forming GR4833 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4833 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4833 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4833 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM113906 precursor RNA, GAM143866 precursor RNA and GAM229631 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM113906 RNA, GAM143866 RNA and GAM229631 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM113906 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM113906 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM113906 target RNA into GAM113906 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM143866 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM143866 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM143866 target RNA into GAM143866 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM229631 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM229631 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM229631 target RNA into GAM229631 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4833 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4833 gene: GAM113906 target protein, GAM143866 target protein and GAM229631 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM113906, GAM143866 and GAM229631

GR4834 BG479631 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4834(GR4834) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4834 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4834 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4834 gene encodes GR4834 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4834 precursor RNA folds spatially, forming GR4834 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4834 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4834 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4834 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1219 precursor RNA and GAM28102 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1219 RNA and GAM28102 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1219 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1219 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1219 target RNA into GAM1219 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM28102 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM28102 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM28102 target RNA into GAM28102 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4834 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4834 gene: GAM1219 target protein and GAM28102 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1219 and GAM28102

GR4835 BF326818 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4835(GR4835) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4835 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4835 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4835 gene encodes GR4835 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4835 precursor RNA folds spatially, forming GR4835 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4835 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4835 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4835 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM101394 precursor RNA, GAM127885 precursor RNA and GAM232626 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM101394 RNA, GAM127885 RNA and GAM232626 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM101394 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM101394 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM101394 target RNA into GAM101394 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM127885 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM127885 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM127885 target RNA into GAM127885 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM232626 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM232626 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM232626 target RNA into GAM232626 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4835 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4835 gene: GAM101394 target protein, GAM127885 target protein and GAM232626 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM101394, GAM127885 and GAM232626

GR4836 AW117887 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4836(GR4836) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4836 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4836 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4836 gene encodes GR4836 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4836 precursor RNA folds spatially, forming GR4836 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4836 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4836 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4836 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM134422 precursor RNA, GAM142846 precursor RNA and GAM151848 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM134422 RNA, GAM142846 RNA and GAM151848 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM134422 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM134422 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM134422 target RNA into GAM134422 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM142846 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM142846 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM142846 target RNA into GAM142846 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM151848 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM151848 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM151848 target RNA into GAM151848 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4836 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4836 gene: GAM134422 target protein, GAM142846 target protein and GAM151848 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM134422, GAM142846 and GAM151848

GR4837 BF870175 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4837(GR4837) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4837 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4837 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4837 gene encodes GR4837 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4837 precursor RNA folds spatially, forming GR4837 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4837 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4837 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4837 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM112069 precursor RNA and GAM178896 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM112069 RNA and GAM178896 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM112069 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM112069 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM112069 target RNA into GAM112069 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM178896 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM178896 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM178896 target RNA into GAM178896 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4837 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4837 gene: GAM112069 target protein and GAM178896 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference,

with references to GAM112069 and GAM178896

GR4838 AA781429 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4838(GR4838) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4838 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4838 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4838 gene encodes GR4838 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4838 precursor RNA folds spatially, forming GR4838 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4838 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4838 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4838 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM6715 precursor RNA, GAM6905 precursor RNA and GAM209604 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6715 RNA, GAM6905 RNA and GAM209604 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6715 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6715 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6715 target RNA into GAM6715 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6905 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM6905 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6905 target RNA into GAM6905 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM209604 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM209604 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM209604 target RNA into GAM209604 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4838 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4838 gene: GAM6715 target protein, GAM6905 target protein and GAM209604 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6715, GAM6905 and GAM209604

GR4839 BG912916 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4839(GR4839) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4839 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4839 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4839 gene encodes GR4839 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4839 precursor RNA folds spatially, forming GR4839 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4839 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4839 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4839 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM5034 precursor RNA, GAM63819 precursor RNA and GAM104402 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5034 RNA, GAM63819 RNA and GAM104402 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5034 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5034 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5034 target RNA into GAM5034 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM63819 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM63819 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM63819 target RNA into GAM63819 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM104402 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM104402 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM104402 target RNA into GAM104402 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4839 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4839 gene: GAM5034 target protein, GAM63819 target protein and GAM104402 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5034, GAM63819 and GAM104402

4840(GR4840) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4840 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4840 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4840 gene encodes GR4840 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4840 precursor RNA folds spatially, forming GR4840 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4840 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4840 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4840 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM97 precursor RNA and GAM210231 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM97 RNA and GAM210231 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM97 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM97 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM97 target RNA into GAM97 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM210231 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM210231 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM210231 target RNA into GAM210231 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4840 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4840 gene: GAM97 target protein and GAM210231 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM97 and GAM210231

GR4841 AA458961 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4841 (GR4841) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4841 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4841 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4841 gene encodes GR4841 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4841 precursor RNA folds spatially, forming GR4841 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4841 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4841 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4841 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM1941 precursor RNA, GAM164954 precursor RNA, GAM195053 precursor RNA and GAM325144 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1941 RNA, GAM164954 RNA, GAM195053 RNA and GAM325144 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1941 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1941 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1941 target RNA into GAM1941 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM164954 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM164954 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM164954 target RNA into GAM164954 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM195053 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM195053 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM195053 target RNA into GAM195053 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM325144 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM325144 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM325144 target RNA into GAM325144 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4841 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4841 gene: GAM1941 target protein, GAM164954 target protein, GAM195053 target protein and GAM325144 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1941, GAM164954, GAM195053 and GAM325144

GR4842 BF576460 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4842(GR4842) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4842 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR4842 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4842 gene encodes GR4842 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4842 precursor RNA folds spatially, forming GR4842 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4842 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4842 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4842 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM48525 precursor RNA and GAM160076 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM48525 RNA and GAM160076 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM48525 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM48525 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM48525 target RNA into GAM48525 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM160076 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM160076 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM160076 target RNA into GAM160076 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4842 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4842 gene: GAM48525 target

protein and GAM160076 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM48525 and GAM160076

GR4843 BG536012 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4843(GR4843) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4843 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4843 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4843 gene encodes GR4843 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4843 precursor RNA folds spatially, forming GR4843 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4843 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4843 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4843 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM77518 precursor RNA, GAM88993 precursor RNA and GAM317435 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM77518 RNA, GAM88993 RNA and GAM317435 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM77518 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM77518 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM77518 target RNA into GAM77518 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM88993 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM88993 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM88993 target RNA into GAM88993 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM317435 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM317435 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM317435 target RNA into GAM317435 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4843 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4843 gene: GAM77518 target protein, GAM88993 target protein and GAM317435 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM77518, GAM88993 and GAM317435

GR4844 BF381868 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4844(GR4844) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4844 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4844 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4844 gene encodes GR4844 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4844 precursor RNA folds spatially, forming GR4844 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4844 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4844 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR4844 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM144421 precursor RNA, GAM185634 precursor RNA and GAM330220 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM144421 RNA, GAM185634 RNA and GAM330220 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM144421 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM144421 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM144421 target RNA into GAM144421 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM185634 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM185634 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM185634 target RNA into GAM185634 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM330220 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM330220 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM330220 target RNA into GAM330220 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4844 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4844 gene: GAM144421 target protein, GAM185634 target protein and GAM330220 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM144421, GAM185634 and GAM330220

GR4845 BF687551 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4845(GR4845) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4845 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4845 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4845 gene encodes GR4845 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4845 precursor RNA folds spatially, forming GR4845 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4845 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4845 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4845 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8002 precursor RNA and GAM274615 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8002 RNA and GAM274615 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8002 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8002 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8002 target RNA into GAM8002 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM274615 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM274615 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM274615 target RNA into GAM274615 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4845 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4845 gene: GAM8002 target protein and GAM274615 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8002 and GAM274615

GR4846 BI223210 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4846(GR4846) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4846 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4846 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4846 gene encodes GR4846 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4846 precursor RNA folds spatially, forming GR4846 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4846 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4846 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4846 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM75 precursor RNA, GAM8466 precursor RNA and GAM58869 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM75 RNA, GAM8466 RNA and GAM58869 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs

corresponding to GAM RNA of Fig. 8.

GAM75 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM75 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM75 target RNA into GAM75 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8466 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8466 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8466 target RNA into GAM8466 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM58869 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM58869 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM58869 target RNA into GAM58869 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4846 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4846 gene: GAM75 target protein, GAM8466 target protein and GAM58869 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM75, GAM8466 and GAM58869

GR4847 BM055115 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4847(GR4847) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4847 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4847 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4847 gene encodes GR4847 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR4847 precursor RNA folds spatially, forming GR4847 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4847 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4847 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4847 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM69648 precursor RNA and GAM190838 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM69648 RNA and GAM190838 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM69648 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM69648 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM69648 target RNA into GAM69648 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM190838 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM190838 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM190838 target RNA into GAM190838 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4847 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4847 gene: GAM69648 target protein and GAM190838 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM69648 and GAM190838

GR4848 AW747804 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4848(GR4848) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4848 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4848 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4848 gene encodes GR4848 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4848 precursor RNA folds spatially, forming GR4848 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4848 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4848 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4848 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM63452 precursor RNA and GAM107063 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM63452 RNA and GAM107063 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM63452 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM63452 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM63452 target RNA into GAM63452 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM107063 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM107063 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM107063 target RNA into GAM107063 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4848 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4848 gene: GAM63452 target protein and GAM107063 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM63452 and GAM107063

GR4849 AA044977 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4849(GR4849) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4849 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4849 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4849 gene encodes GR4849 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4849 precursor RNA folds spatially, forming GR4849 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4849 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4849 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4849 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM416 precursor RNA and GAM207786 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM416 RNA and GAM207786 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM416 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM416 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM416 target RNA into GAM416 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM207786 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM207786 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM207786 target RNA into GAM207786 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4849 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4849 gene: GAM416 target protein and GAM207786 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM416 and GAM207786

GR4850 BF768064 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4850(GR4850) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4850 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4850 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4850 gene encodes GR4850 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4850 precursor RNA folds spatially, forming GR4850 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4850 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4850 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4850 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM90 precursor RNA and GAM261194 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM90 RNA and GAM261194 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM90 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM90 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM90 target RNA into GAM90 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM261194 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM261194 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM261194 target RNA into GAM261194 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4850 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4850 gene: GAM90 target protein and GAM261194 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM90 and GAM261194

GR4851 BG113745 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4851(GR4851) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4851 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4851 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4851 gene encodes GR4851 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4851 precursor RNA folds spatially, forming GR4851 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4851 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4851 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4851 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM8208 precursor RNA, GAM72446 precursor RNA, GAM171345 precursor RNA and GAM282477 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8208 RNA, GAM72446 RNA, GAM171345 RNA and GAM282477 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8208 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8208 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8208 target RNA into GAM8208 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM72446 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM72446 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM72446 target RNA into GAM72446 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM171345 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM171345 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM171345 target RNA into GAM171345 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM282477 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM282477 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM282477 target RNA into GAM282477 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4851 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4851 gene: GAM8208 target protein, GAM72446 target protein, GAM171345 target protein and GAM282477 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8208, GAM72446, GAM171345 and GAM282477

GR4852 R76727 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4852(GR4852) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4852 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4852 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4852 gene encodes GR4852 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4852 precursor RNA folds spatially, forming GR4852 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4852 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4852 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4852 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2801 precursor RNA and GAM74523 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2801 RNA and GAM74523 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2801 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2801 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2801 target RNA into GAM2801 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM74523 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM74523 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM74523 target RNA into GAM74523 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4852 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4852 gene: GAM2801 target protein and GAM74523 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2801 and GAM74523

GR4853 AA969515 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4853(GR4853) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4853 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4853 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4853 gene encodes GR4853 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4853 precursor RNA folds spatially, forming GR4853 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated

that GR4853 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4853 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4853 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM218618 precursor RNA and GAM251040 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM218618 RNA and GAM251040 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM218618 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM218618 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM218618 target RNA into GAM218618 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM251040 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM251040 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM251040 target RNA into GAM251040 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4853 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4853 gene: GAM218618 target protein and GAM251040 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM218618 and GAM251040

GR4854 BI828120 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4854(GR4854) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR4854 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4854 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4854 gene encodes GR4854 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4854 precursor RNA folds spatially, forming GR4854 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4854 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4854 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4854 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM217 precursor RNA, GAM6559 precursor RNA and GAM96767 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM217 RNA, GAM6559 RNA and GAM96767 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM217 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM217 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM217 target RNA into GAM217 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6559 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6559 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6559 target RNA into GAM6559 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM96767 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM96767 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM96767 target RNA into GAM96767 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4854 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4854 gene: GAM217 target protein, GAM6559 target protein and GAM96767 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM217, GAM6559 and GAM96767

GR4855 BI916903 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4855(GR4855) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4855 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4855 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4855 gene encodes GR4855 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4855 precursor RNA folds spatially, forming GR4855 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4855 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4855 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4855 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM6837 precursor RNA, GAM127766 precursor RNA, GAM219932 precursor RNA and GAM294847 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6837 RNA, GAM127766 RNA, GAM219932 RNA and GAM294847 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6837 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6837 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6837 target RNA into GAM6837 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM127766 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM127766 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM127766 target RNA into GAM127766 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM219932 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM219932 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM219932 target RNA into GAM219932 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM294847 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM294847 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM294847 target RNA into GAM294847 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4855 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4855 gene: GAM6837 target protein, GAM127766 target protein, GAM219932 target protein and GAM294847 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6837, GAM127766, GAM219932 and GAM294847

GR4856 BG260443 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4856(GR4856) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4856 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4856 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4856 gene encodes GR4856 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4856 precursor RNA folds spatially, forming GR4856 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4856 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4856 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4856 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM706 precursor RNA, GAM912 precursor RNA and GAM149425 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM706 RNA, GAM912 RNA and GAM149425 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM706 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM706 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM706 target RNA into GAM706 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM912 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM912 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds

to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM912 target RNA into GAM912 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM149425 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM149425 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM149425 target RNA into GAM149425 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4856 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4856 gene: GAM706 target protein, GAM912 target protein and GAM149425 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM706, GAM912 and GAM149425

GR4857 BF210609 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4857(GR4857) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4857 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4857 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4857 gene encodes GR4857 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4857 precursor RNA folds spatially, forming GR4857 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4857 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4857 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4857 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM138153 precursor RNA and GAM335214 precursor

RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM138153 RNA and GAM335214 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM138153 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM138153 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM138153 target RNA into GAM138153 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM335214 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM335214 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM335214 target RNA into GAM335214 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4857 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4857 gene: GAM138153 target protein and GAM335214 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM138153 and GAM335214

GR4858 AI553768 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4858(GR4858) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4858 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4858 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4858 gene encodes GR4858 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4858 precursor RNA folds spatially, forming GR4858 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4858 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4858 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4858 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM36355 precursor RNA and GAM289220 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM36355 RNA and GAM289220 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM36355 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM36355 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM36355 target RNA into GAM36355 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM289220 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM289220 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM289220 target RNA into GAM289220 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4858 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4858 gene: GAM36355 target protein and GAM289220 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM36355 and GAM289220

bioinformatically detected regulatory gene, referred to here as Genomic Record 4859(GR4859) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4859 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4859 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4859 gene encodes GR4859 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4859 precursor RNA folds spatially, forming GR4859 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4859 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4859 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4859 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7478 precursor RNA and GAM223368 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7478 RNA and GAM223368 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7478 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7478 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7478 target RNA into GAM7478 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM223368 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM223368 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM223368

target RNA into GAM223368 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4859 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4859 gene: GAM7478 target protein and GAM223368 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7478 and GAM223368

GR4860 BF951409 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4860(GR4860) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4860 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4860 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4860 gene encodes GR4860 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4860 precursor RNA folds spatially, forming GR4860 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4860 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4860 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4860 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM5276 precursor RNA, GAM168229 precursor RNA and GAM178513 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5276 RNA, GAM168229 RNA and GAM178513 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5276 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5276 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5276 target RNA into GAM5276 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM168229 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM168229 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM168229 target RNA into GAM168229 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM178513 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM178513 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM178513 target RNA into GAM178513 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4860 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4860 gene: GAM5276 target protein, GAM168229 target protein and GAM178513 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5276, GAM168229 and GAM178513

GR4861 BG756599 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4861 (GR4861) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4861 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4861 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4861 gene encodes GR4861 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4861 precursor RNA folds spatially, forming GR4861 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4861 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4861 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4861 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1395 precursor RNA and GAM195046 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1395 RNA and GAM195046 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1395 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1395 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1395 target RNA into GAM1395 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM195046 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM195046 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM195046 target RNA into GAM195046 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4861 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4861 gene: GAM1395 target protein and GAM195046 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1395 and GAM195046

4862(GR4862) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4862 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4862 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4862 gene encodes GR4862 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4862 precursor RNA folds spatially, forming GR4862 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4862 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4862 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4862 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM48962 precursor RNA and GAM237836 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM48962 RNA and GAM237836 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM48962 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM48962 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM48962 target RNA into GAM48962 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM237836 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM237836 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM237836 target RNA into GAM237836 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4862 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4862 gene: GAM48962 target protein and GAM237836 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM48962 and GAM237836

GR4863 AA191438 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4863(GR4863) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4863 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4863 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4863 gene encodes GR4863 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4863 precursor RNA folds spatially, forming GR4863 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4863 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4863 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4863 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM208881 precursor RNA and GAM320203 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM208881 RNA and GAM320203 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM208881 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM208881 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM208881 target RNA into GAM208881 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM320203 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM320203 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM320203 target RNA into GAM320203 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4863 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4863 gene: GAM208881 target protein and GAM320203 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM208881 and GAM320203

GR4864 BM760005 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4864(GR4864) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4864 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4864 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4864 gene encodes GR4864 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4864 precursor RNA folds spatially, forming GR4864 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4864 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4864 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4864 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2

separate GAM precursor RNAs, GAM2269 precursor RNA and GAM4674 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2269 RNA and GAM4674 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2269 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2269 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2269 target RNA into GAM2269 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM4674 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4674 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4674 target RNA into GAM4674 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4864 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4864 gene: GAM2269 target protein and GAM4674 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2269 and GAM4674

GR4865 AI678271 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4865(GR4865) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4865 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4865 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4865 gene encodes GR4865 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR4865 precursor RNA folds spatially, forming GR4865 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4865 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4865 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4865 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM214509 precursor RNA and GAM217302 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM214509 RNA and GAM217302 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM214509 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM214509 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM214509 target RNA into GAM214509 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM217302 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM217302 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM217302 target RNA into GAM217302 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4865 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4865 gene: GAM214509 target protein and GAM217302 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM214509 and GAM217302

GR4866 BE736348 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4866(GR4866) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4866 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4866 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4866 gene encodes GR4866 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4866 precursor RNA folds spatially, forming GR4866 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4866 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4866 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4866 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM659 precursor RNA, GAM803 precursor RNA and GAM5281 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM659 RNA, GAM803 RNA and GAM5281 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM659 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM659 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM659 target RNA into GAM659 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM803 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM803 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds

to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM803 target RNA into GAM803 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5281 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5281 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5281 target RNA into GAM5281 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4866 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4866 gene: GAM659 target protein, GAM803 target protein and GAM5281 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM659, GAM803 and GAM5281

GR4867 BM549475 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4867(GR4867) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4867 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4867 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4867 gene encodes GR4867 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4867 precursor RNA folds spatially, forming GR4867 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4867 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4867 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4867 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM21065 precursor RNA and GAM80862 precursor

RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM21065 RNA and GAM80862 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM21065 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM21065 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM21065 target RNA into GAM21065 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM80862 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM80862 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM80862 target RNA into GAM80862 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4867 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4867 gene: GAM21065 target protein and GAM80862 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM21065 and GAM80862

GR4868 BG424667 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4868(GR4868) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4868 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4868 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4868 gene encodes GR4868 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4868 precursor RNA folds spatially, forming GR4868 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4868 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4868 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4868 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM40123 precursor RNA and GAM225732 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM40123 RNA and GAM225732 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM40123 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM40123 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM40123 target RNA into GAM40123 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM225732 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM225732 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM225732 target RNA into GAM225732 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4868 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4868 gene: GAM40123 target protein and GAM225732 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM40123 and GAM225732

bioinformatically detected regulatory gene, referred to here as Genomic Record 4869(GR4869) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4869 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4869 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4869 gene encodes GR4869 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4869 precursor RNA folds spatially, forming GR4869 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4869 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4869 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4869 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM46611 precursor RNA and GAM196404 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM46611 RNA and GAM196404 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM46611 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM46611 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM46611 target RNA into GAM46611 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM196404 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM196404 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM196404

target RNA into GAM196404 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4869 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4869 gene: GAM46611 target protein and GAM196404 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM46611 and GAM196404

GR4870 BE567232 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4870(GR4870) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4870 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4870 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4870 gene encodes GR4870 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4870 precursor RNA folds spatially, forming GR4870 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4870 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4870 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4870 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8092 precursor RNA and GAM114798 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8092 RNA and GAM114798 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8092 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8092 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8092 target RNA into GAM8092 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM114798 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM114798 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM114798 target RNA into GAM114798 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4870 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4870 gene: GAM8092 target protein and GAM114798 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8092 and GAM114798

GR4871 BE889886 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4871(GR4871) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4871 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4871 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4871 gene encodes GR4871 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4871 precursor RNA folds spatially, forming GR4871 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4871 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4871 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4871 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM117226 precursor RNA, GAM244714 precursor RNA and GAM294030 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM117226 RNA, GAM244714 RNA and GAM294030 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM117226 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM117226 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM117226 target RNA into GAM117226 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM244714 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM244714 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM244714 target RNA into GAM244714 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM294030 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM294030 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM294030 target RNA into GAM294030 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4871 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4871 gene: GAM117226 target protein, GAM244714 target protein and GAM294030 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM117226, GAM244714 and GAM294030

4872(GR4872) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4872 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4872 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4872 gene encodes GR4872 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4872 precursor RNA folds spatially, forming GR4872 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4872 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4872 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4872 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2855 precursor RNA and GAM260847 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2855 RNA and GAM260847 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2855 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2855 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2855 target RNA into GAM2855 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM260847 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM260847 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM260847 target RNA into GAM260847 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4872 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4872 gene: GAM2855 target protein and GAM260847 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2855 and GAM260847

GR4873 BG202365 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4873(GR4873) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4873 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4873 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4873 gene encodes GR4873 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4873 precursor RNA folds spatially, forming GR4873 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4873 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4873 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4873 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 5 separate GAM precursor RNAs, GAM96383 precursor RNA, GAM124103 precursor RNA, GAM151581 precursor RNA, GAM270737 precursor RNA and GAM281761 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM96383 RNA, GAM124103 RNA, GAM151581 RNA, GAM270737 RNA and GAM281761 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM96383 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM96383 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM96383 target RNA into GAM96383 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM124103 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM124103 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM124103 target RNA into GAM124103 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM151581 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM151581 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM151581 target RNA into GAM151581 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM270737 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM270737 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM270737 target RNA into GAM270737 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM281761 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM281761 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM281761 target RNA into GAM281761 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4873 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4873 gene: GAM96383 target protein, GAM124103 target protein, GAM151581 target protein, GAM270737 target protein and GAM281761 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM96383, GAM124103, GAM151581, GAM270737 and GAM281761

GR4874 AW372860 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4874(GR4874) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4874 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4874 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4874 gene encodes GR4874 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4874 precursor RNA folds spatially, forming GR4874 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4874 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4874 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4874 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM164090 precursor RNA and GAM185911 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM164090 RNA and GAM185911 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM164090 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM164090 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM164090 target RNA into GAM164090 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM185911 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM185911 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM185911 target RNA into GAM185911 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4874 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4874 gene: GAM164090 target protein and GAM185911 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM164090 and GAM185911

GR4875 BG003059 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4875(GR4875) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4875 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4875 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4875 gene encodes GR4875 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4875 precursor RNA folds spatially, forming GR4875 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4875 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4875 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4875 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM128120 precursor RNA and GAM204654 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM128120 RNA and GAM204654 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM128120 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM128120 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM128120 target RNA into GAM128120 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM204654 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM204654 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM204654 target RNA into GAM204654 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4875 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4875 gene: GAM128120 target protein and GAM204654 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM128120 and GAM204654

GR4876 AI682437 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4876(GR4876) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4876 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4876 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4876 gene encodes GR4876 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4876 precursor RNA folds spatially, forming GR4876 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4876 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4876 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4876 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1694 precursor RNA and GAM310907 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1694 RNA and GAM310907 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1694 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1694 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1694 target RNA into GAM1694 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM310907 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM310907 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM310907 target RNA into GAM310907 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4876 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4876 gene: GAM1694 target protein and GAM310907 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1694 and GAM310907

GR4877 BG772432 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4877(GR4877) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4877 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4877 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4877 gene encodes GR4877 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4877 precursor RNA folds spatially, forming GR4877 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4877 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4877 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4877 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4059 precursor RNA, GAM224344 precursor RNA and GAM309169 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4059 RNA, GAM224344 RNA and GAM309169 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4059 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4059 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4059 target RNA into GAM4059 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM224344 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM224344 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM224344 target RNA into GAM224344 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM309169 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM309169 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM309169

target RNA into GAM309169 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4877 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4877 gene: GAM4059 target protein, GAM224344 target protein and GAM309169 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4059, GAM224344 and GAM309169

GR4878 AA352336 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4878(GR4878) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4878 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4878 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4878 gene encodes GR4878 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4878 precursor RNA folds spatially, forming GR4878 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4878 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4878 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4878 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM119312 precursor RNA and GAM293131 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM119312 RNA and GAM293131 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM119312 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM119312 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM119312 target RNA into GAM119312 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM293131 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM293131 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM293131 target RNA into GAM293131 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4878 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4878 gene: GAM119312 target protein and GAM293131 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM119312 and GAM293131

GR4879 BI868981 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4879(GR4879) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4879 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4879 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4879 gene encodes GR4879 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4879 precursor RNA folds spatially, forming GR4879 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4879 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4879 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4879 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM187083 precursor RNA and GAM293345 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM187083 RNA and GAM293345 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM187083 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM187083 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM187083 target RNA into GAM187083 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM293345 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM293345 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM293345 target RNA into GAM293345 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4879 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4879 gene: GAM187083 target protein and GAM293345 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM187083 and GAM293345

GR4880 AI341558 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4880(GR4880) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4880 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4880 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4880 gene encodes GR4880 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4880 precursor RNA folds spatially, forming GR4880 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4880 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4880 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4880 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM111858 precursor RNA and GAM315791 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM111858 RNA and GAM315791 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM111858 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM111858 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM111858 target RNA into GAM111858 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM315791 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM315791 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM315791 target RNA into GAM315791 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4880 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4880 gene: GAM111858 target protein and GAM315791 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference,

with references to GAM111858 and GAM315791

GR4881 BQ022290 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4881 (GR4881) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4881 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4881 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4881 gene encodes GR4881 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4881 precursor RNA folds spatially, forming GR4881 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4881 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4881 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4881 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM177967 precursor RNA and GAM293276 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM177967 RNA and GAM293276 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM177967 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM177967 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM177967 target RNA into GAM177967 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM293276 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM293276 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM293276 target RNA into GAM293276 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4881 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4881 gene: GAM177967 target protein and GAM293276 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM177967 and GAM293276

GR4882 AW804716 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4882(GR4882) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4882 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4882 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4882 gene encodes GR4882 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4882 precursor RNA folds spatially, forming GR4882 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4882 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4882 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4882 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4055 precursor RNA and GAM308574 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4055 RNA and GAM308574 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding

to GAM RNA of Fig. 8.

GAM4055 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4055 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4055 target RNA into GAM4055 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM308574 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM308574 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM308574 target RNA into GAM308574 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4882 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4882 gene: GAM4055 target protein and GAM308574 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4055 and GAM308574

GR4883 BE271186 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4883(GR4883) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4883 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4883 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4883 gene encodes GR4883 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4883 precursor RNA folds spatially, forming GR4883 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4883 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4883 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR4883 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2749 precursor RNA and GAM318260 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2749 RNA and GAM318260 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2749 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2749 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2749 target RNA into GAM2749 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM318260 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM318260 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM318260 target RNA into GAM318260 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4883 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4883 gene: GAM2749 target protein and GAM318260 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2749 and GAM318260

GR4884 BF229485 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4884(GR4884) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4884 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4884

gene was detected is described hereinabove with reference to Figs. 8-18.

GR4884 gene encodes GR4884 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4884 precursor RNA folds spatially, forming GR4884 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4884 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4884 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4884 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7722 precursor RNA and GAM186416 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7722 RNA and GAM186416 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7722 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7722 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7722 target RNA into GAM7722 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM186416 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM186416 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM186416 target RNA into GAM186416 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4884 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4884 gene: GAM7722 target protein and GAM186416 target protein, herein schematically represented by GAM1

TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7722 and GAM186416

GR4885 BF184437 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4885(GR4885) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4885 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4885 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4885 gene encodes GR4885 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4885 precursor RNA folds spatially, forming GR4885 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4885 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4885 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4885 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM40407 precursor RNA and GAM290882 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM40407 RNA and GAM290882 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM40407 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM40407 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM40407 target RNA into GAM40407 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM290882 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM290882 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM290882 target RNA into GAM290882 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4885 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4885 gene: GAM40407 target protein and GAM290882 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM40407 and GAM290882

GR4886 AW364244 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4886(GR4886) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4886 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4886 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4886 gene encodes GR4886 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4886 precursor RNA folds spatially, forming GR4886 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4886 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4886 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4886 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM1275 precursor RNA, GAM4220 precursor RNA, GAM108014 precursor RNA and GAM111246 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1275 RNA, GAM4220 RNA, GAM108014 RNA and GAM111246 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1275 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1275 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1275 target RNA into GAM1275 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM4220 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4220 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4220 target RNA into GAM4220 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM108014 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM108014 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM108014 target RNA into GAM108014 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM111246 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM111246 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM111246 target RNA into GAM111246 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4886 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4886 gene: GAM1275 target protein, GAM4220 target protein, GAM108014 target protein and GAM111246 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1275, GAM4220, GAM108014 and GAM111246

4887(GR4887) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4887 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4887 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4887 gene encodes GR4887 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4887 precursor RNA folds spatially, forming GR4887 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4887 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4887 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4887 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM213675 precursor RNA and GAM297843 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM213675 RNA and GAM297843 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM213675 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM213675 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM213675 target RNA into GAM213675 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM297843 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM297843 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM297843 target RNA into GAM297843 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4887 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4887 gene: GAM213675 target protein and GAM297843 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM213675 and GAM297843

GR4888 BE296651 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4888(GR4888) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4888 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4888 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4888 gene encodes GR4888 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4888 precursor RNA folds spatially, forming GR4888 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4888 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4888 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4888 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1346 precursor RNA and GAM24640 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1346 RNA and GAM24640 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1346 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM1346 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1346 target RNA into GAM1346 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM24640 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM24640 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM24640 target RNA into GAM24640 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4888 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4888 gene: GAM1346 target protein and GAM24640 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1346 and GAM24640

GR4889 AV762578 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4889(GR4889) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4889 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4889 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4889 gene encodes GR4889 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4889 precursor RNA folds spatially, forming GR4889 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4889 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4889 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4889 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3

separate GAM precursor RNAs, GAM138583 precursor RNA, GAM161891 precursor RNA and GAM170586 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM138583 RNA, GAM161891 RNA and GAM170586 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM138583 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM138583 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM138583 target RNA into GAM138583 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM161891 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM161891 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM161891 target RNA into GAM161891 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM170586 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM170586 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM170586 target RNA into GAM170586 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4889 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4889 gene: GAM138583 target protein, GAM161891 target protein and GAM170586 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM138583, GAM161891 and GAM170586

GR4890 AA843999 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4890(GR4890) gene, which encodes an `operon-like` cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4890 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4890 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4890 gene encodes GR4890 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4890 precursor RNA folds spatially, forming GR4890 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4890 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4890 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4890 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM34804 precursor RNA, GAM44980 precursor RNA and GAM148777 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM34804 RNA, GAM44980 RNA and GAM148777 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM34804 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM34804 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM34804 target RNA into GAM34804 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM44980 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM44980 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM44980 target RNA into GAM44980 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM148777 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM148777 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM148777 target RNA into GAM148777 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4890 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4890 gene: GAM34804 target protein, GAM44980 target protein and GAM148777 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM34804, GAM44980 and GAM148777

GR4891 AI880150 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4891(GR4891) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4891 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4891 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4891 gene encodes GR4891 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4891 precursor RNA folds spatially, forming GR4891 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4891 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4891 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4891 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM79133 precursor RNA and GAM127825 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM79133 RNA and GAM127825 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM79133 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM79133 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM79133 target RNA into GAM79133 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM127825 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM127825 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM127825 target RNA into GAM127825 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4891 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4891 gene: GAM79133 target protein and GAM127825 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM79133 and GAM127825

GR4892 BG398971 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4892(GR4892) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4892 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4892 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4892 gene encodes GR4892 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4892 precursor RNA folds spatially, forming GR4892 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated

that GR4892 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4892 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4892 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM213956 precursor RNA and GAM304881 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM213956 RNA and GAM304881 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM213956 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM213956 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM213956 target RNA into GAM213956 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM304881 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM304881 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM304881 target RNA into GAM304881 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4892 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4892 gene: GAM213956 target protein and GAM304881 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM213956 and GAM304881

GR4893 BM841317 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4893(GR4893) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR4893 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4893 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4893 gene encodes GR4893 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4893 precursor RNA folds spatially, forming GR4893 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4893 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4893 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4893 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM771 precursor RNA and GAM98917 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM771 RNA and GAM98917 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM771 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM771 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM771 target RNA into GAM771 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM98917 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM98917 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM98917 target RNA into GAM98917 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4893 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4893 gene: GAM771 target protein and GAM98917 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM771 and GAM98917

GR4894 AU100225 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4894(GR4894) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4894 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4894 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4894 gene encodes GR4894 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4894 precursor RNA folds spatially, forming GR4894 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4894 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4894 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4894 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM72836 precursor RNA and GAM146430 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM72836 RNA and GAM146430 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM72836 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM72836 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM72836 target RNA into GAM72836 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM146430 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM146430 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM146430 target RNA into GAM146430 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4894 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4894 gene: GAM72836 target protein and GAM146430 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM72836 and GAM146430

GR4895 AU145086 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4895(GR4895) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4895 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4895 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4895 gene encodes GR4895 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4895 precursor RNA folds spatially, forming GR4895 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4895 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4895 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4895 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2993 precursor RNA, GAM41274 precursor RNA and GAM42035 precursor RNA, herein schematically represented by GAM1 FOLDED

PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2993 RNA, GAM41274 RNA and GAM42035 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2993 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2993 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2993 target RNA into GAM2993 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM41274 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM41274 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM41274 target RNA into GAM41274 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM42035 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM42035 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM42035 target RNA into GAM42035 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4895 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4895 gene: GAM2993 target protein, GAM41274 target protein and GAM42035 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2993, GAM41274 and GAM42035

GR4896 BF218287 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4896(GR4896) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR4896 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4896 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4896 gene encodes GR4896 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4896 precursor RNA folds spatially, forming GR4896 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4896 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4896 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4896 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM133059 precursor RNA and GAM243951 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM133059 RNA and GAM243951 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM133059 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM133059 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM133059 target RNA into GAM133059 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM243951 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM243951 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM243951 target RNA into GAM243951 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly

utilities, of GR4896 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4896 gene: GAM133059 target protein and GAM243951 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM133059 and GAM243951

GR4897 BI063568 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4897(GR4897) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4897 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4897 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4897 gene encodes GR4897 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4897 precursor RNA folds spatially, forming GR4897 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4897 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4897 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4897 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM36336 precursor RNA, GAM40602 precursor RNA and GAM263483 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM36336 RNA, GAM40602 RNA and GAM263483 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM36336 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM36336 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM36336 target RNA into GAM36336 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM40602 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM40602 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM40602 target RNA into GAM40602 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM263483 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM263483 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM263483 target RNA into GAM263483 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4897 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4897 gene: GAM36336 target protein, GAM40602 target protein and GAM263483 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM36336, GAM40602 and GAM263483

GR4898 BI907481 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4898(GR4898) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4898 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4898 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4898 gene encodes GR4898 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4898 precursor RNA folds spatially, forming GR4898 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4898 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR4898 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4898 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1374 precursor RNA, GAM8537 precursor RNA and GAM283661 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1374 RNA, GAM8537 RNA and GAM283661 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1374 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1374 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1374 target RNA into GAM1374 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8537 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8537 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8537 target RNA into GAM8537 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM283661 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM283661 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM283661 target RNA into GAM283661 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4898 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4898 gene: GAM1374 target protein, GAM8537 target protein and GAM283661 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN.

The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1374, GAM8537 and GAM283661

GR4899 AA609684 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4899(GR4899) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4899 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4899 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4899 gene encodes GR4899 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4899 precursor RNA folds spatially, forming GR4899 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4899 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4899 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4899 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM41821 precursor RNA, GAM134165 precursor RNA and GAM213441 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM41821 RNA, GAM134165 RNA and GAM213441 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM41821 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM41821 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM41821 target RNA into GAM41821 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM134165 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM134165 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM134165 target RNA into GAM134165 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM213441 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM213441 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM213441 target RNA into GAM213441 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4899 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4899 gene: GAM41821 target protein, GAM134165 target protein and GAM213441 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM41821, GAM134165 and GAM213441

GR4900 N31877 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4900(GR4900) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4900 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4900 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4900 gene encodes GR4900 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4900 precursor RNA folds spatially, forming GR4900 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4900 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4900 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4900 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8599 precursor RNA and GAM43416 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8599 RNA and GAM43416 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8599 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8599 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8599 target RNA into GAM8599 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM43416 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM43416 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM43416 target RNA into GAM43416 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4900 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4900 gene: GAM8599 target protein and GAM43416 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8599 and GAM43416

GR4901 AI866645 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4901(GR4901) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4901 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4901 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4901 gene encodes GR4901 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4901 precursor RNA folds spatially, forming GR4901 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4901 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4901 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4901 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM158015 precursor RNA and GAM274673 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM158015 RNA and GAM274673 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM158015 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM158015 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM158015 target RNA into GAM158015 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM274673 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM274673 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM274673 target RNA into GAM274673 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4901 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4901 gene: GAM158015 target protein and GAM274673 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes

is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM158015 and GAM274673

GR4902 BE265309 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4902(GR4902) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4902 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4902 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4902 gene encodes GR4902 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4902 precursor RNA folds spatially, forming GR4902 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4902 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4902 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4902 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM678 precursor RNA and GAM209584 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM678 RNA and GAM209584 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM678 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM678 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM678 target RNA into GAM678 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM209584 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM209584 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM209584 target RNA into GAM209584 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4902 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4902 gene: GAM678 target protein and GAM209584 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM678 and GAM209584

GR4903 BG570722 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4903(GR4903) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4903 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4903 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4903 gene encodes GR4903 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4903 precursor RNA folds spatially, forming GR4903 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4903 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4903 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4903 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM646 precursor RNA, GAM4502 precursor RNA and GAM145962 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM646 RNA, GAM4502 RNA and GAM145962 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM646 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM646 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM646 target RNA into GAM646 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM4502 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4502 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4502 target RNA into GAM4502 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM145962 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM145962 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM145962 target RNA into GAM145962 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4903 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4903 gene: GAM646 target protein, GAM4502 target protein and GAM145962 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM646, GAM4502 and GAM145962

GR4904 BG187894 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4904(GR4904) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4904 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4904 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4904 gene encodes GR4904 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4904 precursor RNA folds spatially, forming GR4904 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4904 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4904 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4904 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM100215 precursor RNA and GAM149492 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM100215 RNA and GAM149492 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM100215 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM100215 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM100215 target RNA into GAM100215 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM149492 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM149492 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM149492 target RNA into GAM149492 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4904 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4904 gene: GAM100215 target protein and GAM149492 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference,

with references to GAM100215 and GAM149492

GR4905 BF155649 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4905(GR4905) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4905 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4905 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4905 gene encodes GR4905 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4905 precursor RNA folds spatially, forming GR4905 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4905 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4905 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4905 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1925 precursor RNA, GAM3379 precursor RNA and GAM251840 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1925 RNA, GAM3379 RNA and GAM251840 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1925 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1925 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1925 target RNA into GAM1925 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM3379 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM3379 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3379 target RNA into GAM3379 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM251840 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM251840 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM251840 target RNA into GAM251840 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4905 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4905 gene: GAM1925 target protein, GAM3379 target protein and GAM251840 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1925, GAM3379 and GAM251840

GR4906 AA309076 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4906(GR4906) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4906 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4906 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4906 gene encodes GR4906 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4906 precursor RNA folds spatially, forming GR4906 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4906 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4906 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4906 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2351 precursor RNA and GAM102069 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2351 RNA and GAM102069 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2351 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2351 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2351 target RNA into GAM2351 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM102069 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM102069 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM102069 target RNA into GAM102069 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4906 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4906 gene: GAM2351 target protein and GAM102069 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2351 and GAM102069

GR4907 AI052780 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4907(GR4907) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4907 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4907 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4907 gene encodes GR4907 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4907 precursor RNA folds spatially, forming GR4907 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4907 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4907 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4907 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM71 precursor RNA, GAM6993 precursor RNA and GAM210159 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM71 RNA, GAM6993 RNA and GAM210159 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM71 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM71 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM71 target RNA into GAM71 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6993 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6993 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6993 target RNA into GAM6993 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM210159 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM210159 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM210159 target RNA into GAM210159 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4907 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4907 gene: GAM71 target protein, GAM6993 target protein and GAM210159 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM71, GAM6993 and GAM210159

GR4908 BI048137 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4908(GR4908) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4908 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4908 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4908 gene encodes GR4908 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4908 precursor RNA folds spatially, forming GR4908 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4908 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4908 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4908 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3106 precursor RNA and GAM317260 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3106 RNA and GAM317260 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3106 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM3106 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3106 target RNA into GAM3106 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM317260 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM317260 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM317260 target RNA into GAM317260 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4908 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4908 gene: GAM3106 target protein and GAM317260 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3106 and GAM317260

GR4909 T58354 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4909(GR4909) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4909 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4909 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4909 gene encodes GR4909 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4909 precursor RNA folds spatially, forming GR4909 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4909 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4909 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4909 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2

separate GAM precursor RNAs, GAM1814 precursor RNA and GAM143198 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1814 RNA and GAM143198 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1814 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1814 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1814 target RNA into GAM1814 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM143198 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM143198 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM143198 target RNA into GAM143198 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4909 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4909 gene: GAM1814 target protein and GAM143198 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1814 and GAM143198

GR4910 BF508219 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4910 (GR4910) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4910 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4910 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4910 gene encodes GR4910 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR4910 precursor RNA folds spatially, forming GR4910 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4910 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4910 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4910 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM196622 precursor RNA and GAM323806 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM196622 RNA and GAM323806 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM196622 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM196622 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM196622 target RNA into GAM196622 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM323806 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM323806 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM323806 target RNA into GAM323806 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4910 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4910 gene: GAM196622 target protein and GAM323806 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM196622 and GAM323806

GR4911 BG430930 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4911(GR4911) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4911 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4911 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4911 gene encodes GR4911 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4911 precursor RNA folds spatially, forming GR4911 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4911 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4911 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4911 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5193 precursor RNA and GAM41321 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5193 RNA and GAM41321 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5193 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5193 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5193 target RNA into GAM5193 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM41321 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM41321 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM41321 target RNA into GAM41321 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4911 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4911 gene: GAM5193 target protein and GAM41321 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5193 and GAM41321

GR4912 BG722482 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4912(GR4912) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4912 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4912 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4912 gene encodes GR4912 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4912 precursor RNA folds spatially, forming GR4912 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4912 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4912 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4912 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1337 precursor RNA, GAM4182 precursor RNA and GAM256427 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1337 RNA, GAM4182 RNA and GAM256427 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1337 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1337 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1337 target RNA into GAM1337 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM4182 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4182 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4182 target RNA into GAM4182 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM256427 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM256427 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM256427 target RNA into GAM256427 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4912 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4912 gene: GAM1337 target protein, GAM4182 target protein and GAM256427 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1337, GAM4182 and GAM256427

GR4913 BG392938 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4913(GR4913) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4913 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4913 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4913 gene encodes GR4913 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4913 precursor RNA folds spatially, forming GR4913 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4913 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4913 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4913 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM687 precursor RNA and GAM64681 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM687 RNA and GAM64681 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM687 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM687 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM687 target RNA into GAM687 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM64681 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM64681 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM64681 target RNA into GAM64681 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4913 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4913 gene: GAM687 target protein and GAM64681 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM687 and GAM64681

bioinformatically detected regulatory gene, referred to here as Genomic Record 4914 (GR4914) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4914 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4914 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4914 gene encodes GR4914 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4914 precursor RNA folds spatially, forming GR4914 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4914 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4914 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4914 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM64101 precursor RNA and GAM100611 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM64101 RNA and GAM100611 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM64101 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM64101 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM64101 target RNA into GAM64101 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM100611 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM100611 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM100611

target RNA into GAM100611 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4914 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4914 gene: GAM64101 target protein and GAM100611 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM64101 and GAM100611

GR4915 AI670028 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4915(GR4915) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4915 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4915 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4915 gene encodes GR4915 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4915 precursor RNA folds spatially, forming GR4915 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4915 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4915 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4915 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM13814 precursor RNA and GAM280266 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM13814 RNA and GAM280266 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM13814 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM13814 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM13814 target RNA into GAM13814 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM280266 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM280266 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM280266 target RNA into GAM280266 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4915 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4915 gene: GAM13814 target protein and GAM280266 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM13814 and GAM280266

GR4916 BF542106 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4916(GR4916) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4916 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4916 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4916 gene encodes GR4916 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4916 precursor RNA folds spatially, forming GR4916 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4916 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4916 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4916 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2438 precursor RNA and GAM80582 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2438 RNA and GAM80582 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2438 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2438 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2438 target RNA into GAM2438 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM80582 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM80582 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM80582 target RNA into GAM80582 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4916 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4916 gene: GAM2438 target protein and GAM80582 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2438 and GAM80582

GR4917 BG208850 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4917(GR4917) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4917 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4917 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4917 gene encodes GR4917 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4917 precursor RNA folds spatially, forming GR4917 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4917 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4917 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4917 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM181954 precursor RNA and GAM328075 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM181954 RNA and GAM328075 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM181954 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM181954 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM181954 target RNA into GAM181954 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM328075 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM328075 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM328075 target RNA into GAM328075 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4917 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4917 gene: GAM181954 target protein and GAM328075 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM181954 and GAM328075

GR4918 BQ005519 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4918(GR4918) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4918 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4918 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4918 gene encodes GR4918 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4918 precursor RNA folds spatially, forming GR4918 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4918 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4918 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4918 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM52500 precursor RNA and GAM178045 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM52500 RNA and GAM178045 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM52500 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM52500 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM52500 target RNA into GAM52500 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM178045 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM178045 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM178045 target RNA into GAM178045 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4918 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4918 gene: GAM52500 target protein and GAM178045 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM52500 and GAM178045

GR4919 BF691785 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4919(GR4919) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4919 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4919 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4919 gene encodes GR4919 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4919 precursor RNA folds spatially, forming GR4919 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4919 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4919 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4919 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM8171 precursor RNA, GAM47574 precursor RNA and GAM187498 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8171 RNA, GAM47574 RNA and GAM187498 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs

corresponding to GAM RNA of Fig. 8.

GAM8171 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8171 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8171 target RNA into GAM8171 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM47574 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM47574 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM47574 target RNA into GAM47574 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM187498 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM187498 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM187498 target RNA into GAM187498 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4919 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4919 gene: GAM8171 target protein, GAM47574 target protein and GAM187498 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8171, GAM47574 and GAM187498

GR4920 BM718649 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4920 (GR4920) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4920 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4920 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4920 gene encodes GR4920 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR4920 precursor RNA folds spatially, forming GR4920 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4920 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4920 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4920 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM28017 precursor RNA and GAM168764 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM28017 RNA and GAM168764 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM28017 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM28017 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM28017 target RNA into GAM28017 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM168764 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM168764 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM168764 target RNA into GAM168764 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4920 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4920 gene: GAM28017 target protein and GAM168764 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM28017 and GAM168764

GR4921 N94245 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4921 (GR4921) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4921 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4921 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4921 gene encodes GR4921 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4921 precursor RNA folds spatially, forming GR4921 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4921 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4921 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4921 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM218336 precursor RNA and GAM237998 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM218336 RNA and GAM237998 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM218336 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM218336 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM218336 target RNA into GAM218336 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM237998 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM237998 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM237998 target RNA into GAM237998 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4921 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4921 gene: GAM218336 target protein and GAM237998 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM218336 and GAM237998

GR4922 BG530472 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4922(GR4922) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4922 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4922 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4922 gene encodes GR4922 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4922 precursor RNA folds spatially, forming GR4922 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4922 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4922 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4922 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM623 precursor RNA and GAM92090 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM623 RNA and GAM92090 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM623 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM623 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM623 target RNA into GAM623 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM92090 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM92090 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM92090 target RNA into GAM92090 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4922 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4922 gene: GAM623 target protein and GAM92090 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM623 and GAM92090

GR4923 BM148459 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4923(GR4923) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4923 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4923 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4923 gene encodes GR4923 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4923 precursor RNA folds spatially, forming GR4923 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4923 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4923 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4923 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM88612 precursor RNA and GAM272707 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM88612 RNA and GAM272707 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM88612 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM88612 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM88612 target RNA into GAM88612 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM272707 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM272707 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM272707 target RNA into GAM272707 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4923 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4923 gene: GAM88612 target protein and GAM272707 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM88612 and GAM272707

GR4924 AW615320 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4924(GR4924) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4924 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4924 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4924 gene encodes GR4924 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4924 precursor RNA folds spatially, forming GR4924 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4924 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4924 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4924 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM6128 precursor RNA, GAM141948 precursor RNA and GAM146232 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6128 RNA, GAM141948 RNA and GAM146232 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6128 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6128 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6128 target RNA into GAM6128 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM141948 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM141948 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM141948 target RNA into GAM141948 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM146232 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM146232 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM146232 target RNA into GAM146232 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4924 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4924 gene: GAM6128 target protein, GAM141948 target protein and GAM146232 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6128, GAM141948 and GAM146232

GR4925 BI523518 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4925(GR4925) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4925 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4925 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4925 gene encodes GR4925 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4925 precursor RNA folds spatially, forming GR4925 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4925 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4925 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4925 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7986 precursor RNA and GAM267413 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7986 RNA and GAM267413 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7986 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7986 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7986 target RNA into GAM7986 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM267413 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM267413 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM267413 target RNA into GAM267413 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4925 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4925 gene: GAM7986 target protein and GAM267413 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7986 and GAM267413

GR4926 BE903588 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4926(GR4926) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4926 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4926 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4926 gene encodes GR4926 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4926 precursor RNA folds spatially, forming GR4926 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4926 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4926 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4926 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 5 separate GAM precursor RNAs, GAM17206 precursor RNA, GAM261292 precursor RNA, GAM263278 precursor RNA, GAM290228 precursor RNA and GAM319669 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM17206 RNA, GAM261292 RNA, GAM263278 RNA, GAM290228 RNA and GAM319669 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM17206 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM17206 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM17206 target RNA into GAM17206 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM261292 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM261292 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM261292 target RNA into GAM261292 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM263278 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM263278 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM263278 target RNA into GAM263278 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM290228 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM290228 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM290228 target RNA into GAM290228 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM319669 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM319669 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM319669 target RNA into GAM319669 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4926 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4926 gene: GAM17206 target protein, GAM261292 target protein, GAM263278 target protein, GAM290228 target protein and GAM319669 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM17206, GAM261292, GAM263278, GAM290228 and GAM319669

GR4927 BF743263 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4927(GR4927) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4927 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4927 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4927 gene encodes GR4927 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4927 precursor RNA folds spatially, forming GR4927 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4927 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4927 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4927 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5027 precursor RNA and GAM298955 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5027 RNA and GAM298955 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding

to GAM RNA of Fig. 8.

GAM5027 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5027 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5027 target RNA into GAM5027 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM298955 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM298955 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM298955 target RNA into GAM298955 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4927 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4927 gene: GAM5027 target protein and GAM298955 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5027 and GAM298955

GR4928 BE378668 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4928(GR4928) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4928 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4928 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4928 gene encodes GR4928 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4928 precursor RNA folds spatially, forming GR4928 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4928 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4928 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR4928 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1355 precursor RNA, GAM3592 precursor RNA and GAM224588 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1355 RNA, GAM3592 RNA and GAM224588 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1355 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1355 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1355 target RNA into GAM1355 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM3592 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3592 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3592 target RNA into GAM3592 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM224588 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM224588 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM224588 target RNA into GAM224588 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4928 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4928 gene: GAM1355 target protein, GAM3592 target protein and GAM224588 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1355, GAM3592 and GAM224588

GR4929 BG034356 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4929(GR4929) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4929 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4929 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4929 gene encodes GR4929 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4929 precursor RNA folds spatially, forming GR4929 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4929 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4929 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4929 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM355 precursor RNA, GAM172673 precursor RNA and GAM324521 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM355 RNA, GAM172673 RNA and GAM324521 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM355 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM355 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM355 target RNA into GAM355 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM172673 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM172673 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM172673 target RNA into GAM172673 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM324521 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM324521 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM324521 target RNA into GAM324521 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4929 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4929 gene: GAM355 target protein, GAM172673 target protein and GAM324521 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM355, GAM172673 and GAM324521

GR4930 AI632021 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4930 (GR4930) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4930 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4930 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4930 gene encodes GR4930 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4930 precursor RNA folds spatially, forming GR4930 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4930 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4930 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4930 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2

separate GAM precursor RNAs, GAM213119 precursor RNA and GAM280274 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM213119 RNA and GAM280274 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM213119 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM213119 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM213119 target RNA into GAM213119 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM280274 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM280274 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM280274 target RNA into GAM280274 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4930 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4930 gene: GAM213119 target protein and GAM280274 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM213119 and GAM280274

GR4931 BF129448 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4931 (GR4931) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4931 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4931 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4931 gene encodes GR4931 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR4931 precursor RNA folds spatially, forming GR4931 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4931 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4931 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4931 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM891 precursor RNA and GAM228363 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM891 RNA and GAM228363 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM891 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM891 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM891 target RNA into GAM891 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM228363 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM228363 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM228363 target RNA into GAM228363 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4931 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4931 gene: GAM891 target protein and GAM228363 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM891 and GAM228363

GR4932 BG716336 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4932(GR4932) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4932 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4932 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4932 gene encodes GR4932 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4932 precursor RNA folds spatially, forming GR4932 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4932 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4932 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4932 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM511 precursor RNA and GAM88897 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM511 RNA and GAM88897 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM511 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM511 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM511 target RNA into GAM511 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM88897 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM88897 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM88897 target RNA into GAM88897 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4932 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4932 gene: GAM511 target protein and GAM88897 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM511 and GAM88897

GR4933 AA435616 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4933(GR4933) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4933 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4933 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4933 gene encodes GR4933 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4933 precursor RNA folds spatially, forming GR4933 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4933 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4933 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4933 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM115001 precursor RNA and GAM118521 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM115001 RNA and GAM118521 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM115001 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM115001 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM115001 target RNA into GAM115001 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM118521 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM118521 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM118521 target RNA into GAM118521 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4933 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4933 gene: GAM115001 target protein and GAM118521 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM115001 and GAM118521

GR4934 BE066410 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4934(GR4934) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4934 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4934 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4934 gene encodes GR4934 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4934 precursor RNA folds spatially, forming GR4934 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4934 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4934 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4934 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM1722 precursor RNA, GAM2968 precursor RNA, GAM34834 precursor RNA and GAM148129 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1722 RNA, GAM2968 RNA, GAM34834 RNA and GAM148129 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1722 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1722 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1722 target RNA into GAM1722 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM2968 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2968 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2968 target RNA into GAM2968 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM34834 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM34834 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM34834 target RNA into GAM34834 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM148129 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM148129 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM148129 target RNA into GAM148129 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4934 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR4934 gene: GAM1722 target protein, GAM2968 target protein, GAM34834 target protein and GAM148129 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1722, GAM2968, GAM34834 and GAM148129

GR4935 BQ063283 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4935(GR4935) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4935 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4935 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4935 gene encodes GR4935 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4935 precursor RNA folds spatially, forming GR4935 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4935 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4935 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4935 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1960 precursor RNA and GAM57533 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1960 RNA and GAM57533 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1960 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1960 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1960 target RNA into

GAM1960 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM57533 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM57533 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM57533 target RNA into GAM57533 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4935 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4935 gene: GAM1960 target protein and GAM57533 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1960 and GAM57533

GR4936 BG505752 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4936(GR4936) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4936 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4936 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4936 gene encodes GR4936 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4936 precursor RNA folds spatially, forming GR4936 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4936 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4936 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4936 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4622 precursor RNA, GAM7498 precursor RNA and GAM325758 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED

PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4622 RNA, GAM7498 RNA and GAM325758 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4622 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4622 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4622 target RNA into GAM4622 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7498 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7498 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7498 target RNA into GAM7498 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM325758 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM325758 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM325758 target RNA into GAM325758 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4936 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4936 gene: GAM4622 target protein, GAM7498 target protein and GAM325758 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4622, GAM7498 and GAM325758

GR4937 AI264325 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4937(GR4937) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4937 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4937 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4937 gene encodes GR4937 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4937 precursor RNA folds spatially, forming GR4937 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4937 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4937 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4937 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM916 precursor RNA, GAM14893 precursor RNA and GAM320260 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM916 RNA, GAM14893 RNA and GAM320260 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM916 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM916 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM916 target RNA into GAM916 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM14893 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM14893 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM14893 target RNA into GAM14893 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM320260 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM320260 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM320260 target RNA into GAM320260 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4937 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4937 gene: GAM916 target protein, GAM14893 target protein and GAM320260 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM916, GAM14893 and GAM320260

GR4938 AI110693 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4938(GR4938) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4938 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4938 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4938 gene encodes GR4938 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4938 precursor RNA folds spatially, forming GR4938 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4938 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4938 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4938 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3274 precursor RNA and GAM7923 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3274 RNA and GAM7923 RNA, herein schematically

represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3274 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3274 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3274 target RNA into GAM3274 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7923 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7923 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7923 target RNA into GAM7923 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4938 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4938 gene: GAM3274 target protein and GAM7923 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3274 and GAM7923

GR4939 BG470643 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4939(GR4939) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4939 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4939 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4939 gene encodes GR4939 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4939 precursor RNA folds spatially, forming GR4939 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4939 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4939 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4939 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM64509 precursor RNA and GAM241466 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM64509 RNA and GAM241466 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM64509 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM64509 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM64509 target RNA into GAM64509 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM241466 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM241466 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM241466 target RNA into GAM241466 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4939 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4939 gene: GAM64509 target protein and GAM241466 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM64509 and GAM241466

GR4940 AA757438 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4940(GR4940) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4940 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR4940 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4940 gene encodes GR4940 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4940 precursor RNA folds spatially, forming GR4940 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4940 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4940 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4940 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7557 precursor RNA and GAM240474 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7557 RNA and GAM240474 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7557 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7557 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7557 target RNA into GAM7557 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM240474 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM240474 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM240474 target RNA into GAM240474 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4940 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4940 gene: GAM7557 target

protein and GAM240474 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7557 and GAM240474

GR4941 BE539471 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4941 (GR4941) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4941 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4941 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4941 gene encodes GR4941 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4941 precursor RNA folds spatially, forming GR4941 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4941 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4941 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4941 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2702 precursor RNA and GAM128853 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2702 RNA and GAM128853 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2702 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2702 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2702 target RNA into GAM2702 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM128853 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM128853 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM128853 target RNA into GAM128853 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4941 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4941 gene: GAM2702 target protein and GAM128853 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2702 and GAM128853

GR4942 BG386843 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4942(GR4942) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4942 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4942 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4942 gene encodes GR4942 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4942 precursor RNA folds spatially, forming GR4942 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4942 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4942 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4942 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM147259 precursor RNA and GAM209148 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM147259 RNA and GAM209148 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM147259 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM147259 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM147259 target RNA into GAM147259 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM209148 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM209148 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM209148 target RNA into GAM209148 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4942 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4942 gene: GAM147259 target protein and GAM209148 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM147259 and GAM209148

GR4943 AA292562 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4943(GR4943) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4943 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4943 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4943 gene encodes GR4943 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4943 precursor RNA folds spatially, forming GR4943 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4943 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR4943 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4943 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM103418 precursor RNA and GAM219164 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM103418 RNA and GAM219164 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM103418 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM103418 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM103418 target RNA into GAM103418 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM219164 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM219164 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM219164 target RNA into GAM219164 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4943 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4943 gene: GAM103418 target protein and GAM219164 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM103418 and GAM219164

GR4944 BM354061 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4944(GR4944) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4944 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4944 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4944 gene encodes GR4944 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4944 precursor RNA folds spatially, forming GR4944 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4944 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4944 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4944 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM126769 precursor RNA and GAM302160 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM126769 RNA and GAM302160 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM126769 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM126769 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM126769 target RNA into GAM126769 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM302160 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM302160 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM302160 target RNA into GAM302160 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4944 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4944 gene: GAM126769 target protein and GAM302160 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM126769 and GAM302160

GR4945 AV732170 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4945(GR4945) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4945 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4945 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4945 gene encodes GR4945 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4945 precursor RNA folds spatially, forming GR4945 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4945 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4945 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4945 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3115 precursor RNA and GAM187751 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3115 RNA and GAM187751 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3115 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3115 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3115 target RNA into

GAM3115 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM187751 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM187751 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM187751 target RNA into GAM187751 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4945 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4945 gene: GAM3115 target protein and GAM187751 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3115 and GAM187751

GR4946 AI937497 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4946(GR4946) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4946 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4946 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4946 gene encodes GR4946 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4946 precursor RNA folds spatially, forming GR4946 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4946 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4946 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4946 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM127374 precursor RNA and GAM280541 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM127374 RNA and GAM280541 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM127374 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM127374 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM127374 target RNA into GAM127374 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM280541 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM280541 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM280541 target RNA into GAM280541 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4946 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4946 gene: GAM127374 target protein and GAM280541 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM127374 and GAM280541

GR4947 BG178531 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4947(GR4947) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4947 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4947 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4947 gene encodes GR4947 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4947 precursor RNA folds spatially, forming GR4947 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated

that GR4947 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4947 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4947 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM81704 precursor RNA, GAM208462 precursor RNA and GAM323547 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM81704 RNA, GAM208462 RNA and GAM323547 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM81704 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM81704 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM81704 target RNA into GAM81704 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM208462 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM208462 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM208462 target RNA into GAM208462 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM323547 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM323547 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM323547 target RNA into GAM323547 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4947 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4947 gene: GAM81704 target

protein, GAM208462 target protein and GAM323547 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM81704, GAM208462 and GAM323547

GR4948 BE673464 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4948(GR4948) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4948 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4948 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4948 gene encodes GR4948 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4948 precursor RNA folds spatially, forming GR4948 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4948 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4948 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4948 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM146662 precursor RNA, GAM291765 precursor RNA, GAM332407 precursor RNA and GAM335730 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM146662 RNA, GAM291765 RNA, GAM332407 RNA and GAM335730 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM146662 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM146662 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM146662

target RNA into GAM146662 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM291765 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM291765 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM291765 target RNA into GAM291765 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM332407 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM332407 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM332407 target RNA into GAM332407 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM335730 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM335730 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM335730 target RNA into GAM335730 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4948 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4948 gene: GAM146662 target protein, GAM291765 target protein, GAM332407 target protein and GAM335730 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM146662, GAM291765, GAM332407 and GAM335730

GR4949 BM680642 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4949(GR4949) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4949 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4949 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4949 gene encodes GR4949 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR4949 precursor RNA folds spatially, forming GR4949 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4949 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4949 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4949 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM107044 precursor RNA and GAM224868 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM107044 RNA and GAM224868 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM107044 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM107044 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM107044 target RNA into GAM107044 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM224868 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM224868 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM224868 target RNA into GAM224868 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4949 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4949 gene: GAM107044 target protein and GAM224868 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM107044 and GAM224868

GR4950 BE939208 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4950(GR4950) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4950 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4950 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4950 gene encodes GR4950 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4950 precursor RNA folds spatially, forming GR4950 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4950 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4950 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4950 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM5594 precursor RNA, GAM20885 precursor RNA and GAM328485 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5594 RNA, GAM20885 RNA and GAM328485 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5594 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5594 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5594 target RNA into GAM5594 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM20885 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM20885 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM20885 target RNA into GAM20885 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM328485 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM328485 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM328485 target RNA into GAM328485 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4950 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4950 gene: GAM5594 target protein, GAM20885 target protein and GAM328485 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5594, GAM20885 and GAM328485

GR4951 BF303752 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4951 (GR4951) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4951 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4951 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4951 gene encodes GR4951 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4951 precursor RNA folds spatially, forming GR4951 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4951 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4951 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4951 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8005 precursor RNA and GAM314363 precursor

RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8005 RNA and GAM314363 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8005 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8005 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8005 target RNA into GAM8005 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM314363 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM314363 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM314363 target RNA into GAM314363 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4951 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4951 gene: GAM8005 target protein and GAM314363 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8005 and GAM314363

GR4952 BF832870 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4952(GR4952) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4952 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4952 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4952 gene encodes GR4952 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4952 precursor RNA folds spatially, forming GR4952 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4952 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4952 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4952 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2312 precursor RNA and GAM120565 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2312 RNA and GAM120565 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2312 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2312 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2312 target RNA into GAM2312 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM120565 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM120565 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM120565 target RNA into GAM120565 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4952 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4952 gene: GAM2312 target protein and GAM120565 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2312 and GAM120565

bioinformatically detected regulatory gene, referred to here as Genomic Record 4953(GR4953) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4953 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4953 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4953 gene encodes GR4953 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4953 precursor RNA folds spatially, forming GR4953 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4953 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4953 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4953 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM474 precursor RNA, GAM145393 precursor RNA, GAM161861 precursor RNA and GAM243424 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM474 RNA, GAM145393 RNA, GAM161861 RNA and GAM243424 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM474 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM474 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM474 target RNA into GAM474 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM145393 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM145393 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM145393 target RNA into GAM145393 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM161861 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM161861 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM161861 target RNA into GAM161861 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM243424 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM243424 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM243424 target RNA into GAM243424 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4953 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4953 gene: GAM474 target protein, GAM145393 target protein, GAM161861 target protein and GAM243424 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM474, GAM145393, GAM161861 and GAM243424

GR4954 AW971865 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4954(GR4954) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4954 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4954 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4954 gene encodes GR4954 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4954 precursor RNA folds spatially, forming GR4954 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4954 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4954 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4954 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM85119 precursor RNA, GAM212876 precursor RNA and GAM234234 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM85119 RNA, GAM212876 RNA and GAM234234 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM85119 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM85119 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM85119 target RNA into GAM85119 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM212876 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM212876 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM212876 target RNA into GAM212876 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM234234 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM234234 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM234234 target RNA into GAM234234 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4954 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4954 gene: GAM85119 target protein, GAM212876 target protein and GAM234234 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6,

hereby incorporated by reference, with references to GAM85119, GAM212876 and GAM234234

GR4955 BE620036 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4955(GR4955) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4955 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4955 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4955 gene encodes GR4955 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4955 precursor RNA folds spatially, forming GR4955 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4955 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4955 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4955 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM89635 precursor RNA and GAM134506 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM89635 RNA and GAM134506 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM89635 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM89635 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM89635 target RNA into GAM89635 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM134506 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM134506 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM134506 target RNA into GAM134506 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4955 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4955 gene: GAM89635 target protein and GAM134506 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM89635 and GAM134506

GR4956 AW062437 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4956(GR4956) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4956 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4956 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4956 gene encodes GR4956 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4956 precursor RNA folds spatially, forming GR4956 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4956 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4956 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4956 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2211 precursor RNA and GAM23036 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2211 RNA and GAM23036 RNA, herein schematically

represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2211 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2211 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2211 target RNA into GAM2211 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM23036 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM23036 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM23036 target RNA into GAM23036 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4956 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4956 gene: GAM2211 target protein and GAM23036 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2211 and GAM23036

GR4957 AI417795 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4957(GR4957) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4957 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4957 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4957 gene encodes GR4957 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4957 precursor RNA folds spatially, forming GR4957 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4957 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4957 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4957 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM77385 precursor RNA and GAM82546 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM77385 RNA and GAM82546 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM77385 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM77385 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM77385 target RNA into GAM77385 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM82546 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM82546 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM82546 target RNA into GAM82546 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4957 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4957 gene: GAM77385 target protein and GAM82546 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM77385 and GAM82546

GR4958 AI963134 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4958(GR4958) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4958 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR4958 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4958 gene encodes GR4958 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4958 precursor RNA folds spatially, forming GR4958 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4958 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4958 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4958 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1343 precursor RNA and GAM175210 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1343 RNA and GAM175210 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1343 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1343 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1343 target RNA into GAM1343 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM175210 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM175210 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM175210 target RNA into GAM175210 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4958 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4958 gene: GAM1343 target

protein and GAM175210 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1343 and GAM175210

GR4959 BE255166 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4959(GR4959) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4959 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4959 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4959 gene encodes GR4959 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4959 precursor RNA folds spatially, forming GR4959 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4959 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4959 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4959 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM418 precursor RNA and GAM244993 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM418 RNA and GAM244993 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM418 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM418 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM418 target RNA into GAM418 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM244993 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM244993 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM244993 target RNA into GAM244993 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4959 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4959 gene: GAM418 target protein and GAM244993 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM418 and GAM244993

GR4960 BE259854 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4960(GR4960) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4960 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4960 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4960 gene encodes GR4960 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4960 precursor RNA folds spatially, forming GR4960 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4960 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4960 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4960 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8137 precursor RNA and GAM309094 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8137 RNA and GAM309094 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8137 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8137 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8137 target RNA into GAM8137 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM309094 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM309094 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM309094 target RNA into GAM309094 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4960 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4960 gene: GAM8137 target protein and GAM309094 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8137 and GAM309094

GR4961 BE314095 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4961(GR4961) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4961 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4961 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4961 gene encodes GR4961 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4961 precursor RNA folds spatially, forming GR4961 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4961 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR4961 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4961 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM264 precursor RNA and GAM7063 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM264 RNA and GAM7063 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM264 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM264 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM264 target RNA into GAM264 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7063 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7063 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7063 target RNA into GAM7063 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4961 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4961 gene: GAM264 target protein and GAM7063 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM264 and GAM7063

GR4962 AW405988 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4962(GR4962) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4962 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4962 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4962 gene encodes GR4962 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4962 precursor RNA folds spatially, forming GR4962 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4962 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4962 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4962 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6682 precursor RNA and GAM249678 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6682 RNA and GAM249678 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6682 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6682 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6682 target RNA into GAM6682 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM249678 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM249678 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM249678 target RNA into GAM249678 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4962 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4962 gene: GAM6682 target protein and GAM249678 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6682 and GAM249678

GR4963 AI708665 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4963(GR4963) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4963 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4963 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4963 gene encodes GR4963 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4963 precursor RNA folds spatially, forming GR4963 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4963 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4963 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4963 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4195 precursor RNA and GAM11236 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4195 RNA and GAM11236 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4195 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4195 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4195 target RNA into

GAM4195 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM11236 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM11236 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM11236 target RNA into GAM11236 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4963 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4963 gene: GAM4195 target protein and GAM11236 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4195 and GAM11236

GR4964 BG029926 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4964(GR4964) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4964 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4964 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4964 gene encodes GR4964 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4964 precursor RNA folds spatially, forming GR4964 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4964 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4964 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4964 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM161 precursor RNA, GAM8491 precursor RNA and GAM80079 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED

PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM161 RNA, GAM8491 RNA and GAM80079 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM161 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM161 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM161 target RNA into GAM161 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8491 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8491 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8491 target RNA into GAM8491 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM80079 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM80079 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM80079 target RNA into GAM80079 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4964 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4964 gene: GAM161 target protein, GAM8491 target protein and GAM80079 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM161, GAM8491 and GAM80079

GR4965 H22102 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4965(GR4965) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4965 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4965 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4965 gene encodes GR4965 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4965 precursor RNA folds spatially, forming GR4965 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4965 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4965 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4965 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM298148 precursor RNA and GAM325517 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM298148 RNA and GAM325517 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM298148 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM298148 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM298148 target RNA into GAM298148 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM325517 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM325517 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM325517 target RNA into GAM325517 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4965 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR4965 gene: GAM298148 target protein and GAM325517 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM298148 and GAM325517

GR4966 AI031832 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4966(GR4966) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4966 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4966 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4966 gene encodes GR4966 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4966 precursor RNA folds spatially, forming GR4966 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4966 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4966 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4966 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM47631 precursor RNA and GAM97492 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM47631 RNA and GAM97492 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM47631 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM47631 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM47631 target RNA into GAM47631 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM97492 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM97492 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM97492 target RNA into GAM97492 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4966 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4966 gene: GAM47631 target protein and GAM97492 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM47631 and GAM97492

GR4967 AL698394 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4967(GR4967) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4967 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4967 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4967 gene encodes GR4967 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4967 precursor RNA folds spatially, forming GR4967 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4967 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4967 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4967 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM1114 precursor RNA, GAM43625 precursor RNA, GAM168958 precursor RNA and GAM321804 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1114 RNA, GAM43625 RNA, GAM168958 RNA and GAM321804 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1114 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1114 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1114 target RNA into GAM1114 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM43625 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM43625 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM43625 target RNA into GAM43625 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM168958 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM168958 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM168958 target RNA into GAM168958 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM321804 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM321804 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM321804 target RNA into GAM321804 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4967 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4967 gene: GAM1114 target protein, GAM43625 target protein, GAM168958 target protein and GAM321804 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1114, GAM43625, GAM168958 and GAM321804

GR4968 BG231524 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4968(GR4968) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4968 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4968 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4968 gene encodes GR4968 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4968 precursor RNA folds spatially, forming GR4968 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4968 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4968 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4968 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2558 precursor RNA and GAM106094 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2558 RNA and GAM106094 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2558 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2558 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2558 target RNA into GAM2558 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM106094 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM106094 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM106094 target RNA into GAM106094 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4968 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4968 gene: GAM2558 target protein and GAM106094 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2558 and GAM106094

GR4969 BF915784 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4969(GR4969) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4969 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4969 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4969 gene encodes GR4969 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4969 precursor RNA folds spatially, forming GR4969 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4969 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4969 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4969 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM294 precursor RNA and GAM64903 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM294 RNA and GAM64903 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM294 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM294 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM294 target RNA into GAM294 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM64903 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM64903 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM64903 target RNA into GAM64903 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4969 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4969 gene: GAM294 target protein and GAM64903 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM294 and GAM64903

GR4970 AI640408 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4970(GR4970) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4970 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4970 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4970 gene encodes GR4970 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4970 precursor RNA folds spatially, forming GR4970 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4970 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4970 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4970 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3871 precursor RNA and GAM291407 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3871 RNA and GAM291407 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3871 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3871 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3871 target RNA into GAM3871 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM291407 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM291407 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM291407 target RNA into GAM291407 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4970 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4970 gene: GAM3871 target protein and GAM291407 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3871 and GAM291407

GR4971 AA091126 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4971 (GR4971) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4971 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4971 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4971 gene encodes GR4971 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4971 precursor RNA folds spatially, forming GR4971 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4971 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4971 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4971 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM121327 precursor RNA and GAM157790 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM121327 RNA and GAM157790 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM121327 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM121327 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM121327 target RNA into GAM121327 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM157790 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM157790 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM157790 target RNA into GAM157790 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4971 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4971 gene: GAM121327 target protein and GAM157790 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference,

with references to GAM121327 and GAM157790

GR4972 AA741519 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4972(GR4972) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4972 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4972 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4972 gene encodes GR4972 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4972 precursor RNA folds spatially, forming GR4972 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4972 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4972 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4972 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM155 precursor RNA and GAM182851 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM155 RNA and GAM182851 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM155 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM155 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM155 target RNA into GAM155 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM182851 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM182851 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM182851 target RNA into GAM182851 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4972 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4972 gene: GAM155 target protein and GAM182851 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM155 and GAM182851

GR4973 AW385123 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4973(GR4973) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4973 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4973 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4973 gene encodes GR4973 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4973 precursor RNA folds spatially, forming GR4973 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4973 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4973 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4973 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3007 precursor RNA, GAM4612 precursor RNA and GAM82511 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3007 RNA, GAM4612 RNA and GAM82511 RNA, herein

schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3007 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3007 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3007 target RNA into GAM3007 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM4612 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4612 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4612 target RNA into GAM4612 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM82511 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM82511 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM82511 target RNA into GAM82511 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4973 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4973 gene: GAM3007 target protein, GAM4612 target protein and GAM82511 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3007, GAM4612 and GAM82511

GR4974 BM724792 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4974(GR4974) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4974 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4974 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4974 gene encodes GR4974 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4974 precursor RNA folds spatially, forming GR4974 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4974 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4974 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4974 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM199476 precursor RNA and GAM236353 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM199476 RNA and GAM236353 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM199476 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM199476 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM199476 target RNA into GAM199476 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM236353 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM236353 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM236353 target RNA into GAM236353 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4974 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4974 gene: GAM199476 target protein and GAM236353 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM199476 and GAM236353

GR4975 BF701680 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4975(GR4975) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4975 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4975 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4975 gene encodes GR4975 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4975 precursor RNA folds spatially, forming GR4975 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4975 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4975 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4975 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4124 precursor RNA, GAM103946 precursor RNA and GAM323719 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4124 RNA, GAM103946 RNA and GAM323719 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4124 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4124 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4124 target RNA into GAM4124 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM103946 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM103946 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM103946 target RNA into GAM103946 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM323719 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM323719 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM323719 target RNA into GAM323719 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4975 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4975 gene: GAM4124 target protein, GAM103946 target protein and GAM323719 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4124, GAM103946 and GAM323719

GR4976 BG980005 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4976(GR4976) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4976 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4976 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4976 gene encodes GR4976 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4976 precursor RNA folds spatially, forming GR4976 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4976 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4976 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4976 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2

separate GAM precursor RNAs, GAM1998 precursor RNA and GAM256737 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1998 RNA and GAM256737 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1998 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1998 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1998 target RNA into GAM1998 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM256737 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM256737 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM256737 target RNA into GAM256737 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4976 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4976 gene: GAM1998 target protein and GAM256737 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1998 and GAM256737

GR4977 BF351327 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4977(GR4977) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4977 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4977 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4977 gene encodes GR4977 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR4977 precursor RNA folds spatially, forming GR4977 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4977 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4977 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4977 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM114164 precursor RNA, GAM244071 precursor RNA and GAM291870 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM114164 RNA, GAM244071 RNA and GAM291870 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM114164 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM114164 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM114164 target RNA into GAM114164 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM244071 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM244071 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM244071 target RNA into GAM244071 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM291870 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM291870 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM291870 target RNA into GAM291870 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4977 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4977 gene: GAM114164 target protein, GAM244071 target protein and GAM291870 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM114164, GAM244071 and GAM291870

GR4978 H12380 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4978(GR4978) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4978 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4978 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4978 gene encodes GR4978 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4978 precursor RNA folds spatially, forming GR4978 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4978 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4978 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4978 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM338 precursor RNA and GAM186055 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM338 RNA and GAM186055 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM338 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM338 target RNA, herein schematically represented by

GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM338 target RNA into GAM338 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM186055 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM186055 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM186055 target RNA into GAM186055 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4978 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4978 gene: GAM338 target protein and GAM186055 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM338 and GAM186055

GR4979 BF526443 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4979(GR4979) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4979 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4979 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4979 gene encodes GR4979 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4979 precursor RNA folds spatially, forming GR4979 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4979 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4979 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4979 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM13009 precursor RNA and GAM213913 precursor

RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM13009 RNA and GAM213913 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM13009 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM13009 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM13009 target RNA into GAM13009 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM213913 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM213913 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM213913 target RNA into GAM213913 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4979 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4979 gene: GAM13009 target protein and GAM213913 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM13009 and GAM213913

GR4980 BM264209 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4980 (GR4980) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4980 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4980 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4980 gene encodes GR4980 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4980 precursor RNA folds spatially, forming GR4980 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4980 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4980 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4980 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM7509 precursor RNA, GAM32968 precursor RNA, GAM144894 precursor RNA and GAM264368 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7509 RNA, GAM32968 RNA, GAM144894 RNA and GAM264368 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7509 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7509 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7509 target RNA into GAM7509 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM32968 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM32968 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM32968 target RNA into GAM32968 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM144894 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM144894 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM144894 target RNA into GAM144894 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM264368 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM264368 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM264368 target RNA into GAM264368 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4980 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4980 gene: GAM7509 target protein, GAM32968 target protein, GAM144894 target protein and GAM264368 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7509, GAM32968, GAM144894 and GAM264368

GR4981 BG498058 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4981(GR4981) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4981 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4981 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4981 gene encodes GR4981 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4981 precursor RNA folds spatially, forming GR4981 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4981 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4981 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4981 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM1304 precursor RNA, GAM96867 precursor RNA, GAM253137 precursor RNA and GAM309182 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1304 RNA, GAM96867 RNA, GAM253137 RNA and GAM309182 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1304 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1304 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1304 target RNA into GAM1304 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM96867 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM96867 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM96867 target RNA into GAM96867 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM253137 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM253137 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM253137 target RNA into GAM253137 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM309182 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM309182 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM309182 target RNA into GAM309182 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4981 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4981 gene: GAM1304 target protein, GAM96867 target protein, GAM253137 target protein and GAM309182 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1304, GAM96867, GAM253137 and GAM309182

4982(GR4982) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4982 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4982 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4982 gene encodes GR4982 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4982 precursor RNA folds spatially, forming GR4982 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4982 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4982 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4982 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM179630 precursor RNA and GAM247294 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM179630 RNA and GAM247294 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM179630 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM179630 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM179630 target RNA into GAM179630 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM247294 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM247294 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM247294 target RNA into GAM247294 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4982 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4982 gene: GAM179630 target protein and GAM247294 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM179630 and GAM247294

GR4983 AI018087 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4983(GR4983) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4983 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4983 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4983 gene encodes GR4983 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4983 precursor RNA folds spatially, forming GR4983 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4983 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4983 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4983 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM612 precursor RNA, GAM32996 precursor RNA and GAM259875 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM612 RNA, GAM32996 RNA and GAM259875 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM612 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM612 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM612 target RNA into GAM612 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM32996 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM32996 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM32996 target RNA into GAM32996 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM259875 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM259875 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM259875 target RNA into GAM259875 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4983 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4983 gene: GAM612 target protein, GAM32996 target protein and GAM259875 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM612, GAM32996 and GAM259875

GR4984 BG214720 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4984(GR4984) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4984 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4984 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4984 gene encodes GR4984 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4984 precursor RNA folds spatially, forming GR4984 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4984 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4984 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4984 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM38787 precursor RNA and GAM113616 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM38787 RNA and GAM113616 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM38787 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM38787 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM38787 target RNA into GAM38787 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM113616 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM113616 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM113616 target RNA into GAM113616 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4984 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4984 gene: GAM38787 target protein and GAM113616 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM38787 and GAM113616

GR4985 BF984706 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4985(GR4985) gene, which encodes an `operon-like` cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4985 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4985 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4985 gene encodes GR4985 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4985 precursor RNA folds spatially, forming GR4985 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4985 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4985 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4985 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM89 precursor RNA and GAM5701 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM89 RNA and GAM5701 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM89 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM89 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM89 target RNA into GAM89 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5701 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5701 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5701 target RNA into GAM5701 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4985 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4985 gene: GAM89 target protein and GAM5701 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM89 and GAM5701

GR4986 AW021974 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4986(GR4986) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4986 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4986 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4986 gene encodes GR4986 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4986 precursor RNA folds spatially, forming GR4986 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4986 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4986 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4986 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM222902 precursor RNA and GAM235637 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM222902 RNA and GAM235637 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM222902 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM222902 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM222902 target RNA into GAM222902 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM235637 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM235637 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM235637 target RNA into GAM235637 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4986 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4986 gene: GAM222902 target protein and GAM235637 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM222902 and GAM235637

GR4987 BM023359 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4987(GR4987) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4987 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4987 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4987 gene encodes GR4987 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4987 precursor RNA folds spatially, forming GR4987 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4987 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4987 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4987 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1669 precursor RNA, GAM105589 precursor RNA

and GAM152620 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1669 RNA, GAM105589 RNA and GAM152620 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1669 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1669 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1669 target RNA into GAM1669 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM105589 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM105589 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM105589 target RNA into GAM105589 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM152620 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM152620 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM152620 target RNA into GAM152620 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4987 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4987 gene: GAM1669 target protein, GAM105589 target protein and GAM152620 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1669, GAM105589 and GAM152620

GR4988 BG434715 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4988(GR4988) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR4988 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4988 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4988 gene encodes GR4988 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4988 precursor RNA folds spatially, forming GR4988 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4988 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4988 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4988 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM162526 precursor RNA and GAM207954 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM162526 RNA and GAM207954 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM162526 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM162526 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM162526 target RNA into GAM162526 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM207954 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM207954 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM207954 target RNA into GAM207954 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4988 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4988 gene: GAM162526 target protein and GAM207954 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM162526 and GAM207954

GR4989 BF902557 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4989(GR4989) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4989 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4989 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4989 gene encodes GR4989 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4989 precursor RNA folds spatially, forming GR4989 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4989 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4989 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4989 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM114 precursor RNA and GAM98095 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM114 RNA and GAM98095 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM114 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM114 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds

to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM114 target RNA into GAM114 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM98095 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM98095 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM98095 target RNA into GAM98095 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4989 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4989 gene: GAM114 target protein and GAM98095 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM114 and GAM98095

GR4990 BG707048 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4990(GR4990) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4990 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4990 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4990 gene encodes GR4990 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4990 precursor RNA folds spatially, forming GR4990 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4990 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4990 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4990 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM5979 precursor RNA, GAM49342 precursor RNA, GAM55423 precursor RNA and GAM219565 precursor RNA, herein schematically

represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5979 RNA, GAM49342 RNA, GAM55423 RNA and GAM219565 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5979 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5979 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5979 target RNA into GAM5979 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM49342 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM49342 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM49342 target RNA into GAM49342 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM55423 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM55423 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM55423 target RNA into GAM55423 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM219565 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM219565 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM219565 target RNA into GAM219565 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4990 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4990 gene: GAM5979 target protein, GAM49342 target protein, GAM55423 target protein and GAM219565 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with

reference to Table 6, hereby incorporated by reference, with references to GAM5979, GAM49342, GAM55423 and GAM219565

GR4991 AA524055 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4991 (GR4991) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4991 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4991 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4991 gene encodes GR4991 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4991 precursor RNA folds spatially, forming GR4991 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4991 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4991 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4991 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM187168 precursor RNA and GAM260230 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM187168 RNA and GAM260230 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM187168 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM187168 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM187168 target RNA into GAM187168 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM260230 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM260230 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM260230 target RNA into GAM260230 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4991 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4991 gene: GAM187168 target protein and GAM260230 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM187168 and GAM260230

GR4992 BI089001 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4992(GR4992) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4992 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4992 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4992 gene encodes GR4992 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4992 precursor RNA folds spatially, forming GR4992 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4992 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4992 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4992 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3528 precursor RNA, GAM3907 precursor RNA and GAM122464 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM3528 RNA, GAM3907 RNA and GAM122464 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3528 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3528 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3528 target RNA into GAM3528 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM3907 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3907 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3907 target RNA into GAM3907 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM122464 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM122464 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM122464 target RNA into GAM122464 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4992 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4992 gene: GAM3528 target protein, GAM3907 target protein and GAM122464 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3528, GAM3907 and GAM122464

GR4993 AA640656 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4993(GR4993) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4993 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4993 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4993 gene encodes GR4993 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4993 precursor RNA folds spatially, forming GR4993 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4993 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4993 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4993 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4302 precursor RNA and GAM25033 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4302 RNA and GAM25033 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4302 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4302 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4302 target RNA into GAM4302 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM25033 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM25033 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM25033 target RNA into GAM25033 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4993 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4993 gene: GAM4302 target protein and GAM25033 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference,

with references to GAM4302 and GAM25033

GR4994 BI335003 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4994 (GR4994) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4994 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4994 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4994 gene encodes GR4994 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4994 precursor RNA folds spatially, forming GR4994 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4994 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4994 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4994 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8493 precursor RNA and GAM14586 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8493 RNA and GAM14586 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8493 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8493 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8493 target RNA into GAM8493 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM14586 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM14586 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM14586 target RNA into GAM14586 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4994 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4994 gene: GAM8493 target protein and GAM14586 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8493 and GAM14586

GR4995 BF243066 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4995(GR4995) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4995 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4995 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4995 gene encodes GR4995 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4995 precursor RNA folds spatially, forming GR4995 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4995 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4995 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4995 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3128 precursor RNA, GAM180305 precursor RNA and GAM260773 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3128 RNA, GAM180305 RNA and GAM260773 RNA, herein

schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3128 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3128 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3128 target RNA into GAM3128 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM180305 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM180305 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM180305 target RNA into GAM180305 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM260773 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM260773 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM260773 target RNA into GAM260773 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4995 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4995 gene: GAM3128 target protein, GAM180305 target protein and GAM260773 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3128, GAM180305 and GAM260773

GR4996 BG168830 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4996(GR4996) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4996 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4996 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4996 gene encodes GR4996 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4996 precursor RNA folds spatially, forming GR4996 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4996 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4996 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4996 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM86344 precursor RNA, GAM230375 precursor RNA and GAM324412 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM86344 RNA, GAM230375 RNA and GAM324412 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM86344 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM86344 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM86344 target RNA into GAM86344 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM230375 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM230375 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM230375 target RNA into GAM230375 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM324412 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM324412 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM324412 target RNA into GAM324412 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4996 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4996 gene: GAM86344 target protein, GAM230375 target protein and GAM324412 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM86344, GAM230375 and GAM324412

GR4997 AA258610 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4997(GR4997) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4997 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4997 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4997 gene encodes GR4997 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4997 precursor RNA folds spatially, forming GR4997 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4997 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4997 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4997 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM212130 precursor RNA and GAM264107 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM212130 RNA and GAM264107 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM212130 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM212130 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM212130 target RNA into GAM212130 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM264107 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM264107 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM264107 target RNA into GAM264107 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4997 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4997 gene: GAM212130 target protein and GAM264107 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM212130 and GAM264107

GR4998 BG776604 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4998(GR4998) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4998 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4998 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4998 gene encodes GR4998 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4998 precursor RNA folds spatially, forming GR4998 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4998 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4998 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4998 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3

separate GAM precursor RNAs, GAM138 precursor RNA, GAM6212 precursor RNA and GAM86075 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM138 RNA, GAM6212 RNA and GAM86075 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM138 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM138 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM138 target RNA into GAM138 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6212 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6212 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6212 target RNA into GAM6212 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM86075 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM86075 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM86075 target RNA into GAM86075 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4998 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4998 gene: GAM138 target protein, GAM6212 target protein and GAM86075 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM138, GAM6212 and GAM86075

GR4999 AV725293 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 4999(GR4999) gene, which encodes an `operon-like` cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR4999 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR4999 gene was detected is described hereinabove with reference to Figs. 8-18.

GR4999 gene encodes GR4999 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR4999 precursor RNA folds spatially, forming GR4999 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR4999 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR4999 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR4999 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM48003 precursor RNA, GAM228908 precursor RNA and GAM248102 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM48003 RNA, GAM228908 RNA and GAM248102 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM48003 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM48003 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM48003 target RNA into GAM48003 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM228908 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM228908 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM228908 target RNA into GAM228908 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM248102 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM248102 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM248102 target RNA into GAM248102 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR4999 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR4999 gene: GAM48003 target protein, GAM228908 target protein and GAM248102 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM48003, GAM228908 and GAM248102

GR5000 BE788402 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5000(GR5000) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5000 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5000 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5000 gene encodes GR5000 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5000 precursor RNA folds spatially, forming GR5000 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5000 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5000 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5000 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4206 precursor RNA, GAM5097 precursor RNA and GAM247841 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED

PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4206 RNA, GAM5097 RNA and GAM247841 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4206 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4206 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4206 target RNA into GAM4206 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5097 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5097 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5097 target RNA into GAM5097 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM247841 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM247841 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM247841 target RNA into GAM247841 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5000 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5000 gene: GAM4206 target protein, GAM5097 target protein and GAM247841 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4206, GAM5097 and GAM247841

GR5001 AW888812 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5001(GR5001) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5001 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5001 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5001 gene encodes GR5001 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5001 precursor RNA folds spatially, forming GR5001 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5001 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5001 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5001 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4693 precursor RNA, GAM66706 precursor RNA and GAM120300 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4693 RNA, GAM66706 RNA and GAM120300 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4693 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4693 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4693 target RNA into GAM4693 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM66706 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM66706 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM66706 target RNA into GAM66706 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM120300 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM120300 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM120300 target RNA into GAM120300 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5001 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5001 gene: GAM4693 target protein, GAM66706 target protein and GAM120300 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4693, GAM66706 and GAM120300

GR5002 BF947253 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5002(GR5002) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5002 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5002 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5002 gene encodes GR5002 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5002 precursor RNA folds spatially, forming GR5002 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5002 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5002 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5002 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM69683 precursor RNA and GAM180775 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM69683 RNA and GAM180775 RNA, herein schematically

represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM69683 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM69683 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM69683 target RNA into GAM69683 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM180775 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM180775 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM180775 target RNA into GAM180775 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5002 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5002 gene: GAM69683 target protein and GAM180775 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM69683 and GAM180775

GR5003 AA195537 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5003(GR5003) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5003 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5003 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5003 gene encodes GR5003 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5003 precursor RNA folds spatially, forming GR5003 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5003 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5003 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5003 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM63304 precursor RNA and GAM113890 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM63304 RNA and GAM113890 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM63304 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM63304 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM63304 target RNA into GAM63304 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM113890 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM113890 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM113890 target RNA into GAM113890 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5003 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5003 gene: GAM63304 target protein and GAM113890 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM63304 and GAM113890

GR5004 BF764436 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5004(GR5004) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5004 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR5004 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5004 gene encodes GR5004 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5004 precursor RNA folds spatially, forming GR5004 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5004 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5004 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5004 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5343 precursor RNA and GAM8246 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5343 RNA and GAM8246 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5343 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5343 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5343 target RNA into GAM5343 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8246 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8246 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8246 target RNA into GAM8246 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5004 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5004 gene: GAM5343 target

protein and GAM8246 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5343 and GAM8246

GR5005 AL135326 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5005(GR5005) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5005 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5005 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5005 gene encodes GR5005 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5005 precursor RNA folds spatially, forming GR5005 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5005 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5005 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5005 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM96249 precursor RNA and GAM267556 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM96249 RNA and GAM267556 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM96249 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM96249 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM96249 target RNA into GAM96249 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM267556 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM267556 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM267556 target RNA into GAM267556 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5005 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5005 gene: GAM96249 target protein and GAM267556 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM96249 and GAM267556

GR5006 AW452560 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5006(GR5006) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5006 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5006 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5006 gene encodes GR5006 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5006 precursor RNA folds spatially, forming GR5006 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5006 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5006 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5006 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM86392 precursor RNA, GAM107228 precursor RNA and GAM177998 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM86392 RNA, GAM107228 RNA and GAM177998 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM86392 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM86392 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM86392 target RNA into GAM86392 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM107228 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM107228 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM107228 target RNA into GAM107228 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM177998 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM177998 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM177998 target RNA into GAM177998 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5006 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5006 gene: GAM86392 target protein, GAM107228 target protein and GAM177998 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM86392, GAM107228 and GAM177998

GR5007 AA687197 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5007(GR5007) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5007 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5007

gene was detected is described hereinabove with reference to Figs. 8-18.

GR5007 gene encodes GR5007 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5007 precursor RNA folds spatially, forming GR5007 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5007 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5007 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5007 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM173619 precursor RNA, GAM207170 precursor RNA and GAM213391 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM173619 RNA, GAM207170 RNA and GAM213391 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM173619 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM173619 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM173619 target RNA into GAM173619 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM207170 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM207170 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM207170 target RNA into GAM207170 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM213391 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM213391 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM213391 target RNA into GAM213391 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5007 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5007 gene: GAM173619 target protein, GAM207170 target protein and GAM213391 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM173619, GAM207170 and GAM213391

GR5008 BF590162 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5008(GR5008) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5008 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5008 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5008 gene encodes GR5008 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5008 precursor RNA folds spatially, forming GR5008 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5008 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5008 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5008 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM34801 precursor RNA and GAM336044 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM34801 RNA and GAM336044 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM34801 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM34801 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM34801 target RNA into GAM34801 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336044 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336044 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336044 target RNA into GAM336044 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5008 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5008 gene: GAM34801 target protein and GAM336044 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM34801 and GAM336044

GR5009 AW130590 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5009(GR5009) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5009 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5009 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5009 gene encodes GR5009 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5009 precursor RNA folds spatially, forming GR5009 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5009 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5009 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5009 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM3926 precursor RNA, GAM215648 precursor RNA, GAM240008 precursor RNA and GAM271105 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3926 RNA, GAM215648 RNA, GAM240008 RNA and GAM271105 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3926 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3926 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3926 target RNA into GAM3926 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM215648 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM215648 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM215648 target RNA into GAM215648 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM240008 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM240008 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM240008 target RNA into GAM240008 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM271105 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM271105 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM271105 target RNA into GAM271105 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5009 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5009 gene: GAM3926 target protein, GAM215648 target protein, GAM240008 target protein and GAM271105 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3926, GAM215648, GAM240008 and GAM271105

GR5010 BI253714 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5010(GR5010) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5010 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5010 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5010 gene encodes GR5010 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5010 precursor RNA folds spatially, forming GR5010 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5010 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5010 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5010 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6749 precursor RNA and GAM307118 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6749 RNA and GAM307118 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6749 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6749 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig. 8, thereby inhibiting translation of GAM6749 target RNA into GAM6749 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM307118 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM307118 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM307118 target RNA into GAM307118 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5010 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5010 gene: GAM6749 target protein and GAM307118 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6749 and GAM307118

GR5011 AI242475 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5011(GR5011) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5011 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5011 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5011 gene encodes GR5011 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5011 precursor RNA folds spatially, forming GR5011 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5011 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5011 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5011 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM50729 precursor RNA and GAM127311 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin

shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM50729 RNA and GAM127311 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM50729 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM50729 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM50729 target RNA into GAM50729 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM127311 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM127311 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM127311 target RNA into GAM127311 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5011 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5011 gene: GAM50729 target protein and GAM127311 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM50729 and GAM127311

GR5012 BM991273 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5012(GR5012) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5012 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5012 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5012 gene encodes GR5012 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5012 precursor RNA folds spatially, forming GR5012 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5012 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5012 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5012 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3912 precursor RNA and GAM295495 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3912 RNA and GAM295495 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3912 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3912 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3912 target RNA into GAM3912 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM295495 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM295495 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM295495 target RNA into GAM295495 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5012 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5012 gene: GAM3912 target protein and GAM295495 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3912 and GAM295495

GR5013 H01596 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5013(GR5013) gene, which encodes an `operon-like` cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5013 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5013 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5013 gene encodes GR5013 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5013 precursor RNA folds spatially, forming GR5013 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5013 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5013 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5013 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM31923 precursor RNA and GAM150764 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM31923 RNA and GAM150764 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM31923 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM31923 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM31923 target RNA into GAM31923 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM150764 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM150764 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM150764 target RNA into GAM150764 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5013 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5013 gene: GAM31923 target protein and GAM150764 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM31923 and GAM150764

GR5014 R36354 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5014(GR5014) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5014 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5014 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5014 gene encodes GR5014 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5014 precursor RNA folds spatially, forming GR5014 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5014 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5014 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5014 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3725 precursor RNA and GAM327309 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3725 RNA and GAM327309 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3725 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3725 target RNA, herein schematically represented by

GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3725 target RNA into GAM3725 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM327309 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM327309 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM327309 target RNA into GAM327309 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5014 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5014 gene: GAM3725 target protein and GAM327309 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3725 and GAM327309

GR5015 BE744046 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5015(GR5015) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5015 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5015 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5015 gene encodes GR5015 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5015 precursor RNA folds spatially, forming GR5015 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5015 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5015 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5015 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2874 precursor RNA and GAM96538 precursor

RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2874 RNA and GAM96538 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2874 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2874 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2874 target RNA into GAM2874 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM96538 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM96538 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM96538 target RNA into GAM96538 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5015 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5015 gene: GAM2874 target protein and GAM96538 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2874 and GAM96538

GR5016 BI603207 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5016(GR5016) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5016 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5016 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5016 gene encodes GR5016 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5016 precursor RNA folds spatially, forming GR5016 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5016 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5016 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5016 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM695 precursor RNA and GAM7579 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM695 RNA and GAM7579 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM695 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM695 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM695 target RNA into GAM695 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7579 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7579 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7579 target RNA into GAM7579 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5016 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5016 gene: GAM695 target protein and GAM7579 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM695 and GAM7579

bioinformatically detected regulatory gene, referred to here as Genomic Record 5017 (GR5017) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5017 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5017 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5017 gene encodes GR5017 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5017 precursor RNA folds spatially, forming GR5017 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5017 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5017 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5017 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM219217 precursor RNA and GAM243942 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM219217 RNA and GAM243942 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM219217 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM219217 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM219217 target RNA into GAM219217 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM243942 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM243942 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM243942

target RNA into GAM243942 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5017 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5017 gene: GAM219217 target protein and GAM243942 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM219217 and GAM243942

GR5018 AI571521 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5018(GR5018) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5018 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5018 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5018 gene encodes GR5018 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5018 precursor RNA folds spatially, forming GR5018 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5018 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5018 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5018 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM243261 precursor RNA and GAM256070 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM243261 RNA and GAM256070 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM243261 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM243261 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM243261 target RNA into GAM243261 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM256070 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM256070 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM256070 target RNA into GAM256070 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5018 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5018 gene: GAM243261 target protein and GAM256070 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM243261 and GAM256070

GR5019 BG150840 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5019 (GR5019) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5019 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5019 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5019 gene encodes GR5019 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5019 precursor RNA folds spatially, forming GR5019 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5019 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5019 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5019 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM216870 precursor RNA and GAM316647 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM216870 RNA and GAM316647 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM216870 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM216870 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM216870 target RNA into GAM216870 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM316647 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM316647 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM316647 target RNA into GAM316647 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5019 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5019 gene: GAM216870 target protein and GAM316647 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM216870 and GAM316647

GR5020 BG497189 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5020 (GR5020) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5020 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5020 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5020 gene encodes GR5020 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5020 precursor RNA folds spatially, forming GR5020 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5020 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5020 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5020 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2871 precursor RNA and GAM144463 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2871 RNA and GAM144463 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2871 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2871 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2871 target RNA into GAM2871 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM144463 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM144463 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM144463 target RNA into GAM144463 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5020 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5020 gene: GAM2871 target protein and GAM144463 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2871 and GAM144463

GR5021 BE252777 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5021 (GR5021) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5021 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5021 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5021 gene encodes GR5021 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5021 precursor RNA folds spatially, forming GR5021 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5021 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5021 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5021 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM224397 precursor RNA and GAM294084 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM224397 RNA and GAM294084 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM224397 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM224397 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM224397 target RNA into GAM224397 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM294084 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM294084 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM294084 target RNA into GAM294084 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5021 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5021 gene: GAM224397 target protein and GAM294084 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM224397 and GAM294084

GR5022 BI223832 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5022(GR5022) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5022 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5022 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5022 gene encodes GR5022 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5022 precursor RNA folds spatially, forming GR5022 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5022 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5022 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5022 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3611 precursor RNA and GAM270448 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3611 RNA and GAM270448 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3611 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3611 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3611 target RNA into GAM3611 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM270448 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM270448 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM270448 target RNA into GAM270448 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5022 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5022 gene: GAM3611 target protein and GAM270448 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3611 and GAM270448

GR5023 BM980560 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5023(GR5023) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5023 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5023 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5023 gene encodes GR5023 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5023 precursor RNA folds spatially, forming GR5023 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5023 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5023 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5023 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8281 precursor RNA and GAM322724 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8281 RNA and GAM322724 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8281 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8281 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8281 target RNA into GAM8281 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM322724 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM322724 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM322724 target RNA into GAM322724 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5023 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5023 gene: GAM8281 target protein and GAM322724 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8281 and GAM322724

GR5024 AA659917 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5024(GR5024) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5024 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5024 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5024 gene encodes GR5024 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5024 precursor RNA folds spatially, forming GR5024 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5024 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5024 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5024 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM80 precursor RNA and GAM252908 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM80 RNA and GAM252908 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM80 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM80 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM80 target RNA into GAM80 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM252908 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM252908 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM252908 target RNA into GAM252908 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5024 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5024 gene: GAM80 target protein and GAM252908 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes

is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM80 and GAM252908

GR5025 BF664939 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5025(GR5025) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5025 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5025 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5025 gene encodes GR5025 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5025 precursor RNA folds spatially, forming GR5025 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5025 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5025 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5025 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM7551 precursor RNA, GAM158944 precursor RNA and GAM313817 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7551 RNA, GAM158944 RNA and GAM313817 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7551 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7551 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7551 target RNA into GAM7551 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM158944 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM158944 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM158944 target RNA into GAM158944 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM313817 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM313817 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM313817 target RNA into GAM313817 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5025 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5025 gene: GAM7551 target protein, GAM158944 target protein and GAM313817 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7551, GAM158944 and GAM313817

GR5026 BI600015 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5026(GR5026) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5026 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5026 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5026 gene encodes GR5026 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5026 precursor RNA folds spatially, forming GR5026 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5026 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5026 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5026 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6025 precursor RNA and GAM68218 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6025 RNA and GAM68218 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6025 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6025 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6025 target RNA into GAM6025 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM68218 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM68218 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM68218 target RNA into GAM68218 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5026 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5026 gene: GAM6025 target protein and GAM68218 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6025 and GAM68218

GR5027 BG335692 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5027 (GR5027) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5027 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5027 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5027 gene encodes GR5027 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5027 precursor RNA folds spatially, forming GR5027 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5027 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5027 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5027 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM576 precursor RNA, GAM13570 precursor RNA and GAM224961 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM576 RNA, GAM13570 RNA and GAM224961 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM576 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM576 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM576 target RNA into GAM576 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM13570 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM13570 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM13570 target RNA into GAM13570 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM224961 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM224961 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM224961 target RNA into GAM224961 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5027 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5027 gene: GAM576 target protein, GAM13570 target protein and GAM224961 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM576, GAM13570 and GAM224961

GR5028 AV691952 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5028(GR5028) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5028 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5028 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5028 gene encodes GR5028 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5028 precursor RNA folds spatially, forming GR5028 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5028 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5028 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5028 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2813 precursor RNA and GAM6011 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2813 RNA and GAM6011 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2813 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2813 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2813 target RNA into GAM2813 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6011 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6011 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6011 target RNA into GAM6011 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5028 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5028 gene: GAM2813 target protein and GAM6011 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2813 and GAM6011

GR5029 AA904673 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5029(GR5029) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5029 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5029 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5029 gene encodes GR5029 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5029 precursor RNA folds spatially, forming GR5029 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5029 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5029 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5029 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM218072 precursor RNA and GAM271523 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM218072 RNA and GAM271523 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM218072 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM218072 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM218072 target RNA into GAM218072 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM271523 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM271523 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM271523 target RNA into GAM271523 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5029 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5029 gene: GAM218072 target protein and GAM271523 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM218072 and GAM271523

GR5030 AL042363 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5030 (GR5030) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5030 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5030 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5030 gene encodes GR5030 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5030 precursor RNA folds spatially, forming GR5030 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5030 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5030 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5030 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM30 precursor RNA and GAM220896 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM30 RNA and GAM220896 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM30 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM30 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM30 target RNA into GAM30 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM220896 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM220896 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM220896 target RNA into GAM220896 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5030 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5030 gene: GAM30 target protein and GAM220896 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM30 and GAM220896

GR5031 AW860812 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5031 (GR5031) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5031 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5031 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5031 gene encodes GR5031 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5031 precursor RNA folds spatially, forming GR5031 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5031 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5031 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5031 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM19783 precursor RNA and GAM175474 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM19783 RNA and GAM175474 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM19783 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM19783 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM19783 target RNA into GAM19783 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM175474 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM175474 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM175474 target RNA into GAM175474 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5031 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5031 gene: GAM19783 target protein and GAM175474 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM19783 and GAM175474

GR5032 BI915602 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5032(GR5032) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5032 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5032 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5032 gene encodes GR5032 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5032 precursor RNA folds spatially, forming GR5032 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5032 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5032 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5032 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM102565 precursor RNA and GAM325958 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM102565 RNA and GAM325958 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM102565 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM102565 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM102565 target RNA into GAM102565 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM325958 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM325958 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM325958 target RNA into GAM325958 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5032 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5032 gene: GAM102565 target protein and GAM325958 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM102565 and GAM325958

GR5033 AI554721 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5033(GR5033) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5033 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5033 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5033 gene encodes GR5033 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5033 precursor RNA folds spatially, forming GR5033 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5033 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5033 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5033 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7053 precursor RNA and GAM7838 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7053 RNA and GAM7838 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7053 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7053 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7053 target RNA into GAM7053 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7838 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7838 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7838 target RNA into GAM7838 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5033 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5033 gene: GAM7053 target protein and GAM7838 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7053 and GAM7838

GR5034 BG492519 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5034(GR5034) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5034 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5034 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5034 gene encodes GR5034 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5034 precursor RNA folds spatially, forming GR5034 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5034 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5034 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5034 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM279 precursor RNA, GAM8457 precursor RNA and GAM92648 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM279 RNA, GAM8457 RNA and GAM92648 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM279 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM279 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM279 target RNA into GAM279 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8457 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8457 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8457 target RNA into GAM8457 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM92648 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM92648 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM92648

target RNA into GAM92648 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5034 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5034 gene: GAM279 target protein, GAM8457 target protein and GAM92648 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM279, GAM8457 and GAM92648

GR5035 BG170429 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5035(GR5035) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5035 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5035 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5035 gene encodes GR5035 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5035 precursor RNA folds spatially, forming GR5035 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5035 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5035 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5035 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM664 precursor RNA and GAM223101 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM664 RNA and GAM223101 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM664 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM664 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM664 target RNA into GAM664 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM223101 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM223101 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM223101 target RNA into GAM223101 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5035 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5035 gene: GAM664 target protein and GAM223101 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM664 and GAM223101

GR5036 BG929116 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5036(GR5036) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5036 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5036 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5036 gene encodes GR5036 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5036 precursor RNA folds spatially, forming GR5036 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5036 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5036 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5036 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3235 precursor RNA, GAM5047 precursor RNA and GAM299448 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3235 RNA, GAM5047 RNA and GAM299448 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3235 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3235 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3235 target RNA into GAM3235 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5047 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5047 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5047 target RNA into GAM5047 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM299448 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM299448 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM299448 target RNA into GAM299448 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5036 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5036 gene: GAM3235 target protein, GAM5047 target protein and GAM299448 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3235, GAM5047 and GAM299448

bioinformatically detected regulatory gene, referred to here as Genomic Record 5037(GR5037) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5037 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5037 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5037 gene encodes GR5037 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5037 precursor RNA folds spatially, forming GR5037 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5037 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5037 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5037 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM5398 precursor RNA, GAM198158 precursor RNA and GAM315167 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5398 RNA, GAM198158 RNA and GAM315167 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5398 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5398 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5398 target RNA into GAM5398 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM198158 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM198158 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM198158 target RNA into GAM198158 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM315167 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM315167 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM315167 target RNA into GAM315167 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5037 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5037 gene: GAM5398 target protein, GAM198158 target protein and GAM315167 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5398, GAM198158 and GAM315167

GR5038 AA706741 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5038(GR5038) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5038 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5038 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5038 gene encodes GR5038 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5038 precursor RNA folds spatially, forming GR5038 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5038 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5038 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5038 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM154576 precursor RNA and GAM237687 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3

FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM154576 RNA and GAM237687 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM154576 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM154576 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM154576 target RNA into GAM154576 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM237687 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM237687 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM237687 target RNA into GAM237687 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5038 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5038 gene: GAM154576 target protein and GAM237687 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM154576 and GAM237687

GR5039 BF056985 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5039(GR5039) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5039 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5039 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5039 gene encodes GR5039 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5039 precursor RNA folds spatially, forming GR5039 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5039 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5039 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5039 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM135434 precursor RNA and GAM298683 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM135434 RNA and GAM298683 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM135434 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM135434 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM135434 target RNA into GAM135434 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM298683 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM298683 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM298683 target RNA into GAM298683 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5039 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5039 gene: GAM135434 target protein and GAM298683 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM135434 and GAM298683

5040(GR5040) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5040 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5040 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5040 gene encodes GR5040 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5040 precursor RNA folds spatially, forming GR5040 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5040 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5040 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5040 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM184698 precursor RNA and GAM202692 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM184698 RNA and GAM202692 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM184698 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM184698 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM184698 target RNA into GAM184698 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM202692 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM202692 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM202692 target RNA into GAM202692 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5040 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5040 gene: GAM184698 target protein and GAM202692 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM184698 and GAM202692

GR5041 BM669724 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5041 (GR5041) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5041 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5041 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5041 gene encodes GR5041 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5041 precursor RNA folds spatially, forming GR5041 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5041 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5041 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5041 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM20988 precursor RNA, GAM52987 precursor RNA and GAM180263 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM20988 RNA, GAM52987 RNA and GAM180263 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM20988 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM20988 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM20988 target RNA into GAM20988 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM52987 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM52987 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM52987 target RNA into GAM52987 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM180263 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM180263 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM180263 target RNA into GAM180263 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5041 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5041 gene: GAM20988 target protein, GAM52987 target protein and GAM180263 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM20988, GAM52987 and GAM180263

GR5042 AI819788 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5042(GR5042) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5042 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5042 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5042 gene encodes GR5042 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5042 precursor RNA folds spatially, forming GR5042 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5042 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5042 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5042 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1559 precursor RNA, GAM110638 precursor RNA and GAM121320 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1559 RNA, GAM110638 RNA and GAM121320 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1559 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1559 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1559 target RNA into GAM1559 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM110638 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM110638 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM110638 target RNA into GAM110638 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM121320 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM121320 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM121320 target RNA into GAM121320 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5042 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR5042 gene: GAM1559 target protein, GAM110638 target protein and GAM121320 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1559, GAM110638 and GAM121320

GR5043 AW903817 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5043(GR5043) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5043 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5043 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5043 gene encodes GR5043 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5043 precursor RNA folds spatially, forming GR5043 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5043 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5043 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5043 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM110844 precursor RNA and GAM121563 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM110844 RNA and GAM121563 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM110844 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM110844 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM110844

target RNA into GAM110844 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM121563 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM121563 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM121563 target RNA into GAM121563 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5043 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5043 gene: GAM110844 target protein and GAM121563 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM110844 and GAM121563

GR5044 AL598864 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5044(GR5044) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5044 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5044 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5044 gene encodes GR5044 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5044 precursor RNA folds spatially, forming GR5044 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5044 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5044 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5044 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM766 precursor RNA, GAM4073 precursor RNA, GAM160165 precursor RNA and GAM205567 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment,

corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM766 RNA, GAM4073 RNA, GAM160165 RNA and GAM205567 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM766 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM766 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM766 target RNA into GAM766 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM4073 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4073 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4073 target RNA into GAM4073 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM160165 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM160165 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM160165 target RNA into GAM160165 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM205567 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM205567 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM205567 target RNA into GAM205567 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5044 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5044 gene: GAM766 target protein, GAM4073 target protein, GAM160165 target protein and GAM205567 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM766, GAM4073, GAM160165 and GAM205567

GR5045 BG913485 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5045(GR5045) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5045 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5045 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5045 gene encodes GR5045 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5045 precursor RNA folds spatially, forming GR5045 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5045 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5045 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5045 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1417 precursor RNA, GAM60094 precursor RNA and GAM281215 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1417 RNA, GAM60094 RNA and GAM281215 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1417 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1417 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1417 target RNA into GAM1417 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM60094 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM60094 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM60094 target RNA into GAM60094 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM281215 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM281215 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM281215 target RNA into GAM281215 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5045 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5045 gene: GAM1417 target protein, GAM60094 target protein and GAM281215 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1417, GAM60094 and GAM281215

GR5046 AI754397 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5046(GR5046) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5046 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5046 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5046 gene encodes GR5046 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5046 precursor RNA folds spatially, forming GR5046 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5046 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5046 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5046 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2

separate GAM precursor RNAs, GAM102491 precursor RNA and GAM256049 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM102491 RNA and GAM256049 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM102491 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM102491 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM102491 target RNA into GAM102491 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM256049 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM256049 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM256049 target RNA into GAM256049 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5046 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5046 gene: GAM102491 target protein and GAM256049 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM102491 and GAM256049

GR5047 BF735743 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5047(GR5047) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5047 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5047 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5047 gene encodes GR5047 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR5047 precursor RNA folds spatially, forming GR5047 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5047 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5047 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5047 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4528 precursor RNA and GAM334740 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4528 RNA and GAM334740 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4528 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4528 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4528 target RNA into GAM4528 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM334740 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM334740 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM334740 target RNA into GAM334740 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5047 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5047 gene: GAM4528 target protein and GAM334740 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4528 and GAM334740

GR5048 BF096080 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5048(GR5048) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5048 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5048 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5048 gene encodes GR5048 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5048 precursor RNA folds spatially, forming GR5048 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5048 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5048 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5048 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7824 precursor RNA and GAM133170 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7824 RNA and GAM133170 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7824 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7824 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7824 target RNA into GAM7824 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM133170 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM133170 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM133170 target RNA into GAM133170 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5048 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5048 gene: GAM7824 target protein and GAM133170 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7824 and GAM133170

GR5049 T94751 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5049 (GR5049) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5049 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5049 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5049 gene encodes GR5049 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5049 precursor RNA folds spatially, forming GR5049 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5049 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5049 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5049 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM653 precursor RNA and GAM225177 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM653 RNA and GAM225177 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM653 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM653 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM653 target RNA into GAM653 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM225177 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM225177 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM225177 target RNA into GAM225177 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5049 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5049 gene: GAM653 target protein and GAM225177 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM653 and GAM225177

GR5050 BG742805 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5050(GR5050) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5050 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5050 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5050 gene encodes GR5050 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5050 precursor RNA folds spatially, forming GR5050 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5050 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5050 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5050 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM65335 precursor RNA and GAM190192 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM65335 RNA and GAM190192 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM65335 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM65335 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM65335 target RNA into GAM65335 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM190192 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM190192 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM190192 target RNA into GAM190192 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5050 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5050 gene: GAM65335 target protein and GAM190192 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM65335 and GAM190192

GR5051 BM006648 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5051 (GR5051) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5051 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5051 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5051 gene encodes GR5051 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5051 precursor RNA folds spatially, forming GR5051 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5051 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5051 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5051 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4880 precursor RNA, GAM7862 precursor RNA and GAM191042 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4880 RNA, GAM7862 RNA and GAM191042 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4880 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4880 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4880 target RNA into GAM4880 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7862 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7862 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7862 target RNA into GAM7862 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM191042 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM191042 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM191042 target RNA into GAM191042 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5051 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5051 gene: GAM4880 target protein, GAM7862 target protein and GAM191042 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4880, GAM7862 and GAM191042

GR5052 BF995893 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5052(GR5052) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5052 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5052 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5052 gene encodes GR5052 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5052 precursor RNA folds spatially, forming GR5052 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5052 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5052 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5052 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM106567 precursor RNA and GAM159147 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM106567 RNA and GAM159147 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM106567 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM106567 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM106567 target RNA into GAM106567 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM159147 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM159147 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM159147 target RNA into GAM159147 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5052 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5052 gene: GAM106567 target protein and GAM159147 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM106567 and GAM159147

GR5053 AA437220 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5053(GR5053) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5053 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5053 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5053 gene encodes GR5053 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5053 precursor RNA folds spatially, forming GR5053 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5053 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5053 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5053 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2282 precursor RNA and GAM13500 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2282 RNA and GAM13500 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2282 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2282 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2282 target RNA into GAM2282 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM13500 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM13500 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM13500 target RNA into GAM13500 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5053 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5053 gene: GAM2282 target protein and GAM13500 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2282 and GAM13500

GR5054 BG983572 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5054(GR5054) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5054 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5054 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5054 gene encodes GR5054 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5054 precursor RNA folds spatially, forming GR5054 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5054 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5054 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5054 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7000 precursor RNA and GAM8560 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7000 RNA and GAM8560 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7000 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7000 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7000 target RNA into GAM7000 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8560 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8560 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8560 target RNA into GAM8560 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5054 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5054 gene: GAM7000 target protein and GAM8560 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7000 and GAM8560

GR5055 AW068164 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5055(GR5055) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5055 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5055 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5055 gene encodes GR5055 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5055 precursor RNA folds spatially, forming GR5055 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5055 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5055 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5055 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM66549 precursor RNA, GAM256486 precursor RNA and GAM279794 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM66549 RNA, GAM256486 RNA and GAM279794 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM66549 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM66549 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM66549 target RNA into GAM66549 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM256486 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM256486 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM256486 target RNA into GAM256486 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM279794 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM279794 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM279794 target RNA into GAM279794 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5055 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5055 gene: GAM66549 target protein, GAM256486 target protein and GAM279794 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM66549, GAM256486 and GAM279794

GR5056 BI906405 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5056(GR5056) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5056 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5056 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5056 gene encodes GR5056 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5056 precursor RNA folds spatially, forming GR5056 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5056 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5056 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5056 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3

separate GAM precursor RNAs, GAM4864 precursor RNA, GAM245109 precursor RNA and GAM273195 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4864 RNA, GAM245109 RNA and GAM273195 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4864 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4864 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4864 target RNA into GAM4864 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM245109 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM245109 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM245109 target RNA into GAM245109 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM273195 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM273195 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM273195 target RNA into GAM273195 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5056 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5056 gene: GAM4864 target protein, GAM245109 target protein and GAM273195 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4864, GAM245109 and GAM273195

GR5057 BM048645 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5057(GR5057) gene, which encodes an `operon-like` cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5057 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5057 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5057 gene encodes GR5057 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5057 precursor RNA folds spatially, forming GR5057 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5057 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5057 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5057 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM157886 precursor RNA and GAM206884 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM157886 RNA and GAM206884 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM157886 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM157886 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM157886 target RNA into GAM157886 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM206884 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM206884 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM206884 target RNA into GAM206884 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5057 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5057 gene: GAM157886 target protein and GAM206884 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM157886 and GAM206884

GR5058 AI623475 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5058(GR5058) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5058 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5058 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5058 gene encodes GR5058 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5058 precursor RNA folds spatially, forming GR5058 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5058 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5058 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5058 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2521 precursor RNA and GAM58938 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2521 RNA and GAM58938 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2521 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2521 target RNA, herein schematically represented by

GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2521 target RNA into GAM2521 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM58938 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM58938 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM58938 target RNA into GAM58938 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5058 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5058 gene: GAM2521 target protein and GAM58938 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2521 and GAM58938

GR5059 BE537899 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5059(GR5059) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5059 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5059 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5059 gene encodes GR5059 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5059 precursor RNA folds spatially, forming GR5059 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5059 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5059 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5059 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2064 precursor RNA, GAM4416 precursor RNA and

GAM140513 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2064 RNA, GAM4416 RNA and GAM140513 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2064 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2064 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2064 target RNA into GAM2064 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM4416 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4416 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4416 target RNA into GAM4416 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM140513 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM140513 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM140513 target RNA into GAM140513 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5059 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5059 gene: GAM2064 target protein, GAM4416 target protein and GAM140513 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2064, GAM4416 and GAM140513

GR5060 AA226984 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5060(GR5060) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR5060 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5060 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5060 gene encodes GR5060 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5060 precursor RNA folds spatially, forming GR5060 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5060 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5060 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5060 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3122 precursor RNA, GAM5190 precursor RNA and GAM236414 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3122 RNA, GAM5190 RNA and GAM236414 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3122 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3122 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3122 target RNA into GAM3122 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5190 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5190 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5190 target RNA into GAM5190 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM236414 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM236414 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM236414 target RNA into GAM236414 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5060 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5060 gene: GAM3122 target protein, GAM5190 target protein and GAM236414 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3122, GAM5190 and GAM236414

GR5061 BM930569 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5061 (GR5061) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5061 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5061 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5061 gene encodes GR5061 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5061 precursor RNA folds spatially, forming GR5061 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5061 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5061 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5061 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM120128 precursor RNA and GAM314436 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM120128 RNA and GAM314436 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM120128 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM120128 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM120128 target RNA into GAM120128 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM314436 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM314436 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM314436 target RNA into GAM314436 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5061 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5061 gene: GAM120128 target protein and GAM314436 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM120128 and GAM314436

GR5062 BI117542 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5062(GR5062) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5062 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5062 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5062 gene encodes GR5062 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5062 precursor RNA folds spatially, forming GR5062 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5062 folded precursor RNA comprises a plurality of what is known in the

art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5062 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5062 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3477 precursor RNA and GAM328104 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3477 RNA and GAM328104 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3477 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3477 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3477 target RNA into GAM3477 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM328104 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM328104 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM328104 target RNA into GAM328104 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5062 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5062 gene: GAM3477 target protein and GAM328104 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3477 and GAM328104

GR5063 BQ070657 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5063 (GR5063) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR5063 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5063 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5063 gene encodes GR5063 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5063 precursor RNA folds spatially, forming GR5063 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5063 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5063 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5063 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM16527 precursor RNA and GAM266158 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM16527 RNA and GAM266158 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM16527 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM16527 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM16527 target RNA into GAM16527 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM266158 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM266158 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM266158 target RNA into GAM266158 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly

utilities, of GR5063 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5063 gene: GAM16527 target protein and GAM266158 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM16527 and GAM266158

GR5064 T63066 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5064(GR5064) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5064 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5064 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5064 gene encodes GR5064 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5064 precursor RNA folds spatially, forming GR5064 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5064 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5064 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5064 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM255717 precursor RNA and GAM282389 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM255717 RNA and GAM282389 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM255717 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM255717 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM255717 target RNA into GAM255717 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM282389 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM282389 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM282389 target RNA into GAM282389 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5064 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5064 gene: GAM255717 target protein and GAM282389 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM255717 and GAM282389

GR5065 BG114819 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5065(GR5065) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5065 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5065 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5065 gene encodes GR5065 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5065 precursor RNA folds spatially, forming GR5065 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5065 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5065 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5065 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2202 precursor RNA, GAM2889 precursor RNA and GAM294841 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded

precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2202 RNA, GAM2889 RNA and GAM294841 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2202 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2202 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2202 target RNA into GAM2202 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM2889 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2889 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2889 target RNA into GAM2889 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM294841 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM294841 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM294841 target RNA into GAM294841 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5065 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5065 gene: GAM2202 target protein, GAM2889 target protein and GAM294841 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2202, GAM2889 and GAM294841

GR5066 BM126946 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5066(GR5066) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5066 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5066 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5066 gene encodes GR5066 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5066 precursor RNA folds spatially, forming GR5066 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5066 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5066 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5066 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3847 precursor RNA and GAM8617 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3847 RNA and GAM8617 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3847 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3847 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3847 target RNA into GAM3847 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8617 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8617 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8617 target RNA into GAM8617 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5066 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5066 gene: GAM3847 target protein and GAM8617 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3847 and GAM8617

GR5067 BG748959 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5067(GR5067) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5067 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5067 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5067 gene encodes GR5067 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5067 precursor RNA folds spatially, forming GR5067 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5067 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5067 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5067 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM5024 precursor RNA, GAM97188 precursor RNA and GAM187589 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5024 RNA, GAM97188 RNA and GAM187589 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5024 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5024 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig. 8, thereby inhibiting translation of GAM5024 target RNA into GAM5024 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM97188 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM97188 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM97188 target RNA into GAM97188 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM187589 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM187589 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM187589 target RNA into GAM187589 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5067 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5067 gene: GAM5024 target protein, GAM97188 target protein and GAM187589 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5024, GAM97188 and GAM187589

GR5068 BG831008 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5068 (GR5068) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5068 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5068 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5068 gene encodes GR5068 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5068 precursor RNA folds spatially, forming GR5068 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5068 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5068 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5068 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM8187 precursor RNA, GAM85684 precursor RNA and GAM113071 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8187 RNA, GAM85684 RNA and GAM113071 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8187 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8187 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8187 target RNA into GAM8187 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM85684 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM85684 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM85684 target RNA into GAM85684 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM113071 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM113071 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM113071 target RNA into GAM113071 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5068 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5068 gene: GAM8187 target protein, GAM85684 target protein and GAM113071 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6,

hereby incorporated by reference, with references to GAM8187, GAM85684 and GAM113071

GR5069 BM557612 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5069(GR5069) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5069 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5069 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5069 gene encodes GR5069 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5069 precursor RNA folds spatially, forming GR5069 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5069 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5069 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5069 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM302 precursor RNA, GAM35668 precursor RNA, GAM184098 precursor RNA and GAM223098 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM302 RNA, GAM35668 RNA, GAM184098 RNA and GAM223098 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM302 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM302 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM302 target RNA into GAM302 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM35668 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM35668 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM35668 target RNA into GAM35668 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM184098 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM184098 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM184098 target RNA into GAM184098 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM223098 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM223098 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM223098 target RNA into GAM223098 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5069 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5069 gene: GAM302 target protein, GAM35668 target protein, GAM184098 target protein and GAM223098 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM302, GAM35668, GAM184098 and GAM223098

GR5070 BI551742 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5070(GR5070) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5070 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5070 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5070 gene encodes GR5070 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5070 precursor RNA folds spatially, forming GR5070 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5070 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5070 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5070 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4902 precursor RNA and GAM46306 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4902 RNA and GAM46306 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4902 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4902 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4902 target RNA into GAM4902 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM46306 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM46306 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM46306 target RNA into GAM46306 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5070 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5070 gene: GAM4902 target protein and GAM46306 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4902 and GAM46306

GR5071 BI459909 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5071(GR5071) gene, which encodes an `operon-like` cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5071 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5071 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5071 gene encodes GR5071 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5071 precursor RNA folds spatially, forming GR5071 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5071 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5071 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5071 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM119263 precursor RNA and GAM239610 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM119263 RNA and GAM239610 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM119263 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM119263 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM119263 target RNA into GAM119263 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM239610 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM239610 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM239610 target RNA into GAM239610 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5071 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5071 gene: GAM119263 target protein and GAM239610 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM119263 and GAM239610

GR5072 BG006351 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5072(GR5072) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5072 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5072 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5072 gene encodes GR5072 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5072 precursor RNA folds spatially, forming GR5072 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5072 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5072 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5072 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM65368 precursor RNA and GAM90038 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM65368 RNA and GAM90038 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM65368 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM65368 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM65368 target RNA into GAM65368 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM90038 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM90038 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM90038 target RNA into GAM90038 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5072 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5072 gene: GAM65368 target protein and GAM90038 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM65368 and GAM90038

GR5073 BF675976 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5073(GR5073) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5073 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5073 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5073 gene encodes GR5073 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5073 precursor RNA folds spatially, forming GR5073 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5073 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5073 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5073 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM100476 precursor RNA, GAM234812 precursor RNA

and GAM307651 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM100476 RNA, GAM234812 RNA and GAM307651 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM100476 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM100476 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM100476 target RNA into GAM100476 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM234812 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM234812 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM234812 target RNA into GAM234812 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM307651 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM307651 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM307651 target RNA into GAM307651 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5073 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5073 gene: GAM100476 target protein, GAM234812 target protein and GAM307651 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM100476, GAM234812 and GAM307651

GR5074 BM702323 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5074(GR5074) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR5074 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5074 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5074 gene encodes GR5074 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5074 precursor RNA folds spatially, forming GR5074 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5074 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5074 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5074 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM72211 precursor RNA and GAM274852 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM72211 RNA and GAM274852 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM72211 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM72211 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM72211 target RNA into GAM72211 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM274852 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM274852 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM274852 target RNA into GAM274852 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5074 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5074 gene: GAM72211 target protein and GAM274852 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM72211 and GAM274852

GR5075 BI005744 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5075(GR5075) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5075 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5075 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5075 gene encodes GR5075 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5075 precursor RNA folds spatially, forming GR5075 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5075 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5075 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5075 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7152 precursor RNA and GAM169913 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7152 RNA and GAM169913 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7152 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7152 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds

to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7152 target RNA into GAM7152 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM169913 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM169913 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM169913 target RNA into GAM169913 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5075 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5075 gene: GAM7152 target protein and GAM169913 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7152 and GAM169913

GR5076 BE733434 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5076(GR5076) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5076 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5076 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5076 gene encodes GR5076 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5076 precursor RNA folds spatially, forming GR5076 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5076 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5076 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5076 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3922 precursor RNA and GAM4192 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3

FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3922 RNA and GAM4192 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3922 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3922 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3922 target RNA into GAM3922 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM4192 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4192 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4192 target RNA into GAM4192 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5076 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5076 gene: GAM3922 target protein and GAM4192 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3922 and GAM4192

GR5077 BI912376 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5077(GR5077) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5077 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5077 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5077 gene encodes GR5077 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5077 precursor RNA folds spatially, forming GR5077 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5077 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5077 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5077 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM157301 precursor RNA and GAM322456 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM157301 RNA and GAM322456 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM157301 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM157301 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM157301 target RNA into GAM157301 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM322456 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM322456 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM322456 target RNA into GAM322456 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5077 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5077 gene: GAM157301 target protein and GAM322456 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM157301 and GAM322456

5078(GR5078) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5078 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5078 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5078 gene encodes GR5078 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5078 precursor RNA folds spatially, forming GR5078 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5078 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5078 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5078 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5683 precursor RNA and GAM322118 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5683 RNA and GAM322118 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5683 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5683 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5683 target RNA into GAM5683 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM322118 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM322118 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM322118 target RNA into GAM322118 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5078 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5078 gene: GAM5683 target protein and GAM322118 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5683 and GAM322118

GR5079 BM838105 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5079(GR5079) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5079 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5079 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5079 gene encodes GR5079 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5079 precursor RNA folds spatially, forming GR5079 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5079 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5079 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5079 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2683 precursor RNA and GAM301242 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2683 RNA and GAM301242 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2683 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM2683 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2683 target RNA into GAM2683 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM301242 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM301242 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM301242 target RNA into GAM301242 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5079 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5079 gene: GAM2683 target protein and GAM301242 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2683 and GAM301242

GR5080 BG759195 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5080(GR5080) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5080 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5080 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5080 gene encodes GR5080 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5080 precursor RNA folds spatially, forming GR5080 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5080 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5080 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5080 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2

separate GAM precursor RNAs, GAM8448 precursor RNA and GAM307900 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8448 RNA and GAM307900 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8448 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8448 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8448 target RNA into GAM8448 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM307900 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM307900 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM307900 target RNA into GAM307900 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5080 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5080 gene: GAM8448 target protein and GAM307900 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8448 and GAM307900

GR5081 AW088988 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5081 (GR5081) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5081 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5081 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5081 gene encodes GR5081 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR5081 precursor RNA folds spatially, forming GR5081 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5081 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5081 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5081 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM104952 precursor RNA and GAM111791 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM104952 RNA and GAM111791 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM104952 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM104952 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM104952 target RNA into GAM104952 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM111791 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM111791 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM111791 target RNA into GAM111791 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5081 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5081 gene: GAM104952 target protein and GAM111791 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM104952 and GAM111791

GR5082 BE439986 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5082(GR5082) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5082 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5082 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5082 gene encodes GR5082 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5082 precursor RNA folds spatially, forming GR5082 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5082 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5082 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5082 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3035 precursor RNA, GAM225984 precursor RNA and GAM264551 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3035 RNA, GAM225984 RNA and GAM264551 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3035 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3035 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3035 target RNA into GAM3035 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM225984 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM225984 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM225984 target RNA into GAM225984 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM264551 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM264551 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM264551 target RNA into GAM264551 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5082 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5082 gene: GAM3035 target protein, GAM225984 target protein and GAM264551 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3035, GAM225984 and GAM264551

GR5083 AV659592 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5083(GR5083) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5083 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5083 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5083 gene encodes GR5083 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5083 precursor RNA folds spatially, forming GR5083 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5083 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5083 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5083 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM484 precursor RNA, GAM8374 precursor RNA,

GAM8615 precursor RNA and GAM9386 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM484 RNA, GAM8374 RNA, GAM8615 RNA and GAM9386 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM484 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM484 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM484 target RNA into GAM484 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8374 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8374 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8374 target RNA into GAM8374 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8615 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8615 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8615 target RNA into GAM8615 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM9386 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM9386 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM9386 target RNA into GAM9386 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5083 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5083 gene: GAM484 target protein, GAM8374 target protein, GAM8615 target protein and GAM9386 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3

TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM484, GAM8374, GAM8615 and GAM9386

GR5084 T78864 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5084(GR5084) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5084 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5084 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5084 gene encodes GR5084 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5084 precursor RNA folds spatially, forming GR5084 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5084 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5084 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5084 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4069 precursor RNA and GAM261181 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4069 RNA and GAM261181 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4069 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4069 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4069 target RNA into GAM4069 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM261181 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM261181 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM261181 target RNA into GAM261181 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5084 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5084 gene: GAM4069 target protein and GAM261181 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4069 and GAM261181

GR5085 AI220552 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5085(GR5085) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5085 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5085 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5085 gene encodes GR5085 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5085 precursor RNA folds spatially, forming GR5085 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5085 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5085 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5085 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1790 precursor RNA and GAM131811 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM1790 RNA and GAM131811 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1790 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1790 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1790 target RNA into GAM1790 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM131811 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM131811 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM131811 target RNA into GAM131811 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5085 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5085 gene: GAM1790 target protein and GAM131811 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1790 and GAM131811

GR5086 BF212009 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5086(GR5086) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5086 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5086 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5086 gene encodes GR5086 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5086 precursor RNA folds spatially, forming GR5086 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5086 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5086 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5086 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2343 precursor RNA and GAM113697 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2343 RNA and GAM113697 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2343 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2343 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2343 target RNA into GAM2343 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM113697 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM113697 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM113697 target RNA into GAM113697 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5086 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5086 gene: GAM2343 target protein and GAM113697 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2343 and GAM113697

GR5087 BG204908 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5087(GR5087) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5087 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5087 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5087 gene encodes GR5087 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5087 precursor RNA folds spatially, forming GR5087 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5087 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5087 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5087 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM7329 precursor RNA, GAM89131 precursor RNA and GAM295967 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7329 RNA, GAM89131 RNA and GAM295967 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7329 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7329 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7329 target RNA into GAM7329 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM89131 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM89131 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM89131 target RNA into GAM89131 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM295967 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM295967 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM295967 target RNA into GAM295967 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5087 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5087 gene: GAM7329 target protein, GAM89131 target protein and GAM295967 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7329, GAM89131 and GAM295967

GR5088 BM150666 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5088(GR5088) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5088 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5088 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5088 gene encodes GR5088 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5088 precursor RNA folds spatially, forming GR5088 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5088 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5088 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5088 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM225906 precursor RNA and GAM242081 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM225906 RNA and GAM242081 RNA, herein schematically

represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM225906 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM225906 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM225906 target RNA into GAM225906 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM242081 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM242081 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM242081 target RNA into GAM242081 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5088 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5088 gene: GAM225906 target protein and GAM242081 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM225906 and GAM242081

GR5089 C17757 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5089(GR5089) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5089 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5089 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5089 gene encodes GR5089 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5089 precursor RNA folds spatially, forming GR5089 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5089 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5089 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5089 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM201331 precursor RNA and GAM289325 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM201331 RNA and GAM289325 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM201331 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM201331 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM201331 target RNA into GAM201331 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM289325 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM289325 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM289325 target RNA into GAM289325 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5089 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5089 gene: GAM201331 target protein and GAM289325 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM201331 and GAM289325

GR5090 BF432798 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5090 (GR5090) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5090 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR5090 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5090 gene encodes GR5090 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5090 precursor RNA folds spatially, forming GR5090 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5090 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5090 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5090 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM12462 precursor RNA and GAM279534 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM12462 RNA and GAM279534 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM12462 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM12462 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM12462 target RNA into GAM12462 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM279534 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM279534 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM279534 target RNA into GAM279534 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5090 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5090 gene: GAM12462 target

protein and GAM279534 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM12462 and GAM279534

GR5091 BG675379 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5091 (GR5091) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5091 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5091 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5091 gene encodes GR5091 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5091 precursor RNA folds spatially, forming GR5091 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5091 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5091 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5091 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM181 precursor RNA and GAM77286 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM181 RNA and GAM77286 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM181 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM181 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM181 target RNA into GAM181 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM77286 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM77286 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM77286 target RNA into GAM77286 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5091 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5091 gene: GAM181 target protein and GAM77286 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM181 and GAM77286

GR5092 BF927708 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5092(GR5092) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5092 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5092 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5092 gene encodes GR5092 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5092 precursor RNA folds spatially, forming GR5092 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5092 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5092 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5092 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7697 precursor RNA and GAM63676 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7697 RNA and GAM63676 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7697 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7697 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7697 target RNA into GAM7697 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM63676 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM63676 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM63676 target RNA into GAM63676 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5092 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5092 gene: GAM7697 target protein and GAM63676 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7697 and GAM63676

GR5093 BM713399 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5093(GR5093) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5093 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5093 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5093 gene encodes GR5093 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5093 precursor RNA folds spatially, forming GR5093 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5093 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR5093 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5093 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM644 precursor RNA and GAM4692 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM644 RNA and GAM4692 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM644 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM644 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM644 target RNA into GAM644 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM4692 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4692 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4692 target RNA into GAM4692 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5093 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5093 gene: GAM644 target protein and GAM4692 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM644 and GAM4692

GR5094 BE565263 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5094(GR5094) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5094 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5094 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5094 gene encodes GR5094 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5094 precursor RNA folds spatially, forming GR5094 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5094 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5094 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5094 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6225 precursor RNA and GAM273136 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6225 RNA and GAM273136 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6225 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6225 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6225 target RNA into GAM6225 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM273136 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM273136 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM273136 target RNA into GAM273136 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5094 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5094 gene: GAM6225 target protein and GAM273136 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6225 and GAM273136

GR5095 AA013218 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5095(GR5095) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5095 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5095 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5095 gene encodes GR5095 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5095 precursor RNA folds spatially, forming GR5095 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5095 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5095 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5095 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4517 precursor RNA and GAM290785 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4517 RNA and GAM290785 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4517 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4517 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4517 target RNA into

GAM4517 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM290785 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM290785 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM290785 target RNA into GAM290785 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5095 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5095 gene: GAM4517 target protein and GAM290785 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4517 and GAM290785

GR5096 BF679811 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5096(GR5096) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5096 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5096 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5096 gene encodes GR5096 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5096 precursor RNA folds spatially, forming GR5096 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5096 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5096 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5096 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6724 precursor RNA and GAM205873 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6724 RNA and GAM205873 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6724 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6724 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6724 target RNA into GAM6724 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM205873 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM205873 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM205873 target RNA into GAM205873 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5096 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5096 gene: GAM6724 target protein and GAM205873 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6724 and GAM205873

GR5097 BG540777 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5097(GR5097) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5097 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5097 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5097 gene encodes GR5097 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5097 precursor RNA folds spatially, forming GR5097 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated

that GR5097 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5097 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5097 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7181 precursor RNA and GAM8746 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7181 RNA and GAM8746 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7181 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7181 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7181 target RNA into GAM7181 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8746 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8746 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8746 target RNA into GAM8746 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5097 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5097 gene: GAM7181 target protein and GAM8746 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7181 and GAM8746

GR5098 R67972 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5098(GR5098) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR5098 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5098 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5098 gene encodes GR5098 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5098 precursor RNA folds spatially, forming GR5098 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5098 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5098 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5098 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM17363 precursor RNA, GAM41289 precursor RNA and GAM65752 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM17363 RNA, GAM41289 RNA and GAM65752 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM17363 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM17363 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM17363 target RNA into GAM17363 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM41289 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM41289 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM41289 target RNA into GAM41289 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM65752 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM65752 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM65752 target RNA into GAM65752 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5098 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5098 gene: GAM17363 target protein, GAM41289 target protein and GAM65752 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM17363, GAM41289 and GAM65752

GR5099 BG423715 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5099(GR5099) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5099 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5099 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5099 gene encodes GR5099 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5099 precursor RNA folds spatially, forming GR5099 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5099 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5099 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5099 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM194040 precursor RNA and GAM268219 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM194040 RNA and GAM268219 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM194040 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM194040 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM194040 target RNA into GAM194040 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM268219 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM268219 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM268219 target RNA into GAM268219 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5099 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5099 gene: GAM194040 target protein and GAM268219 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM194040 and GAM268219

GR5100 BI196448 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5100(GR5100) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5100 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5100 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5100 gene encodes GR5100 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5100 precursor RNA folds spatially, forming GR5100 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5100 folded precursor RNA comprises a plurality of what is known in the

art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5100 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5100 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3031 precursor RNA and GAM90317 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3031 RNA and GAM90317 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3031 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3031 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3031 target RNA into GAM3031 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM90317 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM90317 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM90317 target RNA into GAM90317 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5100 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5100 gene: GAM3031 target protein and GAM90317 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3031 and GAM90317

GR5101 BM974253 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5101(GR5101) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR5101 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5101 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5101 gene encodes GR5101 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5101 precursor RNA folds spatially, forming GR5101 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5101 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5101 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5101 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM51442 precursor RNA and GAM142862 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM51442 RNA and GAM142862 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM51442 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM51442 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM51442 target RNA into GAM51442 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM142862 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM142862 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM142862 target RNA into GAM142862 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly

utilities, of GR5101 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5101 gene: GAM51442 target protein and GAM142862 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM51442 and GAM142862

GR5102 BG988890 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5102(GR5102) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5102 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5102 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5102 gene encodes GR5102 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5102 precursor RNA folds spatially, forming GR5102 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5102 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5102 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5102 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM51655 precursor RNA and GAM106689 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM51655 RNA and GAM106689 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM51655 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM51655 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM51655 target RNA into GAM51655 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM106689 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM106689 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM106689 target RNA into GAM106689 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5102 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5102 gene: GAM51655 target protein and GAM106689 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM51655 and GAM106689

GR5103 BQ017630 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5103(GR5103) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5103 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5103 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5103 gene encodes GR5103 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5103 precursor RNA folds spatially, forming GR5103 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5103 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5103 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5103 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM5397 precursor RNA, GAM7096 precursor RNA and GAM8395 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded

precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5397 RNA, GAM7096 RNA and GAM8395 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5397 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5397 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5397 target RNA into GAM5397 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7096 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7096 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7096 target RNA into GAM7096 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8395 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8395 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8395 target RNA into GAM8395 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5103 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5103 gene: GAM5397 target protein, GAM7096 target protein and GAM8395 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5397, GAM7096 and GAM8395

GR5104 BF841544 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5104(GR5104) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5104 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5104 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5104 gene encodes GR5104 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5104 precursor RNA folds spatially, forming GR5104 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5104 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5104 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5104 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4702 precursor RNA and GAM228757 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4702 RNA and GAM228757 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4702 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4702 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4702 target RNA into GAM4702 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM228757 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM228757 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM228757 target RNA into GAM228757 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5104 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5104 gene: GAM4702 target protein and GAM228757 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4702 and GAM228757

GR5105 BE615417 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5105(GR5105) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5105 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5105 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5105 gene encodes GR5105 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5105 precursor RNA folds spatially, forming GR5105 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5105 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5105 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5105 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1044 precursor RNA, GAM96235 precursor RNA and GAM279417 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1044 RNA, GAM96235 RNA and GAM279417 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1044 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1044 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig. 8, thereby inhibiting translation of GAM1044 target RNA into GAM1044 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM96235 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM96235 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM96235 target RNA into GAM96235 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM279417 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM279417 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM279417 target RNA into GAM279417 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5105 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5105 gene: GAM1044 target protein, GAM96235 target protein and GAM279417 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1044, GAM96235 and GAM279417

GR5106 BG428855 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5106(GR5106) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5106 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5106 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5106 gene encodes GR5106 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5106 precursor RNA folds spatially, forming GR5106 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5106 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5106 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5106 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7402 precursor RNA and GAM334071 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7402 RNA and GAM334071 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7402 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7402 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7402 target RNA into GAM7402 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM334071 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM334071 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM334071 target RNA into GAM334071 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5106 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5106 gene: GAM7402 target protein and GAM334071 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7402 and GAM334071

GR5107 BE315498 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5107(GR5107) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5107 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5107 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5107 gene encodes GR5107 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5107 precursor RNA folds spatially, forming GR5107 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5107 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5107 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5107 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM117833 precursor RNA, GAM122956 precursor RNA and GAM281511 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM117833 RNA, GAM122956 RNA and GAM281511 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM117833 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM117833 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM117833 target RNA into GAM117833 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM122956 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM122956 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM122956 target RNA into GAM122956 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM281511 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM281511 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM281511 target RNA into GAM281511 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5107 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5107 gene: GAM117833 target protein, GAM122956 target protein and GAM281511 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM117833, GAM122956 and GAM281511

GR5108 BF509670 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5108(GR5108) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5108 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5108 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5108 gene encodes GR5108 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5108 precursor RNA folds spatially, forming GR5108 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5108 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5108 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5108 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2458 precursor RNA and GAM268376 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2458 RNA and GAM268376 RNA, herein schematically

represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2458 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2458 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2458 target RNA into GAM2458 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM268376 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM268376 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM268376 target RNA into GAM268376 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5108 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5108 gene: GAM2458 target protein and GAM268376 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2458 and GAM268376

GR5109 AI091022 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5109(GR5109) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5109 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5109 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5109 gene encodes GR5109 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5109 precursor RNA folds spatially, forming GR5109 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5109 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5109 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5109 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM299952 precursor RNA and GAM332369 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM299952 RNA and GAM332369 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM299952 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM299952 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM299952 target RNA into GAM299952 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM332369 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM332369 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM332369 target RNA into GAM332369 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5109 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5109 gene: GAM299952 target protein and GAM332369 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM299952 and GAM332369

GR5110 BI497176 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5110 (GR5110) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5110 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR5110 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5110 gene encodes GR5110 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5110 precursor RNA folds spatially, forming GR5110 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5110 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5110 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5110 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM87636 precursor RNA and GAM177630 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM87636 RNA and GAM177630 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM87636 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM87636 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM87636 target RNA into GAM87636 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM177630 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM177630 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM177630 target RNA into GAM177630 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5110 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5110 gene: GAM87636 target

protein and GAM177630 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM87636 and GAM177630

GR5111 AA767997 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5111 (GR5111) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5111 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5111 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5111 gene encodes GR5111 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5111 precursor RNA folds spatially, forming GR5111 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5111 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5111 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5111 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM83177 precursor RNA, GAM165549 precursor RNA, GAM206653 precursor RNA and GAM336116 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM83177 RNA, GAM165549 RNA, GAM206653 RNA and GAM336116 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM83177 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM83177 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM83177 target RNA into GAM83177 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM165549 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM165549 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM165549 target RNA into GAM165549 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM206653 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM206653 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM206653 target RNA into GAM206653 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336116 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336116 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336116 target RNA into GAM336116 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5111 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5111 gene: GAM83177 target protein, GAM165549 target protein, GAM206653 target protein and GAM336116 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM83177, GAM165549, GAM206653 and GAM336116

GR5112 BE048439 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5112(GR5112) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5112 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5112 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5112 gene encodes GR5112 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5112 precursor RNA folds spatially, forming GR5112 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5112 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5112 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5112 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM146390 precursor RNA and GAM269304 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM146390 RNA and GAM269304 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM146390 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM146390 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM146390 target RNA into GAM146390 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM269304 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM269304 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM269304 target RNA into GAM269304 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5112 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5112 gene: GAM146390 target protein and GAM269304 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM146390 and GAM269304

bioinformatically detected regulatory gene, referred to here as Genomic Record 5113(GR5113) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5113 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5113 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5113 gene encodes GR5113 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5113 precursor RNA folds spatially, forming GR5113 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5113 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5113 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5113 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM84068 precursor RNA and GAM146437 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM84068 RNA and GAM146437 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM84068 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM84068 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM84068 target RNA into GAM84068 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM146437 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM146437 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM146437

target RNA into GAM146437 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5113 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5113 gene: GAM84068 target protein and GAM146437 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM84068 and GAM146437

GR5114 AI420656 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5114(GR5114) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5114 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5114 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5114 gene encodes GR5114 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5114 precursor RNA folds spatially, forming GR5114 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5114 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5114 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5114 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1800 precursor RNA, GAM5351 precursor RNA and GAM329951 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1800 RNA, GAM5351 RNA and GAM329951 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1800 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1800 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1800 target RNA into GAM1800 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5351 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5351 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5351 target RNA into GAM5351 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM329951 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM329951 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM329951 target RNA into GAM329951 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5114 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5114 gene: GAM1800 target protein, GAM5351 target protein and GAM329951 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1800, GAM5351 and GAM329951

GR5115 BM850340 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5115(GR5115) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5115 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5115 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5115 gene encodes GR5115 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5115 precursor RNA folds spatially, forming GR5115 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5115 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5115 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5115 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3544 precursor RNA, GAM98769 precursor RNA and GAM294226 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3544 RNA, GAM98769 RNA and GAM294226 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3544 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3544 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3544 target RNA into GAM3544 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM98769 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM98769 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM98769 target RNA into GAM98769 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM294226 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM294226 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM294226 target RNA into GAM294226 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5115 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5115 gene: GAM3544 target protein, GAM98769 target protein and GAM294226 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3544, GAM98769 and GAM294226

GR5116 BM453495 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5116(GR5116) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5116 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5116 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5116 gene encodes GR5116 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5116 precursor RNA folds spatially, forming GR5116 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5116 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5116 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5116 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5865 precursor RNA and GAM336346 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5865 RNA and GAM336346 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5865 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5865 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig. 8, thereby inhibiting translation of GAM5865 target RNA into GAM5865 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336346 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336346 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336346 target RNA into GAM336346 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5116 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5116 gene: GAM5865 target protein and GAM336346 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5865 and GAM336346

GR5117 BM726461 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5117(GR5117) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5117 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5117 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5117 gene encodes GR5117 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5117 precursor RNA folds spatially, forming GR5117 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5117 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5117 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5117 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1229 precursor RNA, GAM8300 precursor RNA and GAM299988 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded

precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1229 RNA, GAM8300 RNA and GAM299988 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1229 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1229 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1229 target RNA into GAM1229 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8300 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8300 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8300 target RNA into GAM8300 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM299988 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM299988 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM299988 target RNA into GAM299988 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5117 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5117 gene: GAM1229 target protein, GAM8300 target protein and GAM299988 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1229, GAM8300 and GAM299988

GR5118 AW978516 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5118(GR5118) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5118 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5118 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5118 gene encodes GR5118 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5118 precursor RNA folds spatially, forming GR5118 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5118 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5118 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5118 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM298 precursor RNA, GAM2416 precursor RNA, GAM3905 precursor RNA and GAM5540 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM298 RNA, GAM2416 RNA, GAM3905 RNA and GAM5540 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM298 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM298 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM298 target RNA into GAM298 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM2416 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2416 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2416 target RNA into GAM2416 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM3905 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM3905 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3905 target RNA into GAM3905 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5540 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5540 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5540 target RNA into GAM5540 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5118 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5118 gene: GAM298 target protein, GAM2416 target protein, GAM3905 target protein and GAM5540 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM298, GAM2416, GAM3905 and GAM5540

GR5119 BF685653 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5119(GR5119) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5119 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5119 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5119 gene encodes GR5119 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5119 precursor RNA folds spatially, forming GR5119 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5119 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5119 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5119 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM8103 precursor RNA, GAM33070 precursor RNA, GAM170201 precursor RNA and GAM224729 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8103 RNA, GAM33070 RNA, GAM170201 RNA and GAM224729 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8103 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8103 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8103 target RNA into GAM8103 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM33070 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM33070 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM33070 target RNA into GAM33070 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM170201 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM170201 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM170201 target RNA into GAM170201 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM224729 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM224729 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM224729 target RNA into GAM224729 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5119 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5119 gene: GAM8103 target

protein, GAM33070 target protein, GAM170201 target protein and GAM224729 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8103, GAM33070, GAM170201 and GAM224729

GR5120 BI052358 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5120(GR5120) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5120 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5120 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5120 gene encodes GR5120 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5120 precursor RNA folds spatially, forming GR5120 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5120 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5120 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5120 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM905 precursor RNA, GAM3397 precursor RNA and GAM175682 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM905 RNA, GAM3397 RNA and GAM175682 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM905 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM905 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM905 target RNA into

GAM905 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM3397 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3397 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3397 target RNA into GAM3397 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM175682 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM175682 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM175682 target RNA into GAM175682 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5120 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5120 gene: GAM905 target protein, GAM3397 target protein and GAM175682 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM905, GAM3397 and GAM175682

GR5121 BF854861 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5121(GR5121) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5121 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5121 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5121 gene encodes GR5121 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5121 precursor RNA folds spatially, forming GR5121 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5121 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5121 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5121 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM181964 precursor RNA and GAM314188 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM181964 RNA and GAM314188 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM181964 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM181964 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM181964 target RNA into GAM181964 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM314188 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM314188 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM314188 target RNA into GAM314188 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5121 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5121 gene: GAM181964 target protein and GAM314188 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM181964 and GAM314188

GR5122 BG773511 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5122(GR5122) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5122 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR5122 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5122 gene encodes GR5122 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5122 precursor RNA folds spatially, forming GR5122 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5122 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5122 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5122 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM102193 precursor RNA and GAM139587 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM102193 RNA and GAM139587 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM102193 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM102193 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM102193 target RNA into GAM102193 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM139587 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM139587 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM139587 target RNA into GAM139587 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5122 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5122 gene: GAM102193 target

protein and GAM139587 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM102193 and GAM139587

GR5123 BM903510 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5123(GR5123) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5123 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5123 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5123 gene encodes GR5123 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5123 precursor RNA folds spatially, forming GR5123 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5123 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5123 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5123 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM270973 precursor RNA and GAM306814 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM270973 RNA and GAM306814 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM270973 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM270973 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM270973 target RNA into GAM270973 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM306814 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM306814 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM306814 target RNA into GAM306814 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5123 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5123 gene: GAM270973 target protein and GAM306814 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM270973 and GAM306814

GR5124 AA583770 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5124(GR5124) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5124 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5124 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5124 gene encodes GR5124 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5124 precursor RNA folds spatially, forming GR5124 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5124 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5124 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5124 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1510 precursor RNA, GAM69674 precursor RNA and GAM198101 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1510 RNA, GAM69674 RNA and GAM198101 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1510 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1510 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1510 target RNA into GAM1510 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM69674 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM69674 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM69674 target RNA into GAM69674 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM198101 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM198101 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM198101 target RNA into GAM198101 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5124 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5124 gene: GAM1510 target protein, GAM69674 target protein and GAM198101 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1510, GAM69674 and GAM198101

GR5125 AI924534 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5125(GR5125) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5125 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5125

gene was detected is described hereinabove with reference to Figs. 8-18.

GR5125 gene encodes GR5125 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5125 precursor RNA folds spatially, forming GR5125 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5125 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5125 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5125 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM92322 precursor RNA and GAM156298 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM92322 RNA and GAM156298 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM92322 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM92322 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM92322 target RNA into GAM92322 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM156298 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM156298 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM156298 target RNA into GAM156298 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5125 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5125 gene: GAM92322 target protein and GAM156298 target protein, herein schematically represented by GAM1

TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM92322 and GAM156298

GR5126 BG036710 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5126(GR5126) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5126 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5126 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5126 gene encodes GR5126 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5126 precursor RNA folds spatially, forming GR5126 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5126 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5126 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5126 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5794 precursor RNA and GAM101098 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5794 RNA and GAM101098 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5794 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5794 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5794 target RNA into GAM5794 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM101098 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM101098 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM101098 target RNA into GAM101098 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5126 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5126 gene: GAM5794 target protein and GAM101098 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5794 and GAM101098

GR5127 BE071563 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5127(GR5127) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5127 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5127 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5127 gene encodes GR5127 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5127 precursor RNA folds spatially, forming GR5127 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5127 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5127 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5127 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4828 precursor RNA and GAM293287 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM4828 RNA and GAM293287 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4828 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4828 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4828 target RNA into GAM4828 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM293287 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM293287 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM293287 target RNA into GAM293287 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5127 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5127 gene: GAM4828 target protein and GAM293287 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4828 and GAM293287

GR5128 BE871977 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5128(GR5128) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5128 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5128 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5128 gene encodes GR5128 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5128 precursor RNA folds spatially, forming GR5128 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5128 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5128 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5128 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6247 precursor RNA and GAM277361 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6247 RNA and GAM277361 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6247 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6247 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6247 target RNA into GAM6247 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM277361 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM277361 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM277361 target RNA into GAM277361 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5128 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5128 gene: GAM6247 target protein and GAM277361 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6247 and GAM277361

GR5129 AI904813 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5129(GR5129) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5129 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5129 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5129 gene encodes GR5129 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5129 precursor RNA folds spatially, forming GR5129 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5129 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5129 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5129 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1271 precursor RNA, GAM71091 precursor RNA and GAM209670 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1271 RNA, GAM71091 RNA and GAM209670 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1271 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1271 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1271 target RNA into GAM1271 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM71091 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM71091 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM71091 target RNA into GAM71091 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM209670 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM209670 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM209670 target RNA into GAM209670 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5129 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5129 gene: GAM1271 target protein, GAM71091 target protein and GAM209670 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1271, GAM71091 and GAM209670

GR5130 AW752668 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5130 (GR5130) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5130 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5130 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5130 gene encodes GR5130 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5130 precursor RNA folds spatially, forming GR5130 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5130 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5130 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5130 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8409 precursor RNA and GAM156817 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8409 RNA and GAM156817 RNA, herein schematically

represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8409 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8409 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8409 target RNA into GAM8409 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM156817 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM156817 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM156817 target RNA into GAM156817 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5130 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5130 gene: GAM8409 target protein and GAM156817 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8409 and GAM156817

GR5131 N39411 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5131(GR5131) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5131 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5131 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5131 gene encodes GR5131 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5131 precursor RNA folds spatially, forming GR5131 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5131 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5131 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5131 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM83373 precursor RNA and GAM162369 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM83373 RNA and GAM162369 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM83373 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM83373 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM83373 target RNA into GAM83373 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM162369 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM162369 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM162369 target RNA into GAM162369 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5131 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5131 gene: GAM83373 target protein and GAM162369 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM83373 and GAM162369

GR5132 BF445613 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5132(GR5132) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5132 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR5132 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5132 gene encodes GR5132 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5132 precursor RNA folds spatially, forming GR5132 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5132 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5132 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5132 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8503 precursor RNA and GAM118056 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8503 RNA and GAM118056 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8503 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8503 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8503 target RNA into GAM8503 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM118056 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM118056 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM118056 target RNA into GAM118056 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5132 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5132 gene: GAM8503 target

protein and GAM118056 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8503 and GAM118056

GR5133 BI522674 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5133(GR5133) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5133 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5133 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5133 gene encodes GR5133 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5133 precursor RNA folds spatially, forming GR5133 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5133 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5133 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5133 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM104656 precursor RNA, GAM255550 precursor RNA and GAM258068 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM104656 RNA, GAM255550 RNA and GAM258068 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM104656 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM104656 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM104656 target RNA into GAM104656 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM255550 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM255550 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM255550 target RNA into GAM255550 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM258068 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM258068 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM258068 target RNA into GAM258068 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5133 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5133 gene: GAM104656 target protein, GAM255550 target protein and GAM258068 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM104656, GAM255550 and GAM258068

GR5134 BG433585 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5134(GR5134) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5134 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5134 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5134 gene encodes GR5134 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5134 precursor RNA folds spatially, forming GR5134 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5134 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5134 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR5134 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM60748 precursor RNA, GAM216085 precursor RNA and GAM264582 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM60748 RNA, GAM216085 RNA and GAM264582 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM60748 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM60748 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM60748 target RNA into GAM60748 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM216085 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM216085 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM216085 target RNA into GAM216085 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM264582 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM264582 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM264582 target RNA into GAM264582 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5134 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5134 gene: GAM60748 target protein, GAM216085 target protein and GAM264582 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM60748, GAM216085 and GAM264582

GR5135 BE383885 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5135(GR5135) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5135 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5135 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5135 gene encodes GR5135 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5135 precursor RNA folds spatially, forming GR5135 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5135 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5135 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5135 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM96719 precursor RNA, GAM176002 precursor RNA and GAM271894 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM96719 RNA, GAM176002 RNA and GAM271894 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM96719 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM96719 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM96719 target RNA into GAM96719 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM176002 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM176002 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM176002 target RNA into GAM176002 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM271894 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM271894 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM271894 target RNA into GAM271894 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5135 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5135 gene: GAM96719 target protein, GAM176002 target protein and GAM271894 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM96719, GAM176002 and GAM271894

GR5136 AA555212 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5136(GR5136) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5136 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5136 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5136 gene encodes GR5136 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5136 precursor RNA folds spatially, forming GR5136 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5136 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5136 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5136 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3

separate GAM precursor RNAs, GAM179491 precursor RNA, GAM212594 precursor RNA and GAM331717 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM179491 RNA, GAM212594 RNA and GAM331717 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM179491 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM179491 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM179491 target RNA into GAM179491 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM212594 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM212594 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM212594 target RNA into GAM212594 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM331717 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM331717 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM331717 target RNA into GAM331717 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5136 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5136 gene: GAM179491 target protein, GAM212594 target protein and GAM331717 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM179491, GAM212594 and GAM331717

GR5137 AI440003 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5137(GR5137) gene, which encodes an `operon-like` cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5137 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5137 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5137 gene encodes GR5137 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5137 precursor RNA folds spatially, forming GR5137 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5137 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5137 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5137 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8330 precursor RNA and GAM113093 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8330 RNA and GAM113093 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8330 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8330 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8330 target RNA into GAM8330 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM113093 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM113093 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM113093 target RNA into GAM113093 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5137 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5137 gene: GAM8330 target protein and GAM113093 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8330 and GAM113093

GR5138 AI874141 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5138(GR5138) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5138 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5138 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5138 gene encodes GR5138 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5138 precursor RNA folds spatially, forming GR5138 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5138 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5138 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5138 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6533 precursor RNA and GAM16178 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6533 RNA and GAM16178 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6533 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6533 target RNA, herein schematically represented by

GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6533 target RNA into GAM6533 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM16178 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM16178 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM16178 target RNA into GAM16178 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5138 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5138 gene: GAM6533 target protein and GAM16178 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6533 and GAM16178

GR5139 AW792914 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5139(GR5139) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5139 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5139 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5139 gene encodes GR5139 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5139 precursor RNA folds spatially, forming GR5139 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5139 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5139 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5139 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1547 precursor RNA, GAM4357 precursor RNA and

GAM100900 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1547 RNA, GAM4357 RNA and GAM100900 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1547 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1547 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1547 target RNA into GAM1547 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM4357 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4357 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4357 target RNA into GAM4357 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM100900 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM100900 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM100900 target RNA into GAM100900 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5139 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5139 gene: GAM1547 target protein, GAM4357 target protein and GAM100900 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1547, GAM4357 and GAM100900

GR5140 BE933135 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5140(GR5140) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR5140 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5140 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5140 gene encodes GR5140 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5140 precursor RNA folds spatially, forming GR5140 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5140 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5140 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5140 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM13893 precursor RNA and GAM162064 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM13893 RNA and GAM162064 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM13893 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM13893 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM13893 target RNA into GAM13893 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM162064 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM162064 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM162064 target RNA into GAM162064 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5140 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5140 gene: GAM13893 target protein and GAM162064 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM13893 and GAM162064

GR5141 BF827140 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5141 (GR5141) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5141 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5141 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5141 gene encodes GR5141 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5141 precursor RNA folds spatially, forming GR5141 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5141 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5141 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5141 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM62350 precursor RNA and GAM274516 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM62350 RNA and GAM274516 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM62350 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM62350 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM62350 target RNA into GAM62350 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM274516 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM274516 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM274516 target RNA into GAM274516 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5141 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5141 gene: GAM62350 target protein and GAM274516 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM62350 and GAM274516

GR5142 AA293587 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5142(GR5142) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5142 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5142 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5142 gene encodes GR5142 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5142 precursor RNA folds spatially, forming GR5142 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5142 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5142 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5142 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1627 precursor RNA and GAM72532 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3

FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1627 RNA and GAM72532 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1627 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1627 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1627 target RNA into GAM1627 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM72532 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM72532 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM72532 target RNA into GAM72532 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5142 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5142 gene: GAM1627 target protein and GAM72532 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1627 and GAM72532

GR5143 AA745503 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5143(GR5143) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5143 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5143 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5143 gene encodes GR5143 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5143 precursor RNA folds spatially, forming GR5143 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5143 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5143 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5143 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM8602 precursor RNA, GAM35046 precursor RNA and GAM288537 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8602 RNA, GAM35046 RNA and GAM288537 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8602 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8602 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8602 target RNA into GAM8602 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM35046 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM35046 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM35046 target RNA into GAM35046 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM288537 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM288537 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM288537 target RNA into GAM288537 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5143 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5143 gene: GAM8602 target protein, GAM35046 target protein and GAM288537 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8602, GAM35046 and GAM288537

GR5144 AU099049 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5144(GR5144) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5144 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5144 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5144 gene encodes GR5144 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5144 precursor RNA folds spatially, forming GR5144 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5144 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5144 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5144 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM238 precursor RNA and GAM266403 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM238 RNA and GAM266403 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM238 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM238 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig. 8, thereby inhibiting translation of GAM238 target RNA into GAM238 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM266403 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM266403 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM266403 target RNA into GAM266403 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5144 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5144 gene: GAM238 target protein and GAM266403 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM238 and GAM266403

GR5145 AI700953 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5145(GR5145) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5145 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5145 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5145 gene encodes GR5145 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5145 precursor RNA folds spatially, forming GR5145 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5145 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5145 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5145 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM415 precursor RNA and GAM285214 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin

shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM415 RNA and GAM285214 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM415 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM415 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM415 target RNA into GAM415 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM285214 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM285214 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM285214 target RNA into GAM285214 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5145 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5145 gene: GAM415 target protein and GAM285214 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM415 and GAM285214

GR5146 AW362049 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5146(GR5146) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5146 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5146 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5146 gene encodes GR5146 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5146 precursor RNA folds spatially, forming GR5146 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5146 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5146 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5146 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM32592 precursor RNA, GAM247787 precursor RNA and GAM258898 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM32592 RNA, GAM247787 RNA and GAM258898 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM32592 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM32592 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM32592 target RNA into GAM32592 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM247787 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM247787 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM247787 target RNA into GAM247787 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM258898 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM258898 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM258898 target RNA into GAM258898 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5146 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR5146 gene: GAM32592 target protein, GAM247787 target protein and GAM258898 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM32592, GAM247787 and GAM258898

GR5147 AW970014 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5147(GR5147) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5147 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5147 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5147 gene encodes GR5147 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5147 precursor RNA folds spatially, forming GR5147 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5147 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5147 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5147 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1379 precursor RNA, GAM12930 precursor RNA and GAM158124 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1379 RNA, GAM12930 RNA and GAM158124 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1379 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1379 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig. 8, thereby inhibiting translation of GAM1379 target RNA into GAM1379 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM12930 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM12930 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM12930 target RNA into GAM12930 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM158124 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM158124 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM158124 target RNA into GAM158124 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5147 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5147 gene: GAM1379 target protein, GAM12930 target protein and GAM158124 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1379, GAM12930 and GAM158124

GR5148 BE618485 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5148(GR5148) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5148 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5148 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5148 gene encodes GR5148 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5148 precursor RNA folds spatially, forming GR5148 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5148 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5148 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5148 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2369 precursor RNA and GAM313793 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2369 RNA and GAM313793 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2369 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2369 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2369 target RNA into GAM2369 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM313793 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM313793 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM313793 target RNA into GAM313793 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5148 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5148 gene: GAM2369 target protein and GAM313793 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2369 and GAM313793

GR5149 BG534310 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5149(GR5149) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5149 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5149 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5149 gene encodes GR5149 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5149 precursor RNA folds spatially, forming GR5149 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5149 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5149 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5149 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM12607 precursor RNA and GAM320866 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM12607 RNA and GAM320866 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM12607 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM12607 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM12607 target RNA into GAM12607 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM320866 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM320866 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM320866 target RNA into GAM320866 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5149 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR5149 gene: GAM12607 target protein and GAM320866 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM12607 and GAM320866

GR5150 N71366 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5150(GR5150) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5150 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5150 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5150 gene encodes GR5150 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5150 precursor RNA folds spatially, forming GR5150 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5150 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5150 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5150 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM56804 precursor RNA and GAM77493 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM56804 RNA and GAM77493 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM56804 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM56804 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM56804 target RNA into GAM56804 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM77493 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM77493 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM77493 target RNA into GAM77493 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5150 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5150 gene: GAM56804 target protein and GAM77493 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM56804 and GAM77493

GR5151 AI935379 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5151(GR5151) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5151 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5151 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5151 gene encodes GR5151 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5151 precursor RNA folds spatially, forming GR5151 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5151 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5151 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5151 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2067 precursor RNA and GAM105624 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2067 RNA and GAM105624 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2067 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2067 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2067 target RNA into GAM2067 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM105624 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM105624 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM105624 target RNA into GAM105624 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5151 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5151 gene: GAM2067 target protein and GAM105624 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2067 and GAM105624

GR5152 AW270749 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5152(GR5152) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5152 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5152 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5152 gene encodes GR5152 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5152 precursor RNA folds spatially, forming GR5152 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5152 folded precursor RNA comprises a plurality of what is known in the

art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5152 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5152 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5382 precursor RNA and GAM160956 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5382 RNA and GAM160956 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5382 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5382 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5382 target RNA into GAM5382 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM160956 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM160956 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM160956 target RNA into GAM160956 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5152 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5152 gene: GAM5382 target protein and GAM160956 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5382 and GAM160956

GR5153 BM272529 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5153(GR5153) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR5153 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5153 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5153 gene encodes GR5153 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5153 precursor RNA folds spatially, forming GR5153 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5153 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5153 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5153 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM647 precursor RNA and GAM268176 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM647 RNA and GAM268176 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM647 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM647 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM647 target RNA into GAM647 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM268176 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM268176 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM268176 target RNA into GAM268176 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly

utilities, of GR5153 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5153 gene: GAM647 target protein and GAM268176 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM647 and GAM268176

GR5154 AI350741 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5154(GR5154) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5154 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5154 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5154 gene encodes GR5154 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5154 precursor RNA folds spatially, forming GR5154 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5154 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5154 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5154 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM57733 precursor RNA, GAM143177 precursor RNA and GAM257698 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM57733 RNA, GAM143177 RNA and GAM257698 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM57733 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM57733 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM57733 target RNA into GAM57733 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM143177 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM143177 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM143177 target RNA into GAM143177 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM257698 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM257698 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM257698 target RNA into GAM257698 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5154 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5154 gene: GAM57733 target protein, GAM143177 target protein and GAM257698 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM57733, GAM143177 and GAM257698

GR5155 BM543335 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5155(GR5155) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5155 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5155 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5155 gene encodes GR5155 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5155 precursor RNA folds spatially, forming GR5155 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5155 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR5155 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5155 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM7821 precursor RNA, GAM96602 precursor RNA, GAM227628 precursor RNA and GAM277538 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7821 RNA, GAM96602 RNA, GAM227628 RNA and GAM277538 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7821 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7821 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7821 target RNA into GAM7821 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM96602 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM96602 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM96602 target RNA into GAM96602 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM227628 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM227628 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM227628 target RNA into GAM227628 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM277538 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM277538 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM277538 target RNA into GAM277538 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5155 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5155 gene: GAM7821 target protein, GAM96602 target protein, GAM227628 target protein and GAM277538 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7821, GAM96602, GAM227628 and GAM277538

GR5156 BF878415 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5156(GR5156) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5156 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5156 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5156 gene encodes GR5156 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5156 precursor RNA folds spatially, forming GR5156 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5156 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5156 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5156 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM57 precursor RNA and GAM51152 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM57 RNA and GAM51152 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM57 RNA, herein schematically represented by GAM1 RNA through GAM3

RNA, binds complementarily to a target binding site located in an untranslated region of GAM57 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM57 target RNA into GAM57 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM51152 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM51152 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM51152 target RNA into GAM51152 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5156 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5156 gene: GAM57 target protein and GAM51152 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM57 and GAM51152

GR5157 BE835231 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5157(GR5157) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5157 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5157 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5157 gene encodes GR5157 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5157 precursor RNA folds spatially, forming GR5157 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5157 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5157 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5157 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM23631 precursor RNA and GAM177659 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM23631 RNA and GAM177659 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM23631 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM23631 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM23631 target RNA into GAM23631 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM177659 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM177659 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM177659 target RNA into GAM177659 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5157 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5157 gene: GAM23631 target protein and GAM177659 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM23631 and GAM177659

GR5158 BQ027892 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5158(GR5158) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5158 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5158 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5158 gene encodes GR5158 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5158 precursor RNA folds spatially, forming GR5158 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5158 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5158 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5158 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM904 precursor RNA, GAM13558 precursor RNA, GAM83004 precursor RNA and GAM283478 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM904 RNA, GAM13558 RNA, GAM83004 RNA and GAM283478 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM904 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM904 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM904 target RNA into GAM904 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM13558 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM13558 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM13558 target RNA into GAM13558 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM83004 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM83004 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM83004 target RNA into GAM83004 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM283478 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM283478 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM283478 target RNA into GAM283478 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5158 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5158 gene: GAM904 target protein, GAM13558 target protein, GAM83004 target protein and GAM283478 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM904, GAM13558, GAM83004 and GAM283478

GR5159 BF675082 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5159(GR5159) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5159 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5159 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5159 gene encodes GR5159 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5159 precursor RNA folds spatially, forming GR5159 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5159 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5159 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5159 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7444 precursor RNA and GAM93569 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7444 RNA and GAM93569 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7444 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7444 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7444 target RNA into GAM7444 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM93569 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM93569 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM93569 target RNA into GAM93569 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5159 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5159 gene: GAM7444 target protein and GAM93569 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7444 and GAM93569

GR5160 BG768112 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5160(GR5160) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5160 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5160 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5160 gene encodes GR5160 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5160 precursor RNA folds spatially, forming GR5160 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5160 folded precursor RNA comprises a plurality of what is known in the

art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5160 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5160 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM60513 precursor RNA and GAM95059 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM60513 RNA and GAM95059 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM60513 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM60513 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM60513 target RNA into GAM60513 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM95059 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM95059 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM95059 target RNA into GAM95059 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5160 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5160 gene: GAM60513 target protein and GAM95059 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM60513 and GAM95059

GR5161 BI830984 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5161(GR5161) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR5161 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5161 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5161 gene encodes GR5161 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5161 precursor RNA folds spatially, forming GR5161 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5161 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5161 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5161 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4841 precursor RNA and GAM5564 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4841 RNA and GAM5564 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4841 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4841 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4841 target RNA into GAM4841 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5564 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5564 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5564 target RNA into GAM5564 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly

utilities, of GR5161 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5161 gene: GAM4841 target protein and GAM5564 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4841 and GAM5564

GR5162 BG569069 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5162(GR5162) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5162 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5162 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5162 gene encodes GR5162 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5162 precursor RNA folds spatially, forming GR5162 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5162 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5162 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5162 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM23486 precursor RNA and GAM214289 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM23486 RNA and GAM214289 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM23486 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM23486 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM23486 target RNA into GAM23486 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM214289 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM214289 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM214289 target RNA into GAM214289 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5162 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5162 gene: GAM23486 target protein and GAM214289 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM23486 and GAM214289

GR5163 AI333032 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5163(GR5163) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5163 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5163 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5163 gene encodes GR5163 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5163 precursor RNA folds spatially, forming GR5163 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5163 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5163 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5163 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM53629 precursor RNA, GAM77370 precursor RNA and GAM188583 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded

precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM53629 RNA, GAM77370 RNA and GAM188583 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM53629 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM53629 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM53629 target RNA into GAM53629 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM77370 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM77370 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM77370 target RNA into GAM77370 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM188583 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM188583 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM188583 target RNA into GAM188583 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5163 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5163 gene: GAM53629 target protein, GAM77370 target protein and GAM188583 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM53629, GAM77370 and GAM188583

GR5164 BG528639 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5164(GR5164) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5164 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5164 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5164 gene encodes GR5164 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5164 precursor RNA folds spatially, forming GR5164 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5164 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5164 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5164 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6032 precursor RNA and GAM47745 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6032 RNA and GAM47745 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6032 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6032 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6032 target RNA into GAM6032 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM47745 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM47745 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM47745 target RNA into GAM47745 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5164 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5164 gene: GAM6032 target protein and GAM47745 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6032 and GAM47745

GR5165 AA622198 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5165(GR5165) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5165 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5165 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5165 gene encodes GR5165 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5165 precursor RNA folds spatially, forming GR5165 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5165 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5165 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5165 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM237688 precursor RNA, GAM260957 precursor RNA and GAM304372 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM237688 RNA, GAM260957 RNA and GAM304372 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM237688 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM237688 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM237688 target RNA into GAM237688 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM260957 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM260957 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM260957 target RNA into GAM260957 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM304372 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM304372 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM304372 target RNA into GAM304372 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5165 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5165 gene: GAM237688 target protein, GAM260957 target protein and GAM304372 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM237688, GAM260957 and GAM304372

GR5166 BF359059 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5166(GR5166) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5166 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5166 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5166 gene encodes GR5166 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5166 precursor RNA folds spatially, forming GR5166 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5166 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5166 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5166 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM192759 precursor RNA and GAM261254 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM192759 RNA and GAM261254 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM192759 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM192759 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM192759 target RNA into GAM192759 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM261254 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM261254 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM261254 target RNA into GAM261254 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5166 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5166 gene: GAM192759 target protein and GAM261254 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM192759 and GAM261254

GR5167 BM923769 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5167(GR5167) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5167 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5167 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5167 gene encodes GR5167 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5167 precursor RNA folds spatially, forming GR5167 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5167 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5167 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5167 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8575 precursor RNA and GAM253907 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8575 RNA and GAM253907 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8575 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8575 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8575 target RNA into GAM8575 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM253907 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM253907 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM253907 target RNA into GAM253907 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5167 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR5167 gene: GAM8575 target protein and GAM253907 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8575 and GAM253907

GR5168 BI548538 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5168(GR5168) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5168 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5168 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5168 gene encodes GR5168 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5168 precursor RNA folds spatially, forming GR5168 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5168 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5168 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5168 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6782 precursor RNA and GAM64619 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6782 RNA and GAM64619 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6782 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6782 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6782 target RNA into GAM6782 target protein, herein schematically represented by GAM1 TARGET

PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM64619 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM64619 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM64619 target RNA into GAM64619 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5168 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5168 gene: GAM6782 target protein and GAM64619 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6782 and GAM64619

GR5169 AA424304 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5169(GR5169) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5169 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5169 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5169 gene encodes GR5169 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5169 precursor RNA folds spatially, forming GR5169 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5169 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5169 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5169 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM106779 precursor RNA and GAM327754 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM106779 RNA and GAM327754 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM106779 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM106779 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM106779 target RNA into GAM106779 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM327754 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM327754 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM327754 target RNA into GAM327754 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5169 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5169 gene: GAM106779 target protein and GAM327754 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM106779 and GAM327754

GR5170 BE396656 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5170(GR5170) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5170 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5170 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5170 gene encodes GR5170 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5170 precursor RNA folds spatially, forming GR5170 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5170 folded precursor RNA comprises a plurality of what is known in the

art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5170 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5170 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM155110 precursor RNA and GAM196165 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM155110 RNA and GAM196165 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM155110 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM155110 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM155110 target RNA into GAM155110 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM196165 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM196165 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM196165 target RNA into GAM196165 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5170 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5170 gene: GAM155110 target protein and GAM196165 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM155110 and GAM196165

GR5171 BF814830 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5171(GR5171) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR5171 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5171 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5171 gene encodes GR5171 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5171 precursor RNA folds spatially, forming GR5171 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5171 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5171 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5171 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM66832 precursor RNA and GAM123848 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM66832 RNA and GAM123848 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM66832 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM66832 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM66832 target RNA into GAM66832 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM123848 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM123848 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM123848 target RNA into GAM123848 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly

utilities, of GR5171 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5171 gene: GAM66832 target protein and GAM123848 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM66832 and GAM123848

GR5172 AI672241 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5172(GR5172) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5172 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5172 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5172 gene encodes GR5172 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5172 precursor RNA folds spatially, forming GR5172 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5172 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5172 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5172 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2191 precursor RNA and GAM5553 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2191 RNA and GAM5553 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2191 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2191 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig. 8, thereby inhibiting translation of GAM2191 target RNA into GAM2191 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5553 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5553 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5553 target RNA into GAM5553 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5172 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5172 gene: GAM2191 target protein and GAM5553 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2191 and GAM5553

GR5173 BE549931 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5173(GR5173) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5173 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5173 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5173 gene encodes GR5173 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5173 precursor RNA folds spatially, forming GR5173 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5173 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5173 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5173 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM170464 precursor RNA and GAM184865 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin

shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM170464 RNA and GAM184865 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM170464 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM170464 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM170464 target RNA into GAM170464 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM184865 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM184865 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM184865 target RNA into GAM184865 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5173 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5173 gene: GAM170464 target protein and GAM184865 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM170464 and GAM184865

GR5174 BG189386 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5174(GR5174) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5174 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5174 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5174 gene encodes GR5174 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5174 precursor RNA folds spatially, forming GR5174 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5174 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5174 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5174 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM107242 precursor RNA and GAM144550 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM107242 RNA and GAM144550 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM107242 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM107242 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM107242 target RNA into GAM107242 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM144550 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM144550 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM144550 target RNA into GAM144550 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5174 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5174 gene: GAM107242 target protein and GAM144550 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM107242 and GAM144550

GR5175 BF695147 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5175(GR5175) gene, which encodes an `operon-like` cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5175 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5175 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5175 gene encodes GR5175 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5175 precursor RNA folds spatially, forming GR5175 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5175 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5175 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5175 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3148 precursor RNA and GAM234968 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3148 RNA and GAM234968 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3148 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3148 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3148 target RNA into GAM3148 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM234968 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM234968 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM234968 target RNA into GAM234968 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5175 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5175 gene: GAM3148 target protein and GAM234968 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3148 and GAM234968

GR5176 BI762945 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5176(GR5176) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5176 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5176 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5176 gene encodes GR5176 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5176 precursor RNA folds spatially, forming GR5176 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5176 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5176 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5176 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM65976 precursor RNA and GAM108401 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM65976 RNA and GAM108401 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM65976 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM65976 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM65976 target RNA into GAM65976 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM108401 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM108401 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM108401 target RNA into GAM108401 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5176 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5176 gene: GAM65976 target protein and GAM108401 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM65976 and GAM108401

GR5177 AI734188 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5177(GR5177) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5177 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5177 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5177 gene encodes GR5177 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5177 precursor RNA folds spatially, forming GR5177 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5177 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5177 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5177 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM7209 precursor RNA, GAM227895 precursor RNA

and GAM283593 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7209 RNA, GAM227895 RNA and GAM283593 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7209 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7209 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7209 target RNA into GAM7209 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM227895 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM227895 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM227895 target RNA into GAM227895 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM283593 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM283593 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM283593 target RNA into GAM283593 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5177 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5177 gene: GAM7209 target protein, GAM227895 target protein and GAM283593 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7209, GAM227895 and GAM283593

GR5178 BF983947 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5178(GR5178) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR5178 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5178 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5178 gene encodes GR5178 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5178 precursor RNA folds spatially, forming GR5178 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5178 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5178 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5178 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM218128 precursor RNA and GAM226974 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM218128 RNA and GAM226974 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM218128 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM218128 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM218128 target RNA into GAM218128 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM226974 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM226974 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM226974 target RNA into GAM226974 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5178 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5178 gene: GAM218128 target protein and GAM226974 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM218128 and GAM226974

GR5179 BQ004441 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5179(GR5179) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5179 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5179 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5179 gene encodes GR5179 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5179 precursor RNA folds spatially, forming GR5179 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5179 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5179 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5179 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM179325 precursor RNA and GAM200168 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM179325 RNA and GAM200168 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM179325 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM179325 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM179325 target RNA into GAM179325 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM200168 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM200168 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM200168 target RNA into GAM200168 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5179 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5179 gene: GAM179325 target protein and GAM200168 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM179325 and GAM200168

GR5180 AL704197 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5180(GR5180) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5180 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5180 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5180 gene encodes GR5180 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5180 precursor RNA folds spatially, forming GR5180 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5180 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5180 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5180 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7062 precursor RNA and GAM126834 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3

FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7062 RNA and GAM126834 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7062 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7062 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7062 target RNA into GAM7062 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM126834 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM126834 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM126834 target RNA into GAM126834 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5180 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5180 gene: GAM7062 target protein and GAM126834 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7062 and GAM126834

GR5181 AU159560 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5181(GR5181) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5181 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5181 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5181 gene encodes GR5181 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5181 precursor RNA folds spatially, forming GR5181 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5181 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5181 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5181 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM6191 precursor RNA, GAM14403 precursor RNA and GAM242754 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6191 RNA, GAM14403 RNA and GAM242754 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6191 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6191 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6191 target RNA into GAM6191 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM14403 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM14403 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM14403 target RNA into GAM14403 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM242754 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM242754 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM242754 target RNA into GAM242754 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5181 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5181 gene: GAM6191 target protein, GAM14403 target protein and GAM242754 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6191, GAM14403 and GAM242754

GR5182 BE796430 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5182(GR5182) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5182 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5182 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5182 gene encodes GR5182 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5182 precursor RNA folds spatially, forming GR5182 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5182 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5182 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5182 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3171 precursor RNA and GAM271084 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3171 RNA and GAM271084 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3171 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3171 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig. 8, thereby inhibiting translation of GAM3171 target RNA into GAM3171 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM271084 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM271084 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM271084 target RNA into GAM271084 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5182 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5182 gene: GAM3171 target protein and GAM271084 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3171 and GAM271084

GR5183 AW578879 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5183(GR5183) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5183 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5183 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5183 gene encodes GR5183 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5183 precursor RNA folds spatially, forming GR5183 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5183 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5183 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5183 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2688 precursor RNA and GAM291116 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin

shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2688 RNA and GAM291116 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2688 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2688 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2688 target RNA into GAM2688 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM291116 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM291116 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM291116 target RNA into GAM291116 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5183 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5183 gene: GAM2688 target protein and GAM291116 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2688 and GAM291116

GR5184 AA127815 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5184(GR5184) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5184 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5184 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5184 gene encodes GR5184 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5184 precursor RNA folds spatially, forming GR5184 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5184 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5184 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5184 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM54046 precursor RNA, GAM138900 precursor RNA and GAM301775 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM54046 RNA, GAM138900 RNA and GAM301775 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM54046 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM54046 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM54046 target RNA into GAM54046 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM138900 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM138900 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM138900 target RNA into GAM138900 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM301775 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM301775 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM301775 target RNA into GAM301775 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5184 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR5184 gene: GAM54046 target protein, GAM138900 target protein and GAM301775 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM54046, GAM138900 and GAM301775

GR5185 AW844873 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5185(GR5185) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5185 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5185 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5185 gene encodes GR5185 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5185 precursor RNA folds spatially, forming GR5185 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5185 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5185 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5185 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1368 precursor RNA and GAM282491 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1368 RNA and GAM282491 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1368 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1368 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1368 target RNA into

GAM1368 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM282491 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM282491 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM282491 target RNA into GAM282491 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5185 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5185 gene: GAM1368 target protein and GAM282491 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1368 and GAM282491

GR5186 BF526713 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5186(GR5186) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5186 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5186 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5186 gene encodes GR5186 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5186 precursor RNA folds spatially, forming GR5186 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5186 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5186 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5186 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7101 precursor RNA and GAM24634 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7101 RNA and GAM24634 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7101 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7101 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7101 target RNA into GAM7101 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM24634 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM24634 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM24634 target RNA into GAM24634 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5186 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5186 gene: GAM7101 target protein and GAM24634 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7101 and GAM24634

GR5187 BG253815 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5187(GR5187) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5187 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5187 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5187 gene encodes GR5187 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5187 precursor RNA folds spatially, forming GR5187 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated

that GR5187 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5187 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5187 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM197386 precursor RNA, GAM219722 precursor RNA and GAM255928 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM197386 RNA, GAM219722 RNA and GAM255928 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM197386 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM197386 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM197386 target RNA into GAM197386 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM219722 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM219722 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM219722 target RNA into GAM219722 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM255928 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM255928 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM255928 target RNA into GAM255928 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5187 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5187 gene: GAM197386 target

protein, GAM219722 target protein and GAM255928 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM197386, GAM219722 and GAM255928

GR5188 BQ062176 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5188(GR5188) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5188 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5188 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5188 gene encodes GR5188 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5188 precursor RNA folds spatially, forming GR5188 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5188 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5188 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5188 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1428 precursor RNA and GAM297762 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1428 RNA and GAM297762 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1428 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1428 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1428 target RNA into GAM1428 target protein, herein schematically represented by GAM1 TARGET

PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM297762 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM297762 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM297762 target RNA into GAM297762 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5188 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5188 gene: GAM1428 target protein and GAM297762 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1428 and GAM297762

GR5189 BG615479 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5189(GR5189) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5189 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5189 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5189 gene encodes GR5189 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5189 precursor RNA folds spatially, forming GR5189 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5189 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5189 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5189 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM231435 precursor RNA and GAM293747 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM231435 RNA and GAM293747 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM231435 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM231435 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM231435 target RNA into GAM231435 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM293747 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM293747 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM293747 target RNA into GAM293747 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5189 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5189 gene: GAM231435 target protein and GAM293747 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM231435 and GAM293747

GR5190 BG106075 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5190(GR5190) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5190 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5190 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5190 gene encodes GR5190 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5190 precursor RNA folds spatially, forming GR5190 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5190 folded precursor RNA comprises a plurality of what is known in the

art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5190 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5190 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2029 precursor RNA and GAM107997 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2029 RNA and GAM107997 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2029 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2029 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2029 target RNA into GAM2029 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM107997 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM107997 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM107997 target RNA into GAM107997 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5190 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5190 gene: GAM2029 target protein and GAM107997 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2029 and GAM107997

GR5191 BF244204 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5191(GR5191) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR5191 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5191 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5191 gene encodes GR5191 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5191 precursor RNA folds spatially, forming GR5191 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5191 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5191 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5191 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5128 precursor RNA and GAM167636 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5128 RNA and GAM167636 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5128 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5128 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5128 target RNA into GAM5128 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM167636 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM167636 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM167636 target RNA into GAM167636 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly

utilities, of GR5191 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5191 gene: GAM5128 target protein and GAM167636 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5128 and GAM167636

GR5192 AA527159 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5192(GR5192) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5192 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5192 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5192 gene encodes GR5192 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5192 precursor RNA folds spatially, forming GR5192 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5192 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5192 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5192 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM200015 precursor RNA and GAM305501 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM200015 RNA and GAM305501 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM200015 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM200015 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM200015 target RNA into GAM200015 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM305501 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM305501 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM305501 target RNA into GAM305501 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5192 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5192 gene: GAM200015 target protein and GAM305501 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM200015 and GAM305501

GR5193 BE783956 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5193(GR5193) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5193 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5193 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5193 gene encodes GR5193 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5193 precursor RNA folds spatially, forming GR5193 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5193 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5193 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5193 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7970 precursor RNA and GAM266462 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin

shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7970 RNA and GAM266462 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7970 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7970 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7970 target RNA into GAM7970 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM266462 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM266462 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM266462 target RNA into GAM266462 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5193 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5193 gene: GAM7970 target protein and GAM266462 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7970 and GAM266462

GR5194 BI091105 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5194(GR5194) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5194 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5194 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5194 gene encodes GR5194 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5194 precursor RNA folds spatially, forming GR5194 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5194 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5194 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5194 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4212 precursor RNA and GAM100753 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4212 RNA and GAM100753 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4212 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4212 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4212 target RNA into GAM4212 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM100753 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM100753 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM100753 target RNA into GAM100753 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5194 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5194 gene: GAM4212 target protein and GAM100753 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4212 and GAM100753

GR5195 AA400923 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5195(GR5195) gene, which encodes an `operon-like` cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5195 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5195 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5195 gene encodes GR5195 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5195 precursor RNA folds spatially, forming GR5195 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5195 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5195 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5195 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3403 precursor RNA and GAM320046 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3403 RNA and GAM320046 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3403 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3403 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3403 target RNA into GAM3403 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM320046 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM320046 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM320046 target RNA into GAM320046 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5195 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5195 gene: GAM3403 target protein and GAM320046 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3403 and GAM320046

GR5196 AW381367 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5196(GR5196) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5196 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5196 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5196 gene encodes GR5196 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5196 precursor RNA folds spatially, forming GR5196 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5196 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5196 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5196 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM250042 precursor RNA and GAM291617 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM250042 RNA and GAM291617 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM250042 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM250042 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM250042 target RNA into GAM250042 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM291617 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM291617 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM291617 target RNA into GAM291617 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5196 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5196 gene: GAM250042 target protein and GAM291617 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM250042 and GAM291617

GR5197 AA723478 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5197(GR5197) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5197 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5197 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5197 gene encodes GR5197 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5197 precursor RNA folds spatially, forming GR5197 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5197 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5197 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5197 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4303 precursor RNA and GAM226747 precursor

RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4303 RNA and GAM226747 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4303 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4303 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4303 target RNA into GAM4303 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM226747 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM226747 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM226747 target RNA into GAM226747 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5197 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5197 gene: GAM4303 target protein and GAM226747 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4303 and GAM226747

GR5198 BG179684 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5198(GR5198) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5198 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5198 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5198 gene encodes GR5198 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5198 precursor RNA folds spatially, forming GR5198 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5198 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5198 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5198 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM527 precursor RNA and GAM195076 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM527 RNA and GAM195076 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM527 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM527 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM527 target RNA into GAM527 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM195076 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM195076 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM195076 target RNA into GAM195076 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5198 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5198 gene: GAM527 target protein and GAM195076 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM527 and GAM195076

bioinformatically detected regulatory gene, referred to here as Genomic Record 5199(GR5199) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5199 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5199 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5199 gene encodes GR5199 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5199 precursor RNA folds spatially, forming GR5199 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5199 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5199 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5199 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2550 precursor RNA, GAM4807 precursor RNA and GAM7085 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2550 RNA, GAM4807 RNA and GAM7085 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2550 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2550 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2550 target RNA into GAM2550 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM4807 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4807 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig. 8, thereby inhibiting translation of GAM4807 target RNA into GAM4807 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7085 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7085 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7085 target RNA into GAM7085 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5199 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5199 gene: GAM2550 target protein, GAM4807 target protein and GAM7085 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2550, GAM4807 and GAM7085

GR5200 BG575531 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5200(GR5200) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5200 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5200 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5200 gene encodes GR5200 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5200 precursor RNA folds spatially, forming GR5200 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5200 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5200 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5200 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM734 precursor RNA, GAM2606 precursor RNA and GAM257963 precursor RNA, herein schematically represented by GAM1 FOLDED

PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM734 RNA, GAM2606 RNA and GAM257963 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM734 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM734 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM734 target RNA into GAM734 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM2606 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2606 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2606 target RNA into GAM2606 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM257963 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM257963 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM257963 target RNA into GAM257963 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5200 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5200 gene: GAM734 target protein, GAM2606 target protein and GAM257963 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM734, GAM2606 and GAM257963

GR5201 BE544799 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5201(GR5201) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR5201 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5201 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5201 gene encodes GR5201 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5201 precursor RNA folds spatially, forming GR5201 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5201 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5201 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5201 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM59301 precursor RNA and GAM145554 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM59301 RNA and GAM145554 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM59301 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM59301 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM59301 target RNA into GAM59301 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM145554 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM145554 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM145554 target RNA into GAM145554 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly

utilities, of GR5201 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5201 gene: GAM59301 target protein and GAM145554 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM59301 and GAM145554

GR5202 BF513739 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5202(GR5202) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5202 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5202 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5202 gene encodes GR5202 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5202 precursor RNA folds spatially, forming GR5202 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5202 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5202 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5202 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5195 precursor RNA and GAM7540 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5195 RNA and GAM7540 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5195 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5195 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig. 8, thereby inhibiting translation of GAM5195 target RNA into GAM5195 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7540 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7540 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7540 target RNA into GAM7540 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5202 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5202 gene: GAM5195 target protein and GAM7540 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5195 and GAM7540

GR5203 BG951229 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5203(GR5203) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5203 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5203 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5203 gene encodes GR5203 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5203 precursor RNA folds spatially, forming GR5203 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5203 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5203 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5203 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4660 precursor RNA and GAM193166 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin

shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4660 RNA and GAM193166 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4660 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4660 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4660 target RNA into GAM4660 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM193166 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM193166 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM193166 target RNA into GAM193166 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5203 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5203 gene: GAM4660 target protein and GAM193166 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4660 and GAM193166

GR5204 BG779273 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5204(GR5204) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5204 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5204 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5204 gene encodes GR5204 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5204 precursor RNA folds spatially, forming GR5204 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5204 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5204 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5204 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM1804 precursor RNA, GAM132933 precursor RNA, GAM156673 precursor RNA and GAM240201 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1804 RNA, GAM132933 RNA, GAM156673 RNA and GAM240201 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1804 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1804 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1804 target RNA into GAM1804 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM132933 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM132933 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM132933 target RNA into GAM132933 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM156673 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM156673 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM156673 target RNA into GAM156673 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM240201 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM240201 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM240201 target RNA into GAM240201 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5204 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5204 gene: GAM1804 target protein, GAM132933 target protein, GAM156673 target protein and GAM240201 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1804, GAM132933, GAM156673 and GAM240201

GR5205 BF343823 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5205(GR5205) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5205 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5205 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5205 gene encodes GR5205 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5205 precursor RNA folds spatially, forming GR5205 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5205 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5205 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5205 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1186 precursor RNA and GAM283617 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1186 RNA and GAM283617 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding

to GAM RNA of Fig. 8.

GAM1186 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1186 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1186 target RNA into GAM1186 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM283617 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM283617 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM283617 target RNA into GAM283617 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5205 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5205 gene: GAM1186 target protein and GAM283617 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1186 and GAM283617

GR5206 AI287653 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5206(GR5206) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5206 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5206 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5206 gene encodes GR5206 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5206 precursor RNA folds spatially, forming GR5206 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5206 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5206 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR5206 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM170613 precursor RNA and GAM327980 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM170613 RNA and GAM327980 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM170613 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM170613 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM170613 target RNA into GAM170613 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM327980 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM327980 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM327980 target RNA into GAM327980 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5206 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5206 gene: GAM170613 target protein and GAM327980 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM170613 and GAM327980

GR5207 BM682752 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5207(GR5207) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5207 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5207

gene was detected is described hereinabove with reference to Figs. 8-18.

GR5207 gene encodes GR5207 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5207 precursor RNA folds spatially, forming GR5207 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5207 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5207 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5207 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM59903 precursor RNA and GAM253888 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM59903 RNA and GAM253888 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM59903 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM59903 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM59903 target RNA into GAM59903 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM253888 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM253888 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM253888 target RNA into GAM253888 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5207 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5207 gene: GAM59903 target protein and GAM253888 target protein, herein schematically represented by GAM1

TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM59903 and GAM253888

GR5208 BI837761 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5208(GR5208) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5208 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5208 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5208 gene encodes GR5208 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5208 precursor RNA folds spatially, forming GR5208 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5208 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5208 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5208 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM131003 precursor RNA, GAM214215 precursor RNA, GAM316759 precursor RNA and GAM319766 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM131003 RNA, GAM214215 RNA, GAM316759 RNA and GAM319766 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM131003 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM131003 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM131003 target RNA into GAM131003 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM214215 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM214215 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM214215 target RNA into GAM214215 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM316759 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM316759 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM316759 target RNA into GAM316759 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM319766 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM319766 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM319766 target RNA into GAM319766 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5208 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5208 gene: GAM131003 target protein, GAM214215 target protein, GAM316759 target protein and GAM319766 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM131003, GAM214215, GAM316759 and GAM319766

GR5209 BG395173 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5209(GR5209) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5209 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5209 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5209 gene encodes GR5209 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5209 precursor RNA folds spatially, forming GR5209 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5209 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5209 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5209 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM123800 precursor RNA and GAM307274 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM123800 RNA and GAM307274 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM123800 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM123800 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM123800 target RNA into GAM123800 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM307274 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM307274 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM307274 target RNA into GAM307274 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5209 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5209 gene: GAM123800 target protein and GAM307274 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM123800 and GAM307274

5210(GR5210) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5210 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5210 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5210 gene encodes GR5210 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5210 precursor RNA folds spatially, forming GR5210 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5210 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5210 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5210 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM237096 precursor RNA and GAM294817 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM237096 RNA and GAM294817 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM237096 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM237096 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM237096 target RNA into GAM237096 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM294817 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM294817 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM294817 target RNA into GAM294817 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5210 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5210 gene: GAM237096 target protein and GAM294817 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM237096 and GAM294817

GR5211 AA244003 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5211(GR5211) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5211 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5211 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5211 gene encodes GR5211 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5211 precursor RNA folds spatially, forming GR5211 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5211 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5211 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5211 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM167594 precursor RNA, GAM210306 precursor RNA and GAM295168 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM167594 RNA, GAM210306 RNA and GAM295168 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM167594 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM167594 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM167594 target RNA into GAM167594 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM210306 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM210306 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM210306 target RNA into GAM210306 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM295168 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM295168 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM295168 target RNA into GAM295168 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5211 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5211 gene: GAM167594 target protein, GAM210306 target protein and GAM295168 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM167594, GAM210306 and GAM295168

GR5212 BF126651 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5212(GR5212) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5212 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5212 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5212 gene encodes GR5212 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5212 precursor RNA folds spatially, forming GR5212 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5212 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5212 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5212 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM890 precursor RNA, GAM8010 precursor RNA, GAM138939 precursor RNA and GAM213664 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM890 RNA, GAM8010 RNA, GAM138939 RNA and GAM213664 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM890 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM890 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM890 target RNA into GAM890 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8010 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8010 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8010 target RNA into GAM8010 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM138939 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM138939 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM138939 target RNA into GAM138939 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM213664 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM213664 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM213664 target RNA into GAM213664 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5212 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5212 gene: GAM890 target protein, GAM8010 target protein, GAM138939 target protein and GAM213664 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM890, GAM8010, GAM138939 and GAM213664

GR5213 BE260720 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5213(GR5213) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5213 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5213 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5213 gene encodes GR5213 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5213 precursor RNA folds spatially, forming GR5213 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5213 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5213 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5213 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM221289 precursor RNA and GAM231351 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM221289 RNA and GAM231351 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding

to GAM RNA of Fig. 8.

GAM221289 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM221289 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM221289 target RNA into GAM221289 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM231351 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM231351 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM231351 target RNA into GAM231351 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5213 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5213 gene: GAM221289 target protein and GAM231351 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM221289 and GAM231351

GR5214 BM912357 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5214(GR5214) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5214 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5214 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5214 gene encodes GR5214 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5214 precursor RNA folds spatially, forming GR5214 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5214 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5214 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR5214 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM72341 precursor RNA and GAM103444 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM72341 RNA and GAM103444 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM72341 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM72341 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM72341 target RNA into GAM72341 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM103444 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM103444 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM103444 target RNA into GAM103444 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5214 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5214 gene: GAM72341 target protein and GAM103444 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM72341 and GAM103444

GR5215 AW024637 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5215(GR5215) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5215 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5215

gene was detected is described hereinabove with reference to Figs. 8-18.

GR5215 gene encodes GR5215 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5215 precursor RNA folds spatially, forming GR5215 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5215 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5215 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5215 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7048 precursor RNA and GAM163881 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7048 RNA and GAM163881 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7048 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7048 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7048 target RNA into GAM7048 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM163881 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM163881 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM163881 target RNA into GAM163881 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5215 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5215 gene: GAM7048 target protein and GAM163881 target protein, herein schematically represented by GAM1

TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7048 and GAM163881

GR5216 BE390740 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5216(GR5216) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5216 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5216 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5216 gene encodes GR5216 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5216 precursor RNA folds spatially, forming GR5216 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5216 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5216 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5216 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6104 precursor RNA and GAM323343 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6104 RNA and GAM323343 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6104 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6104 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6104 target RNA into GAM6104 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM323343 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM323343 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM323343 target RNA into GAM323343 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5216 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5216 gene: GAM6104 target protein and GAM323343 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6104 and GAM323343

GR5217 BG715355 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5217(GR5217) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5217 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5217 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5217 gene encodes GR5217 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5217 precursor RNA folds spatially, forming GR5217 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5217 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5217 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5217 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM566 precursor RNA and GAM334952 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM566 RNA and GAM334952 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM566 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM566 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM566 target RNA into GAM566 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM334952 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM334952 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM334952 target RNA into GAM334952 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5217 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5217 gene: GAM566 target protein and GAM334952 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM566 and GAM334952

GR5218 BM743139 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5218(GR5218) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5218 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5218 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5218 gene encodes GR5218 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5218 precursor RNA folds spatially, forming GR5218 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5218 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5218 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5218 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM3542 precursor RNA, GAM92353 precursor RNA, GAM237200 precursor RNA and GAM261647 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3542 RNA, GAM92353 RNA, GAM237200 RNA and GAM261647 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3542 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3542 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3542 target RNA into GAM3542 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM92353 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM92353 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM92353 target RNA into GAM92353 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM237200 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM237200 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM237200 target RNA into GAM237200 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM261647 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM261647 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM261647 target RNA into GAM261647 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5218 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5218 gene: GAM3542 target protein, GAM92353 target protein, GAM237200 target protein and GAM261647 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3542, GAM92353, GAM237200 and GAM261647

GR5219 AA507289 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5219(GR5219) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5219 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5219 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5219 gene encodes GR5219 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5219 precursor RNA folds spatially, forming GR5219 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5219 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5219 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5219 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM79401 precursor RNA and GAM269940 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM79401 RNA and GAM269940 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM79401 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM79401 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM79401 target RNA into GAM79401 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM269940 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM269940 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM269940 target RNA into GAM269940 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5219 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5219 gene: GAM79401 target protein and GAM269940 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM79401 and GAM269940

GR5220 BI084404 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5220(GR5220) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5220 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5220 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5220 gene encodes GR5220 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5220 precursor RNA folds spatially, forming GR5220 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5220 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5220 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5220 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2

separate GAM precursor RNAs, GAM8119 precursor RNA and GAM223840 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8119 RNA and GAM223840 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8119 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8119 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8119 target RNA into GAM8119 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM223840 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM223840 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM223840 target RNA into GAM223840 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5220 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5220 gene: GAM8119 target protein and GAM223840 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8119 and GAM223840

GR5221 AW205795 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5221 (GR5221) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5221 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5221 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5221 gene encodes GR5221 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR5221 precursor RNA folds spatially, forming GR5221 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5221 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5221 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5221 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM7138 precursor RNA, GAM82775 precursor RNA and GAM112643 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7138 RNA, GAM82775 RNA and GAM112643 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7138 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7138 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7138 target RNA into GAM7138 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM82775 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM82775 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM82775 target RNA into GAM82775 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM112643 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM112643 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM112643 target RNA into GAM112643 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5221 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5221 gene: GAM7138 target protein, GAM82775 target protein and GAM112643 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7138, GAM82775 and GAM112643

GR5222 BG505321 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5222(GR5222) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5222 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5222 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5222 gene encodes GR5222 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5222 precursor RNA folds spatially, forming GR5222 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5222 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5222 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5222 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM39834 precursor RNA and GAM161748 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM39834 RNA and GAM161748 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM39834 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM39834 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM39834 target RNA into GAM39834 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM161748 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM161748 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM161748 target RNA into GAM161748 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5222 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5222 gene: GAM39834 target protein and GAM161748 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM39834 and GAM161748

GR5223 BE089486 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5223(GR5223) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5223 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5223 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5223 gene encodes GR5223 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5223 precursor RNA folds spatially, forming GR5223 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5223 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5223 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5223 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM3696 precursor RNA, GAM185897 precursor RNA,

GAM224858 precursor RNA and GAM330666 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3696 RNA, GAM185897 RNA, GAM224858 RNA and GAM330666 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3696 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3696 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3696 target RNA into GAM3696 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM185897 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM185897 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM185897 target RNA into GAM185897 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM224858 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM224858 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM224858 target RNA into GAM224858 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM330666 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM330666 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM330666 target RNA into GAM330666 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5223 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5223 gene: GAM3696 target protein, GAM185897 target protein, GAM224858 target protein and GAM330666 target protein, herein schematically represented by GAM1 TARGET PROTEIN

through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3696, GAM185897, GAM224858 and GAM330666

GR5224 AA100898 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5224(GR5224) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5224 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5224 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5224 gene encodes GR5224 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5224 precursor RNA folds spatially, forming GR5224 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5224 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5224 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5224 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM128241 precursor RNA and GAM307302 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM128241 RNA and GAM307302 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM128241 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM128241 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM128241 target RNA into GAM128241 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM307302 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM307302 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM307302 target RNA into GAM307302 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5224 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5224 gene: GAM128241 target protein and GAM307302 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM128241 and GAM307302

GR5225 BE963225 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5225(GR5225) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5225 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5225 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5225 gene encodes GR5225 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5225 precursor RNA folds spatially, forming GR5225 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5225 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5225 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5225 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 5 separate GAM precursor RNAs, GAM5607 precursor RNA, GAM6930 precursor RNA, GAM69527 precursor RNA, GAM128380 precursor RNA and GAM331849 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5607 RNA, GAM6930 RNA, GAM69527 RNA, GAM128380 RNA and GAM331849 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5607 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5607 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5607 target RNA into GAM5607 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6930 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6930 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6930 target RNA into GAM6930 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM69527 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM69527 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM69527 target RNA into GAM69527 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM128380 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM128380 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM128380 target RNA into GAM128380 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM331849 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM331849 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM331849 target RNA into GAM331849 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5225 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5225 gene: GAM5607 target

protein, GAM6930 target protein, GAM69527 target protein, GAM128380 target protein and GAM331849 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5607, GAM6930, GAM69527, GAM128380 and GAM331849

GR5226 AA836595 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5226(GR5226) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5226 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5226 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5226 gene encodes GR5226 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5226 precursor RNA folds spatially, forming GR5226 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5226 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5226 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5226 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM76601 precursor RNA and GAM331712 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM76601 RNA and GAM331712 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM76601 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM76601 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM76601 target RNA into GAM76601 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM331712 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM331712 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM331712 target RNA into GAM331712 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5226 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5226 gene: GAM76601 target protein and GAM331712 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM76601 and GAM331712

GR5227 BI713735 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5227(GR5227) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5227 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5227 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5227 gene encodes GR5227 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5227 precursor RNA folds spatially, forming GR5227 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5227 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5227 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5227 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM5200 precursor RNA, GAM57379 precursor RNA, GAM158313 precursor RNA and GAM180823 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5200 RNA, GAM57379 RNA, GAM158313 RNA and GAM180823 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5200 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5200 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5200 target RNA into GAM5200 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM57379 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM57379 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM57379 target RNA into GAM57379 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM158313 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM158313 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM158313 target RNA into GAM158313 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM180823 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM180823 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM180823 target RNA into GAM180823 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5227 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5227 gene: GAM5200 target protein, GAM57379 target protein, GAM158313 target protein and GAM180823 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5200, GAM57379, GAM158313 and GAM180823

GR5228 AU146237 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5228(GR5228) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5228 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5228 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5228 gene encodes GR5228 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5228 precursor RNA folds spatially, forming GR5228 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5228 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5228 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5228 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2665 precursor RNA, GAM282296 precursor RNA and GAM306098 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2665 RNA, GAM282296 RNA and GAM306098 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2665 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2665 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2665 target RNA into GAM2665 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM282296 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM282296 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM282296 target RNA into GAM282296 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM306098 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM306098 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM306098 target RNA into GAM306098 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5228 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5228 gene: GAM2665 target protein, GAM282296 target protein and GAM306098 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2665, GAM282296 and GAM306098

GR5229 AW816958 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5229(GR5229) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5229 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5229 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5229 gene encodes GR5229 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5229 precursor RNA folds spatially, forming GR5229 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5229 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5229 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5229 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5779 precursor RNA and GAM195793 precursor

RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5779 RNA and GAM195793 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5779 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5779 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5779 target RNA into GAM5779 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM195793 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM195793 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM195793 target RNA into GAM195793 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5229 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5229 gene: GAM5779 target protein and GAM195793 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5779 and GAM195793

GR5230 AA453686 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5230 (GR5230) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5230 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5230 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5230 gene encodes GR5230 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5230 precursor RNA folds spatially, forming GR5230 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5230 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5230 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5230 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2869 precursor RNA and GAM217652 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2869 RNA and GAM217652 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2869 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2869 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2869 target RNA into GAM2869 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM217652 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM217652 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM217652 target RNA into GAM217652 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5230 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5230 gene: GAM2869 target protein and GAM217652 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2869 and GAM217652

bioinformatically detected regulatory gene, referred to here as Genomic Record 5231 (GR5231) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5231 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5231 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5231 gene encodes GR5231 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5231 precursor RNA folds spatially, forming GR5231 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5231 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5231 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5231 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM1716 precursor RNA, GAM108653 precursor RNA, GAM205995 precursor RNA and GAM312612 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1716 RNA, GAM108653 RNA, GAM205995 RNA and GAM312612 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1716 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1716 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1716 target RNA into GAM1716 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM108653 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM108653 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM108653 target RNA into GAM108653 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM205995 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM205995 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM205995 target RNA into GAM205995 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM312612 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM312612 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM312612 target RNA into GAM312612 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5231 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5231 gene: GAM1716 target protein, GAM108653 target protein, GAM205995 target protein and GAM312612 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1716, GAM108653, GAM205995 and GAM312612

GR5232 AI816253 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5232(GR5232) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5232 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5232 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5232 gene encodes GR5232 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5232 precursor RNA folds spatially, forming GR5232 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5232 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5232 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5232 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM190770 precursor RNA and GAM219969 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM190770 RNA and GAM219969 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM190770 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM190770 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM190770 target RNA into GAM190770 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM219969 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM219969 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM219969 target RNA into GAM219969 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5232 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5232 gene: GAM190770 target protein and GAM219969 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM190770 and GAM219969

GR5233 AW499811 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5233(GR5233) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5233 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5233 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5233 gene encodes GR5233 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5233 precursor RNA folds spatially, forming GR5233 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5233 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5233 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5233 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM93953 precursor RNA, GAM293414 precursor RNA and GAM327190 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM93953 RNA, GAM293414 RNA and GAM327190 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM93953 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM93953 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM93953 target RNA into GAM93953 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM293414 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM293414 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM293414 target RNA into GAM293414 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM327190 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM327190 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM327190 target RNA into GAM327190 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5233 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5233 gene: GAM93953 target protein, GAM293414 target protein and GAM327190 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM93953, GAM293414 and GAM327190

GR5234 BF790693 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5234(GR5234) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5234 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5234 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5234 gene encodes GR5234 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5234 precursor RNA folds spatially, forming GR5234 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5234 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5234 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5234 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM54277 precursor RNA, GAM89506 precursor RNA and GAM116138 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM54277 RNA, GAM89506 RNA and GAM116138 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM54277 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM54277 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM54277 target RNA into GAM54277 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM89506 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM89506 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM89506 target RNA into GAM89506 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM116138 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM116138 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM116138 target RNA into GAM116138 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5234 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5234 gene: GAM54277 target protein, GAM89506 target protein and GAM116138 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM54277, GAM89506 and GAM116138

GR5235 BG924704 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5235(GR5235) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5235 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5235 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5235 gene encodes GR5235 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5235 precursor RNA folds spatially, forming GR5235 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5235 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5235 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5235 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1846 precursor RNA, GAM36129 precursor RNA and GAM136360 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1846 RNA, GAM36129 RNA and GAM136360 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1846 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1846 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1846 target RNA into GAM1846 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM36129 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM36129 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM36129 target RNA into GAM36129 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM136360 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM136360 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM136360 target RNA into GAM136360 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5235 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5235 gene: GAM1846 target protein, GAM36129 target protein and GAM136360 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1846, GAM36129 and GAM136360

GR5236 BF092969 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5236(GR5236) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5236 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5236 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5236 gene encodes GR5236 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5236 precursor RNA folds spatially, forming GR5236 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5236 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5236 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5236 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM97145 precursor RNA, GAM129581 precursor RNA and GAM170306 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM97145 RNA, GAM129581 RNA and GAM170306 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM97145 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM97145 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM97145 target RNA into GAM97145 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM129581 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM129581 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM129581 target RNA into GAM129581 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM170306 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM170306 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM170306 target RNA into GAM170306 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5236 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5236 gene: GAM97145 target protein, GAM129581 target protein and GAM170306 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM97145, GAM129581 and GAM170306

GR5237 BG165197 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5237(GR5237) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5237 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5237 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5237 gene encodes GR5237 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5237 precursor RNA folds spatially, forming GR5237 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5237 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5237 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5237 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6333 precursor RNA and GAM12280 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6333 RNA and GAM12280 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6333 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6333 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6333 target RNA into GAM6333 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM12280 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM12280 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM12280 target RNA into GAM12280 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5237 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5237 gene: GAM6333 target protein and GAM12280 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6333 and GAM12280

5238(GR5238) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5238 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5238 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5238 gene encodes GR5238 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5238 precursor RNA folds spatially, forming GR5238 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5238 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5238 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5238 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM6040 precursor RNA, GAM8614 precursor RNA and GAM177805 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6040 RNA, GAM8614 RNA and GAM177805 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6040 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6040 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6040 target RNA into GAM6040 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8614 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8614 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8614 target RNA into

GAM8614 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM177805 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM177805 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM177805 target RNA into GAM177805 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5238 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5238 gene: GAM6040 target protein, GAM8614 target protein and GAM177805 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6040, GAM8614 and GAM177805

GR5239 BG496092 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5239(GR5239) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5239 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5239 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5239 gene encodes GR5239 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5239 precursor RNA folds spatially, forming GR5239 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5239 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5239 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5239 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM108070 precursor RNA and GAM193374 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin

shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM108070 RNA and GAM193374 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM108070 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM108070 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM108070 target RNA into GAM108070 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM193374 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM193374 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM193374 target RNA into GAM193374 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5239 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5239 gene: GAM108070 target protein and GAM193374 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM108070 and GAM193374

GR5240 F37411 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5240(GR5240) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5240 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5240 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5240 gene encodes GR5240 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5240 precursor RNA folds spatially, forming GR5240 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5240 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5240 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5240 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2800 precursor RNA, GAM178573 precursor RNA and GAM336693 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2800 RNA, GAM178573 RNA and GAM336693 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2800 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2800 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2800 target RNA into GAM2800 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM178573 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM178573 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM178573 target RNA into GAM178573 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336693 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336693 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336693 target RNA into GAM336693 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5240 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR5240 gene: GAM2800 target protein, GAM178573 target protein and GAM336693 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2800, GAM178573 and GAM336693

GR5241 AV692886 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5241 (GR5241) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5241 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5241 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5241 gene encodes GR5241 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5241 precursor RNA folds spatially, forming GR5241 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5241 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5241 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5241 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM194812 precursor RNA and GAM256902 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM194812 RNA and GAM256902 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM194812 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM194812 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM194812

target RNA into GAM194812 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM256902 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM256902 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM256902 target RNA into GAM256902 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5241 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5241 gene: GAM194812 target protein and GAM256902 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM194812 and GAM256902

GR5242 BG701038 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5242(GR5242) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5242 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5242 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5242 gene encodes GR5242 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5242 precursor RNA folds spatially, forming GR5242 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5242 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5242 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5242 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM1055 precursor RNA, GAM5489 precursor RNA, GAM30143 precursor RNA and GAM117278 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment,

corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1055 RNA, GAM5489 RNA, GAM30143 RNA and GAM117278 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1055 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1055 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1055 target RNA into GAM1055 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5489 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5489 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5489 target RNA into GAM5489 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM30143 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM30143 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM30143 target RNA into GAM30143 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM117278 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM117278 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM117278 target RNA into GAM117278 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5242 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5242 gene: GAM1055 target protein, GAM5489 target protein, GAM30143 target protein and GAM117278 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1055, GAM5489, GAM30143 and GAM117278

GR5243 BG504185 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5243(GR5243) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5243 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5243 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5243 gene encodes GR5243 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5243 precursor RNA folds spatially, forming GR5243 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5243 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5243 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5243 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM22111 precursor RNA, GAM182934 precursor RNA and GAM330781 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM22111 RNA, GAM182934 RNA and GAM330781 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM22111 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM22111 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM22111 target RNA into GAM22111 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM182934 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM182934 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM182934 target RNA into GAM182934 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM330781 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM330781 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM330781 target RNA into GAM330781 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5243 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5243 gene: GAM22111 target protein, GAM182934 target protein and GAM330781 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM22111, GAM182934 and GAM330781

GR5244 AA679654 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5244(GR5244) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5244 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5244 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5244 gene encodes GR5244 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5244 precursor RNA folds spatially, forming GR5244 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5244 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5244 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5244 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2

separate GAM precursor RNAs, GAM4551 precursor RNA and GAM43965 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4551 RNA and GAM43965 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4551 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4551 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4551 target RNA into GAM4551 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM43965 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM43965 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM43965 target RNA into GAM43965 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5244 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5244 gene: GAM4551 target protein and GAM43965 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4551 and GAM43965

GR5245 AW135055 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5245(GR5245) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5245 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5245 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5245 gene encodes GR5245 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR5245 precursor RNA folds spatially, forming GR5245 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5245 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5245 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5245 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM4269 precursor RNA, GAM136289 precursor RNA, GAM224445 precursor RNA and GAM315321 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4269 RNA, GAM136289 RNA, GAM224445 RNA and GAM315321 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4269 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4269 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4269 target RNA into GAM4269 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM136289 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM136289 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM136289 target RNA into GAM136289 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM224445 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM224445 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM224445 target RNA into GAM224445 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM315321 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM315321 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM315321 target RNA into GAM315321 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5245 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5245 gene: GAM4269 target protein, GAM136289 target protein, GAM224445 target protein and GAM315321 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4269, GAM136289, GAM224445 and GAM315321

GR5246 BG292030 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5246(GR5246) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5246 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5246 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5246 gene encodes GR5246 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5246 precursor RNA folds spatially, forming GR5246 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5246 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5246 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5246 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM121248 precursor RNA, GAM196164 precursor RNA and GAM229072 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM121248 RNA, GAM196164 RNA and GAM229072 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM121248 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM121248 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM121248 target RNA into GAM121248 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM196164 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM196164 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM196164 target RNA into GAM196164 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM229072 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM229072 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM229072 target RNA into GAM229072 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5246 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5246 gene: GAM121248 target protein, GAM196164 target protein and GAM229072 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM121248, GAM196164 and GAM229072

GR5247 AL110321 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5247(GR5247) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5247 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5247

gene was detected is described hereinabove with reference to Figs. 8-18.

GR5247 gene encodes GR5247 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5247 precursor RNA folds spatially, forming GR5247 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5247 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5247 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5247 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM54496 precursor RNA, GAM73000 precursor RNA and GAM166027 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM54496 RNA, GAM73000 RNA and GAM166027 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM54496 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM54496 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM54496 target RNA into GAM54496 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM73000 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM73000 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM73000 target RNA into GAM73000 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM166027 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM166027 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM166027 target RNA into GAM166027 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5247 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5247 gene: GAM54496 target protein, GAM73000 target protein and GAM166027 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM54496, GAM73000 and GAM166027

GR5248 BE771689 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5248(GR5248) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5248 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5248 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5248 gene encodes GR5248 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5248 precursor RNA folds spatially, forming GR5248 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5248 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5248 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5248 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM4871 precursor RNA, GAM6432 precursor RNA, GAM8695 precursor RNA and GAM11799 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4871 RNA, GAM6432 RNA, GAM8695 RNA and GAM11799 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which

GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4871 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4871 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4871 target RNA into GAM4871 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6432 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6432 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6432 target RNA into GAM6432 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8695 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8695 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8695 target RNA into GAM8695 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM11799 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM11799 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM11799 target RNA into GAM11799 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5248 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5248 gene: GAM4871 target protein, GAM6432 target protein, GAM8695 target protein and GAM11799 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4871, GAM6432, GAM8695 and GAM11799

GR5249 BM783262 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5249(GR5249) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR5249 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5249 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5249 gene encodes GR5249 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5249 precursor RNA folds spatially, forming GR5249 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5249 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5249 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5249 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5356 precursor RNA and GAM219379 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5356 RNA and GAM219379 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5356 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5356 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5356 target RNA into GAM5356 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM219379 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM219379 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM219379 target RNA into GAM219379 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly

utilities, of GR5249 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5249 gene: GAM5356 target protein and GAM219379 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5356 and GAM219379

GR5250 BF971005 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5250(GR5250) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5250 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5250 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5250 gene encodes GR5250 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5250 precursor RNA folds spatially, forming GR5250 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5250 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5250 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5250 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1704 precursor RNA and GAM168262 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1704 RNA and GAM168262 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1704 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1704 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig. 8, thereby inhibiting translation of GAM1704 target RNA into GAM1704 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM168262 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM168262 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM168262 target RNA into GAM168262 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5250 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5250 gene: GAM1704 target protein and GAM168262 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1704 and GAM168262

GR5251 BG705921 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5251(GR5251) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5251 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5251 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5251 gene encodes GR5251 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5251 precursor RNA folds spatially, forming GR5251 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5251 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5251 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5251 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM207874 precursor RNA and GAM218645 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin

shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM207874 RNA and GAM218645 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM207874 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM207874 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM207874 target RNA into GAM207874 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM218645 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM218645 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM218645 target RNA into GAM218645 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5251 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5251 gene: GAM207874 target protein and GAM218645 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM207874 and GAM218645

GR5252 BM996870 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5252(GR5252) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5252 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5252 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5252 gene encodes GR5252 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5252 precursor RNA folds spatially, forming GR5252 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5252 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5252 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5252 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM592 precursor RNA, GAM43687 precursor RNA and GAM104282 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM592 RNA, GAM43687 RNA and GAM104282 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM592 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM592 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM592 target RNA into GAM592 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM43687 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM43687 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM43687 target RNA into GAM43687 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM104282 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM104282 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM104282 target RNA into GAM104282 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5252 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR5252 gene: GAM592 target protein, GAM43687 target protein and GAM104282 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM592, GAM43687 and GAM104282

GR5253 BI677280 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5253(GR5253) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5253 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5253 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5253 gene encodes GR5253 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5253 precursor RNA folds spatially, forming GR5253 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5253 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5253 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5253 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM7586 precursor RNA, GAM167025 precursor RNA and GAM282549 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7586 RNA, GAM167025 RNA and GAM282549 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7586 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7586 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig. 8, thereby inhibiting translation of GAM7586 target RNA into GAM7586 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM167025 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM167025 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM167025 target RNA into GAM167025 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM282549 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM282549 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM282549 target RNA into GAM282549 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5253 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5253 gene: GAM7586 target protein, GAM167025 target protein and GAM282549 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7586, GAM167025 and GAM282549

GR5254 H10866 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5254(GR5254) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5254 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5254 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5254 gene encodes GR5254 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5254 precursor RNA folds spatially, forming GR5254 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5254 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5254 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5254 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM237345 precursor RNA and GAM304173 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM237345 RNA and GAM304173 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM237345 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM237345 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM237345 target RNA into GAM237345 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM304173 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM304173 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM304173 target RNA into GAM304173 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5254 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5254 gene: GAM237345 target protein and GAM304173 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM237345 and GAM304173

GR5255 BE538682 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5255(GR5255) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5255 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5255 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5255 gene encodes GR5255 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5255 precursor RNA folds spatially, forming GR5255 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5255 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5255 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5255 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM671 precursor RNA and GAM135665 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM671 RNA and GAM135665 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM671 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM671 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM671 target RNA into GAM671 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM135665 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM135665 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM135665 target RNA into GAM135665 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5255 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR5255 gene: GAM671 target protein and GAM135665 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM671 and GAM135665

GR5256 W67625 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5256(GR5256) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5256 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5256 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5256 gene encodes GR5256 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5256 precursor RNA folds spatially, forming GR5256 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5256 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5256 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5256 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM254560 precursor RNA and GAM285780 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM254560 RNA and GAM285780 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM254560 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM254560 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM254560 target RNA into GAM254560 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM285780 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM285780 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM285780 target RNA into GAM285780 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5256 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5256 gene: GAM254560 target protein and GAM285780 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM254560 and GAM285780

GR5257 AA721238 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5257(GR5257) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5257 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5257 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5257 gene encodes GR5257 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5257 precursor RNA folds spatially, forming GR5257 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5257 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5257 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5257 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM86821 precursor RNA, GAM122246 precursor RNA, GAM178170 precursor RNA and GAM304510 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM86821 RNA, GAM122246 RNA, GAM178170 RNA and GAM304510 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM86821 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM86821 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM86821 target RNA into GAM86821 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM122246 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM122246 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM122246 target RNA into GAM122246 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM178170 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM178170 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM178170 target RNA into GAM178170 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM304510 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM304510 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM304510 target RNA into GAM304510 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5257 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5257 gene: GAM86821 target protein, GAM122246 target protein, GAM178170 target protein and GAM304510 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM86821, GAM122246, GAM178170 and GAM304510

GR5258 AI192530 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5258(GR5258) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5258 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5258 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5258 gene encodes GR5258 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5258 precursor RNA folds spatially, forming GR5258 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5258 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5258 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5258 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3073 precursor RNA, GAM7853 precursor RNA and GAM264878 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3073 RNA, GAM7853 RNA and GAM264878 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3073 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3073 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3073 target RNA into GAM3073 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7853 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7853 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds

to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7853 target RNA into GAM7853 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM264878 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM264878 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM264878 target RNA into GAM264878 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5258 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5258 gene: GAM3073 target protein, GAM7853 target protein and GAM264878 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3073, GAM7853 and GAM264878

GR5259 AI826853 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5259(GR5259) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5259 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5259 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5259 gene encodes GR5259 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5259 precursor RNA folds spatially, forming GR5259 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5259 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5259 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5259 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM211384 precursor RNA and GAM302000 precursor

RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM211384 RNA and GAM302000 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM211384 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM211384 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM211384 target RNA into GAM211384 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM302000 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM302000 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM302000 target RNA into GAM302000 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5259 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5259 gene: GAM211384 target protein and GAM302000 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM211384 and GAM302000

GR5260 AA442799 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5260 (GR5260) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5260 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5260 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5260 gene encodes GR5260 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5260 precursor RNA folds spatially, forming GR5260 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5260 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5260 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5260 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8336 precursor RNA and GAM136324 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8336 RNA and GAM136324 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8336 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8336 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8336 target RNA into GAM8336 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM136324 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM136324 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM136324 target RNA into GAM136324 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5260 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5260 gene: GAM8336 target protein and GAM136324 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8336 and GAM136324

bioinformatically detected regulatory gene, referred to here as Genomic Record 5261 (GR5261) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5261 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5261 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5261 gene encodes GR5261 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5261 precursor RNA folds spatially, forming GR5261 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5261 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5261 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5261 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM75033 precursor RNA and GAM279297 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM75033 RNA and GAM279297 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM75033 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM75033 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM75033 target RNA into GAM75033 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM279297 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM279297 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM279297

target RNA into GAM279297 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5261 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5261 gene: GAM75033 target protein and GAM279297 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM75033 and GAM279297

GR5262 BM990090 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5262(GR5262) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5262 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5262 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5262 gene encodes GR5262 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5262 precursor RNA folds spatially, forming GR5262 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5262 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5262 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5262 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM444 precursor RNA and GAM5768 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM444 RNA and GAM5768 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM444 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM444 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM444 target RNA into GAM444 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5768 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5768 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5768 target RNA into GAM5768 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5262 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5262 gene: GAM444 target protein and GAM5768 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM444 and GAM5768

GR5263 BE783285 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5263(GR5263) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5263 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5263 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5263 gene encodes GR5263 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5263 precursor RNA folds spatially, forming GR5263 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5263 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5263 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5263 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM132897 precursor RNA and GAM147770 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM132897 RNA and GAM147770 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM132897 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM132897 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM132897 target RNA into GAM132897 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM147770 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM147770 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM147770 target RNA into GAM147770 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5263 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5263 gene: GAM132897 target protein and GAM147770 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM132897 and GAM147770

GR5264 AW409623 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5264(GR5264) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5264 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5264 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5264 gene encodes GR5264 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5264 precursor RNA folds spatially, forming GR5264 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5264 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5264 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5264 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM57072 precursor RNA and GAM299488 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM57072 RNA and GAM299488 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM57072 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM57072 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM57072 target RNA into GAM57072 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM299488 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM299488 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM299488 target RNA into GAM299488 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5264 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5264 gene: GAM57072 target protein and GAM299488 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM57072 and GAM299488

GR5265 BF108189 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5265(GR5265) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5265 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5265 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5265 gene encodes GR5265 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5265 precursor RNA folds spatially, forming GR5265 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5265 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5265 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5265 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM148357 precursor RNA and GAM213994 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM148357 RNA and GAM213994 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM148357 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM148357 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM148357 target RNA into GAM148357 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM213994 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM213994 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM213994 target RNA into GAM213994 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5265 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5265 gene: GAM148357 target protein and GAM213994 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM148357 and GAM213994

GR5266 AW511872 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5266(GR5266) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5266 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5266 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5266 gene encodes GR5266 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5266 precursor RNA folds spatially, forming GR5266 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5266 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5266 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5266 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4140 precursor RNA and GAM294212 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4140 RNA and GAM294212 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4140 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4140 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4140 target RNA into GAM4140 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM294212 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM294212 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM294212 target RNA into GAM294212 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5266 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5266 gene: GAM4140 target protein and GAM294212 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4140 and GAM294212

GR5267 BF332528 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5267(GR5267) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5267 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5267 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5267 gene encodes GR5267 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5267 precursor RNA folds spatially, forming GR5267 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5267 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5267 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5267 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5452 precursor RNA and GAM75573 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5452 RNA and GAM75573 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5452 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5452 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5452 target RNA into GAM5452 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM75573 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM75573 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM75573 target RNA into GAM75573 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5267 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5267 gene: GAM5452 target protein and GAM75573 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5452 and GAM75573

GR5268 BI602512 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5268(GR5268) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5268 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5268 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5268 gene encodes GR5268 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5268 precursor RNA folds spatially, forming GR5268 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5268 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5268 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5268 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2228 precursor RNA and GAM72034 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2228 RNA and GAM72034 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2228 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2228 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2228 target RNA into GAM2228 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM72034 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM72034 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM72034 target RNA into GAM72034 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5268 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5268 gene: GAM2228 target protein and GAM72034 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes

is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2228 and GAM72034

GR5269 AW947642 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5269(GR5269) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5269 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5269 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5269 gene encodes GR5269 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5269 precursor RNA folds spatially, forming GR5269 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5269 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5269 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5269 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7924 precursor RNA and GAM148584 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7924 RNA and GAM148584 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7924 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7924 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7924 target RNA into GAM7924 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM148584 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM148584 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM148584 target RNA into GAM148584 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5269 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5269 gene: GAM7924 target protein and GAM148584 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7924 and GAM148584

GR5270 BI459454 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5270(GR5270) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5270 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5270 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5270 gene encodes GR5270 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5270 precursor RNA folds spatially, forming GR5270 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5270 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5270 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5270 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7234 precursor RNA and GAM315781 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7234 RNA and GAM315781 RNA, herein schematically

represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7234 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7234 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7234 target RNA into GAM7234 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM315781 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM315781 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM315781 target RNA into GAM315781 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5270 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5270 gene: GAM7234 target protein and GAM315781 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7234 and GAM315781

GR5271 BF305520 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5271(GR5271) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5271 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5271 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5271 gene encodes GR5271 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5271 precursor RNA folds spatially, forming GR5271 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5271 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5271 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5271 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM59861 precursor RNA and GAM123022 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM59861 RNA and GAM123022 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM59861 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM59861 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM59861 target RNA into GAM59861 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM123022 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM123022 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM123022 target RNA into GAM123022 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5271 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5271 gene: GAM59861 target protein and GAM123022 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM59861 and GAM123022

GR5272 BQ009172 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5272(GR5272) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5272 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR5272 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5272 gene encodes GR5272 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5272 precursor RNA folds spatially, forming GR5272 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5272 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5272 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5272 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM6520 precursor RNA, GAM54143 precursor RNA and GAM204763 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6520 RNA, GAM54143 RNA and GAM204763 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6520 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6520 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6520 target RNA into GAM6520 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM54143 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM54143 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM54143 target RNA into GAM54143 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM204763 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM204763 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM204763 target RNA into GAM204763 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5272 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5272 gene: GAM6520 target protein, GAM54143 target protein and GAM204763 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6520, GAM54143 and GAM204763

GR5273 AA890201 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5273(GR5273) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5273 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5273 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5273 gene encodes GR5273 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5273 precursor RNA folds spatially, forming GR5273 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5273 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5273 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5273 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7273 precursor RNA and GAM97399 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7273 RNA and GAM97399 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding

to GAM RNA of Fig. 8.

GAM7273 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7273 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7273 target RNA into GAM7273 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM97399 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM97399 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM97399 target RNA into GAM97399 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5273 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5273 gene: GAM7273 target protein and GAM97399 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7273 and GAM97399

GR5274 BE732260 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5274(GR5274) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5274 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5274 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5274 gene encodes GR5274 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5274 precursor RNA folds spatially, forming GR5274 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5274 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5274 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR5274 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM5983 precursor RNA, GAM7104 precursor RNA and GAM110640 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5983 RNA, GAM7104 RNA and GAM110640 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5983 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5983 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5983 target RNA into GAM5983 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7104 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7104 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7104 target RNA into GAM7104 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM110640 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM110640 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM110640 target RNA into GAM110640 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5274 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5274 gene: GAM5983 target protein, GAM7104 target protein and GAM110640 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5983, GAM7104 and GAM110640

GR5275 R51293 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5275(GR5275) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5275 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5275 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5275 gene encodes GR5275 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5275 precursor RNA folds spatially, forming GR5275 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5275 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5275 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5275 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3775 precursor RNA and GAM79511 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3775 RNA and GAM79511 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3775 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3775 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3775 target RNA into GAM3775 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM79511 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM79511 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM79511 target RNA into GAM79511 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5275 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5275 gene: GAM3775 target protein and GAM79511 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3775 and GAM79511

GR5276 AI768802 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5276(GR5276) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5276 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5276 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5276 gene encodes GR5276 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5276 precursor RNA folds spatially, forming GR5276 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5276 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5276 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5276 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM50641 precursor RNA, GAM187052 precursor RNA and GAM279866 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM50641 RNA, GAM187052 RNA and GAM279866 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs

corresponding to GAM RNA of Fig. 8.

GAM50641 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM50641 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM50641 target RNA into GAM50641 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM187052 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM187052 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM187052 target RNA into GAM187052 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM279866 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM279866 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM279866 target RNA into GAM279866 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5276 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5276 gene: GAM50641 target protein, GAM187052 target protein and GAM279866 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM50641, GAM187052 and GAM279866

GR5277 BM824873 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5277(GR5277) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5277 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5277 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5277 gene encodes GR5277 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR5277 precursor RNA folds spatially, forming GR5277 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5277 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5277 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5277 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM154697 precursor RNA and GAM197177 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM154697 RNA and GAM197177 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM154697 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM154697 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM154697 target RNA into GAM154697 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM197177 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM197177 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM197177 target RNA into GAM197177 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5277 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5277 gene: GAM154697 target protein and GAM197177 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM154697 and GAM197177

GR5278 AA974540 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5278(GR5278) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5278 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5278 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5278 gene encodes GR5278 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5278 precursor RNA folds spatially, forming GR5278 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5278 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5278 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5278 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1633 precursor RNA, GAM251239 precursor RNA and GAM267066 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1633 RNA, GAM251239 RNA and GAM267066 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1633 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1633 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1633 target RNA into GAM1633 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM251239 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM251239 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM251239 target RNA into GAM251239 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM267066 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM267066 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM267066 target RNA into GAM267066 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5278 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5278 gene: GAM1633 target protein, GAM251239 target protein and GAM267066 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1633, GAM251239 and GAM267066

GR5279 BF528428 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5279(GR5279) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5279 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5279 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5279 gene encodes GR5279 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5279 precursor RNA folds spatially, forming GR5279 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5279 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5279 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5279 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM813 precursor RNA, GAM4418 precursor RNA and

GAM99556 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM813 RNA, GAM4418 RNA and GAM99556 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM813 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM813 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM813 target RNA into GAM813 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM4418 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4418 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4418 target RNA into GAM4418 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM99556 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM99556 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM99556 target RNA into GAM99556 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5279 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5279 gene: GAM813 target protein, GAM4418 target protein and GAM99556 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM813, GAM4418 and GAM99556

GR5280 BG400640 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5280(GR5280) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR5280 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5280 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5280 gene encodes GR5280 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5280 precursor RNA folds spatially, forming GR5280 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5280 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5280 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5280 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1657 precursor RNA, GAM6789 precursor RNA and GAM57070 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1657 RNA, GAM6789 RNA and GAM57070 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1657 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1657 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1657 target RNA into GAM1657 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6789 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6789 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6789 target RNA into GAM6789 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM57070 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM57070 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM57070 target RNA into GAM57070 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5280 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5280 gene: GAM1657 target protein, GAM6789 target protein and GAM57070 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1657, GAM6789 and GAM57070

GR5281 BG255611 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5281 (GR5281) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5281 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5281 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5281 gene encodes GR5281 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5281 precursor RNA folds spatially, forming GR5281 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5281 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5281 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5281 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8183 precursor RNA and GAM209541 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8183 RNA and GAM209541 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8183 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8183 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8183 target RNA into GAM8183 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM209541 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM209541 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM209541 target RNA into GAM209541 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5281 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5281 gene: GAM8183 target protein and GAM209541 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8183 and GAM209541

GR5282 BI093272 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5282(GR5282) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5282 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5282 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5282 gene encodes GR5282 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5282 precursor RNA folds spatially, forming GR5282 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5282 folded precursor RNA comprises a plurality of what is known in the

art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5282 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5282 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3060 precursor RNA, GAM4695 precursor RNA and GAM5108 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3060 RNA, GAM4695 RNA and GAM5108 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3060 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3060 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3060 target RNA into GAM3060 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM4695 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4695 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4695 target RNA into GAM4695 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5108 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5108 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5108 target RNA into GAM5108 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5282 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5282 gene: GAM3060 target protein, GAM4695 target protein and GAM5108 target protein, herein

schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3060, GAM4695 and GAM5108

GR5283 BG826942 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5283(GR5283) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5283 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5283 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5283 gene encodes GR5283 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5283 precursor RNA folds spatially, forming GR5283 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5283 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5283 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5283 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM158934 precursor RNA, GAM197866 precursor RNA and GAM223012 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM158934 RNA, GAM197866 RNA and GAM223012 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM158934 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM158934 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM158934 target RNA into GAM158934 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM197866 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM197866 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM197866 target RNA into GAM197866 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM223012 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM223012 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM223012 target RNA into GAM223012 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5283 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5283 gene: GAM158934 target protein, GAM197866 target protein and GAM223012 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM158934, GAM197866 and GAM223012

GR5284 BG744040 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5284(GR5284) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5284 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5284 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5284 gene encodes GR5284 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5284 precursor RNA folds spatially, forming GR5284 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5284 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5284 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR5284 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM395 precursor RNA and GAM262630 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM395 RNA and GAM262630 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM395 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM395 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM395 target RNA into GAM395 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM262630 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM262630 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM262630 target RNA into GAM262630 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5284 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5284 gene: GAM395 target protein and GAM262630 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM395 and GAM262630

GR5285 T54611 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5285(GR5285) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5285 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5285

gene was detected is described hereinabove with reference to Figs. 8-18.

GR5285 gene encodes GR5285 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5285 precursor RNA folds spatially, forming GR5285 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5285 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5285 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5285 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM880 precursor RNA and GAM57945 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM880 RNA and GAM57945 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM880 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM880 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM880 target RNA into GAM880 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM57945 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM57945 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM57945 target RNA into GAM57945 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5285 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5285 gene: GAM880 target protein and GAM57945 target protein, herein schematically represented by GAM1

TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM880 and GAM57945

GR5286 C05763 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5286(GR5286) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5286 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5286 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5286 gene encodes GR5286 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5286 precursor RNA folds spatially, forming GR5286 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5286 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5286 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5286 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM172145 precursor RNA, GAM178072 precursor RNA and GAM204670 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM172145 RNA, GAM178072 RNA and GAM204670 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM172145 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM172145 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM172145 target RNA into GAM172145 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM178072 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM178072 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM178072 target RNA into GAM178072 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM204670 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM204670 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM204670 target RNA into GAM204670 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5286 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5286 gene: GAM172145 target protein, GAM178072 target protein and GAM204670 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM172145, GAM178072 and GAM204670

GR5287 H60802 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5287(GR5287) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5287 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5287 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5287 gene encodes GR5287 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5287 precursor RNA folds spatially, forming GR5287 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5287 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5287 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5287 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM120234 precursor RNA and GAM149328 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM120234 RNA and GAM149328 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM120234 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM120234 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM120234 target RNA into GAM120234 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM149328 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM149328 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM149328 target RNA into GAM149328 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5287 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5287 gene: GAM120234 target protein and GAM149328 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM120234 and GAM149328

GR5288 BM693645 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5288(GR5288) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5288 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5288 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5288 gene encodes GR5288 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5288 precursor RNA folds spatially, forming GR5288 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5288 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5288 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5288 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM107209 precursor RNA and GAM269318 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM107209 RNA and GAM269318 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM107209 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM107209 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM107209 target RNA into GAM107209 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM269318 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM269318 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM269318 target RNA into GAM269318 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5288 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5288 gene: GAM107209 target protein and GAM269318 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes

is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM107209 and GAM269318

GR5289 BG189871 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5289(GR5289) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5289 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5289 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5289 gene encodes GR5289 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5289 precursor RNA folds spatially, forming GR5289 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5289 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5289 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5289 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM8325 precursor RNA, GAM261787 precursor RNA and GAM276820 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8325 RNA, GAM261787 RNA and GAM276820 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8325 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8325 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8325 target RNA into GAM8325 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM261787 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM261787 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM261787 target RNA into GAM261787 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM276820 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM276820 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM276820 target RNA into GAM276820 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5289 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5289 gene: GAM8325 target protein, GAM261787 target protein and GAM276820 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8325, GAM261787 and GAM276820

GR5290 BF197066 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5290 (GR5290) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5290 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5290 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5290 gene encodes GR5290 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5290 precursor RNA folds spatially, forming GR5290 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5290 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5290 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5290 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1702 precursor RNA, GAM5224 precursor RNA and GAM281770 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1702 RNA, GAM5224 RNA and GAM281770 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1702 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1702 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1702 target RNA into GAM1702 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5224 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5224 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5224 target RNA into GAM5224 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM281770 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM281770 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM281770 target RNA into GAM281770 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5290 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5290 gene: GAM1702 target protein, GAM5224 target protein and GAM281770 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1702, GAM5224 and GAM281770

bioinformatically detected regulatory gene, referred to here as Genomic Record 5291 (GR5291) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5291 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5291 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5291 gene encodes GR5291 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5291 precursor RNA folds spatially, forming GR5291 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5291 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5291 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5291 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM85964 precursor RNA and GAM317988 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM85964 RNA and GAM317988 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM85964 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM85964 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM85964 target RNA into GAM85964 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM317988 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM317988 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM317988

target RNA into GAM317988 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5291 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5291 gene: GAM85964 target protein and GAM317988 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM85964 and GAM317988

GR5292 BI463499 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5292(GR5292) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5292 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5292 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5292 gene encodes GR5292 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5292 precursor RNA folds spatially, forming GR5292 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5292 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5292 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5292 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM17636 precursor RNA, GAM78390 precursor RNA and GAM263399 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM17636 RNA, GAM78390 RNA and GAM263399 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM17636 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM17636 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM17636 target RNA into GAM17636 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM78390 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM78390 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM78390 target RNA into GAM78390 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM263399 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM263399 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM263399 target RNA into GAM263399 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5292 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5292 gene: GAM17636 target protein, GAM78390 target protein and GAM263399 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM17636, GAM78390 and GAM263399

GR5293 BE563937 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5293(GR5293) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5293 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5293 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5293 gene encodes GR5293 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5293 precursor RNA folds spatially, forming GR5293 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5293 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5293 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5293 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM1537 precursor RNA, GAM2783 precursor RNA, GAM121860 precursor RNA and GAM283284 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1537 RNA, GAM2783 RNA, GAM121860 RNA and GAM283284 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1537 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1537 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1537 target RNA into GAM1537 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM2783 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2783 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2783 target RNA into GAM2783 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM121860 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM121860 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM121860 target RNA into GAM121860 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM283284 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM283284 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM283284 target RNA into GAM283284 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5293 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5293 gene: GAM1537 target protein, GAM2783 target protein, GAM121860 target protein and GAM283284 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1537, GAM2783, GAM121860 and GAM283284

GR5294 BF923147 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5294(GR5294) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5294 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5294 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5294 gene encodes GR5294 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5294 precursor RNA folds spatially, forming GR5294 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5294 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5294 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5294 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4153 precursor RNA and GAM7108 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4153 RNA and GAM7108 RNA, herein schematically

represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4153 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4153 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4153 target RNA into GAM4153 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7108 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7108 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7108 target RNA into GAM7108 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5294 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5294 gene: GAM4153 target protein and GAM7108 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4153 and GAM7108

GR5295 BF997324 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5295(GR5295) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5295 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5295 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5295 gene encodes GR5295 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5295 precursor RNA folds spatially, forming GR5295 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5295 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5295 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5295 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM79727 precursor RNA and GAM163417 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM79727 RNA and GAM163417 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM79727 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM79727 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM79727 target RNA into GAM79727 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM163417 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM163417 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM163417 target RNA into GAM163417 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5295 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5295 gene: GAM79727 target protein and GAM163417 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM79727 and GAM163417

GR5296 BI910381 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5296(GR5296) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5296 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR5296 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5296 gene encodes GR5296 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5296 precursor RNA folds spatially, forming GR5296 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5296 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5296 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5296 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM8308 precursor RNA, GAM128856 precursor RNA and GAM205314 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8308 RNA, GAM128856 RNA and GAM205314 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8308 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8308 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8308 target RNA into GAM8308 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM128856 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM128856 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM128856 target RNA into GAM128856 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM205314 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM205314 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM205314 target RNA into GAM205314 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5296 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5296 gene: GAM8308 target protein, GAM128856 target protein and GAM205314 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8308, GAM128856 and GAM205314

GR5297 BG539527 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5297(GR5297) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5297 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5297 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5297 gene encodes GR5297 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5297 precursor RNA folds spatially, forming GR5297 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5297 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5297 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5297 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM118555 precursor RNA and GAM139754 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM118555 RNA and GAM139754 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding

to GAM RNA of Fig. 8.

GAM118555 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM118555 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM118555 target RNA into GAM118555 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM139754 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM139754 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM139754 target RNA into GAM139754 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5297 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5297 gene: GAM118555 target protein and GAM139754 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM118555 and GAM139754

GR5298 BE183938 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5298(GR5298) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5298 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5298 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5298 gene encodes GR5298 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5298 precursor RNA folds spatially, forming GR5298 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5298 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5298 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR5298 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4287 precursor RNA and GAM278846 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4287 RNA and GAM278846 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4287 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4287 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4287 target RNA into GAM4287 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM278846 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM278846 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM278846 target RNA into GAM278846 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5298 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5298 gene: GAM4287 target protein and GAM278846 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4287 and GAM278846

GR5299 BI560207 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5299(GR5299) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5299 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5299

gene was detected is described hereinabove with reference to Figs. 8-18.

GR5299 gene encodes GR5299 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5299 precursor RNA folds spatially, forming GR5299 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5299 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5299 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5299 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM122616 precursor RNA and GAM273202 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM122616 RNA and GAM273202 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM122616 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM122616 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM122616 target RNA into GAM122616 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM273202 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM273202 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM273202 target RNA into GAM273202 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5299 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5299 gene: GAM122616 target protein and GAM273202 target protein, herein schematically represented by GAM1

TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM122616 and GAM273202

GR5300 BG482928 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5300(GR5300) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5300 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5300 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5300 gene encodes GR5300 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5300 precursor RNA folds spatially, forming GR5300 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5300 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5300 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5300 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM54850 precursor RNA and GAM241635 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM54850 RNA and GAM241635 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM54850 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM54850 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM54850 target RNA into GAM54850 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM241635 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM241635 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM241635 target RNA into GAM241635 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5300 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5300 gene: GAM54850 target protein and GAM241635 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM54850 and GAM241635

GR5301 BE741575 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5301(GR5301) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5301 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5301 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5301 gene encodes GR5301 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5301 precursor RNA folds spatially, forming GR5301 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5301 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5301 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5301 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM115804 precursor RNA and GAM276466 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM115804 RNA and GAM276466 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM115804 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM115804 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM115804 target RNA into GAM115804 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM276466 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM276466 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM276466 target RNA into GAM276466 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5301 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5301 gene: GAM115804 target protein and GAM276466 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM115804 and GAM276466

GR5302 BI008000 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5302(GR5302) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5302 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5302 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5302 gene encodes GR5302 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5302 precursor RNA folds spatially, forming GR5302 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5302 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5302 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5302 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2065 precursor RNA, GAM175152 precursor RNA and GAM256419 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2065 RNA, GAM175152 RNA and GAM256419 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2065 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2065 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2065 target RNA into GAM2065 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM175152 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM175152 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM175152 target RNA into GAM175152 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM256419 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM256419 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM256419 target RNA into GAM256419 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5302 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5302 gene: GAM2065 target protein, GAM175152 target protein and GAM256419 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6,

hereby incorporated by reference, with references to GAM2065, GAM175152 and GAM256419

GR5303 BF569704 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5303(GR5303) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5303 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5303 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5303 gene encodes GR5303 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5303 precursor RNA folds spatially, forming GR5303 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5303 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5303 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5303 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3717 precursor RNA, GAM6477 precursor RNA and GAM251839 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3717 RNA, GAM6477 RNA and GAM251839 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3717 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3717 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3717 target RNA into GAM3717 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6477 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6477 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6477 target RNA into GAM6477 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM251839 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM251839 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM251839 target RNA into GAM251839 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5303 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5303 gene: GAM3717 target protein, GAM6477 target protein and GAM251839 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3717, GAM6477 and GAM251839

GR5304 BG014030 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5304(GR5304) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5304 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5304 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5304 gene encodes GR5304 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5304 precursor RNA folds spatially, forming GR5304 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5304 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5304 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5304 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3314 precursor RNA and GAM68763 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3314 RNA and GAM68763 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3314 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3314 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3314 target RNA into GAM3314 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM68763 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM68763 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM68763 target RNA into GAM68763 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5304 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5304 gene: GAM3314 target protein and GAM68763 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3314 and GAM68763

GR5305 BM847445 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5305(GR5305) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5305 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5305 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5305 gene encodes GR5305 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5305 precursor RNA folds spatially, forming GR5305 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5305 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5305 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5305 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM6030 precursor RNA, GAM8504 precursor RNA, GAM115064 precursor RNA and GAM246060 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6030 RNA, GAM8504 RNA, GAM115064 RNA and GAM246060 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6030 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6030 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6030 target RNA into GAM6030 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8504 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8504 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8504 target RNA into GAM8504 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM115064 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM115064 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM115064 target RNA into GAM115064 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM246060 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM246060 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM246060 target RNA into GAM246060 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5305 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5305 gene: GAM6030 target protein, GAM8504 target protein, GAM115064 target protein and GAM246060 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6030, GAM8504, GAM115064 and GAM246060

GR5306 H84149 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5306(GR5306) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5306 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5306 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5306 gene encodes GR5306 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5306 precursor RNA folds spatially, forming GR5306 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5306 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5306 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5306 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM266383 precursor RNA and GAM276918 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM266383 RNA and GAM276918 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM266383 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM266383 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM266383 target RNA into GAM266383 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM276918 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM276918 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM276918 target RNA into GAM276918 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5306 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5306 gene: GAM266383 target protein and GAM276918 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM266383 and GAM276918

GR5307 BG283773 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5307(GR5307) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5307 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5307 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5307 gene encodes GR5307 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5307 precursor RNA folds spatially, forming GR5307 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated

that GR5307 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5307 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5307 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM38061 precursor RNA, GAM142151 precursor RNA and GAM185311 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM38061 RNA, GAM142151 RNA and GAM185311 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM38061 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM38061 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM38061 target RNA into GAM38061 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM142151 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM142151 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM142151 target RNA into GAM142151 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM185311 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM185311 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM185311 target RNA into GAM185311 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5307 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5307 gene: GAM38061 target

protein, GAM142151 target protein and GAM185311 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM38061, GAM142151 and GAM185311

GR5308 BG750383 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5308(GR5308) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5308 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5308 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5308 gene encodes GR5308 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5308 precursor RNA folds spatially, forming GR5308 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5308 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5308 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5308 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM7258 precursor RNA, GAM53921 precursor RNA, GAM117358 precursor RNA and GAM237530 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7258 RNA, GAM53921 RNA, GAM117358 RNA and GAM237530 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7258 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7258 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7258 target RNA into

GAM7258 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM53921 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM53921 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM53921 target RNA into GAM53921 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM117358 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM117358 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM117358 target RNA into GAM117358 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM237530 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM237530 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM237530 target RNA into GAM237530 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5308 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5308 gene: GAM7258 target protein, GAM53921 target protein, GAM117358 target protein and GAM237530 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7258, GAM53921, GAM117358 and GAM237530

GR5309 BI914936 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5309(GR5309) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5309 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5309 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5309 gene encodes GR5309 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR5309 precursor RNA folds spatially, forming GR5309 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5309 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5309 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5309 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM121386 precursor RNA and GAM215676 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM121386 RNA and GAM215676 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM121386 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM121386 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM121386 target RNA into GAM121386 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM215676 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM215676 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM215676 target RNA into GAM215676 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5309 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5309 gene: GAM121386 target protein and GAM215676 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM121386 and GAM215676

GR5310 BF082134 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5310 (GR5310) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5310 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5310 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5310 gene encodes GR5310 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5310 precursor RNA folds spatially, forming GR5310 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5310 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5310 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5310 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM275433 precursor RNA and GAM293878 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM275433 RNA and GAM293878 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM275433 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM275433 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM275433 target RNA into GAM275433 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM293878 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM293878 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM293878 target RNA into GAM293878 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5310 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5310 gene: GAM275433 target protein and GAM293878 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM275433 and GAM293878

GR5311 BE275424 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5311 (GR5311) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5311 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5311 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5311 gene encodes GR5311 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5311 precursor RNA folds spatially, forming GR5311 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5311 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5311 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5311 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5192 precursor RNA and GAM253043 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5192 RNA and GAM253043 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5192 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5192 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5192 target RNA into GAM5192 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM253043 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM253043 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM253043 target RNA into GAM253043 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5311 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5311 gene: GAM5192 target protein and GAM253043 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5192 and GAM253043

GR5312 BF839952 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5312(GR5312) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5312 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5312 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5312 gene encodes GR5312 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5312 precursor RNA folds spatially, forming GR5312 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5312 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5312 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5312 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM207935 precursor RNA and GAM308190 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM207935 RNA and GAM308190 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM207935 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM207935 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM207935 target RNA into GAM207935 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM308190 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM308190 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM308190 target RNA into GAM308190 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5312 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5312 gene: GAM207935 target protein and GAM308190 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM207935 and GAM308190

GR5313 BQ020871 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5313(GR5313) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5313 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5313 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5313 gene encodes GR5313 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5313 precursor RNA folds spatially, forming GR5313 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5313 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5313 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5313 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM42550 precursor RNA, GAM112507 precursor RNA and GAM241462 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM42550 RNA, GAM112507 RNA and GAM241462 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM42550 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM42550 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM42550 target RNA into GAM42550 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM112507 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM112507 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM112507 target RNA into GAM112507 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM241462 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM241462 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM241462 target RNA into GAM241462 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5313 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5313 gene: GAM42550 target protein, GAM112507 target protein and GAM241462 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM42550, GAM112507 and GAM241462

GR5314 BG491682 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5314(GR5314) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5314 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5314 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5314 gene encodes GR5314 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5314 precursor RNA folds spatially, forming GR5314 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5314 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5314 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5314 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM193143 precursor RNA and GAM279635 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM193143 RNA and GAM279635 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM193143 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM193143 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM193143 target RNA into GAM193143 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM279635 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM279635 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM279635 target RNA into GAM279635 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5314 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5314 gene: GAM193143 target protein and GAM279635 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM193143 and GAM279635

GR5315 BI160981 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5315(GR5315) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5315 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5315 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5315 gene encodes GR5315 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5315 precursor RNA folds spatially, forming GR5315 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5315 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5315 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5315 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3862 precursor RNA, GAM70314 precursor RNA and GAM88727 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3862 RNA, GAM70314 RNA and GAM88727 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3862 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3862 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3862 target RNA into GAM3862 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM70314 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM70314 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM70314 target RNA into GAM70314 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM88727 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM88727 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM88727 target RNA into GAM88727 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5315 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5315 gene: GAM3862 target protein, GAM70314 target protein and GAM88727 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3862, GAM70314 and GAM88727

5316(GR5316) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5316 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5316 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5316 gene encodes GR5316 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5316 precursor RNA folds spatially, forming GR5316 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5316 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5316 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5316 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM65667 precursor RNA, GAM141398 precursor RNA and GAM178148 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM65667 RNA, GAM141398 RNA and GAM178148 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM65667 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM65667 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM65667 target RNA into GAM65667 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM141398 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM141398 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM141398

target RNA into GAM141398 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM178148 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM178148 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM178148 target RNA into GAM178148 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5316 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5316 gene: GAM65667 target protein, GAM141398 target protein and GAM178148 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM65667, GAM141398 and GAM178148

GR5317 AW883923 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5317(GR5317) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5317 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5317 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5317 gene encodes GR5317 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5317 precursor RNA folds spatially, forming GR5317 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5317 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5317 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5317 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM289047 precursor RNA and GAM304866 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin

shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM289047 RNA and GAM304866 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM289047 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM289047 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM289047 target RNA into GAM289047 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM304866 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM304866 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM304866 target RNA into GAM304866 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5317 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5317 gene: GAM289047 target protein and GAM304866 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM289047 and GAM304866

GR5318 R16273 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5318(GR5318) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5318 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5318 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5318 gene encodes GR5318 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5318 precursor RNA folds spatially, forming GR5318 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5318 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5318 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5318 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM109434 precursor RNA and GAM256829 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM109434 RNA and GAM256829 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM109434 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM109434 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM109434 target RNA into GAM109434 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM256829 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM256829 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM256829 target RNA into GAM256829 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5318 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5318 gene: GAM109434 target protein and GAM256829 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM109434 and GAM256829

GR5319 BG421540 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5319(GR5319) gene, which encodes an `operon-like` cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5319 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5319 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5319 gene encodes GR5319 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5319 precursor RNA folds spatially, forming GR5319 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5319 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5319 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5319 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM98286 precursor RNA, GAM101221 precursor RNA and GAM252357 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM98286 RNA, GAM101221 RNA and GAM252357 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM98286 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM98286 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM98286 target RNA into GAM98286 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM101221 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM101221 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM101221 target RNA into GAM101221 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM252357 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM252357 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM252357 target RNA into GAM252357 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5319 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5319 gene: GAM98286 target protein, GAM101221 target protein and GAM252357 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM98286, GAM101221 and GAM252357

GR5320 BG831985 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5320(GR5320) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5320 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5320 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5320 gene encodes GR5320 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5320 precursor RNA folds spatially, forming GR5320 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5320 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5320 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5320 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2999 precursor RNA, GAM126830 precursor RNA and GAM246161 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED

PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2999 RNA, GAM126830 RNA and GAM246161 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2999 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2999 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2999 target RNA into GAM2999 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM126830 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM126830 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM126830 target RNA into GAM126830 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM246161 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM246161 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM246161 target RNA into GAM246161 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5320 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5320 gene: GAM2999 target protein, GAM126830 target protein and GAM246161 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2999, GAM126830 and GAM246161

GR5321 BM764003 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5321(GR5321) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5321 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5321 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5321 gene encodes GR5321 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5321 precursor RNA folds spatially, forming GR5321 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5321 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5321 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5321 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM217608 precursor RNA and GAM283673 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM217608 RNA and GAM283673 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM217608 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM217608 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM217608 target RNA into GAM217608 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM283673 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM283673 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM283673 target RNA into GAM283673 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5321 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR5321 gene: GAM217608 target protein and GAM283673 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM217608 and GAM283673

GR5322 BF308922 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5322(GR5322) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5322 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5322 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5322 gene encodes GR5322 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5322 precursor RNA folds spatially, forming GR5322 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5322 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5322 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5322 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5245 precursor RNA and GAM314335 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5245 RNA and GAM314335 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5245 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5245 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5245 target RNA into GAM5245 target protein, herein schematically represented by GAM1 TARGET

PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM314335 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM314335 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM314335 target RNA into GAM314335 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5322 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5322 gene: GAM5245 target protein and GAM314335 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5245 and GAM314335

GR5323 AW451425 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5323(GR5323) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5323 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5323 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5323 gene encodes GR5323 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5323 precursor RNA folds spatially, forming GR5323 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5323 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5323 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5323 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8132 precursor RNA and GAM320542 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8132 RNA and GAM320542 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8132 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8132 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8132 target RNA into GAM8132 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM320542 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM320542 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM320542 target RNA into GAM320542 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5323 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5323 gene: GAM8132 target protein and GAM320542 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8132 and GAM320542

GR5324 BE246058 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5324(GR5324) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5324 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5324 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5324 gene encodes GR5324 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5324 precursor RNA folds spatially, forming GR5324 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5324 folded precursor RNA comprises a plurality of what is known in the

art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5324 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5324 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM152237 precursor RNA and GAM240163 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM152237 RNA and GAM240163 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM152237 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM152237 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM152237 target RNA into GAM152237 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM240163 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM240163 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM240163 target RNA into GAM240163 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5324 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5324 gene: GAM152237 target protein and GAM240163 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM152237 and GAM240163

GR5325 AA580224 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5325(GR5325) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR5325 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5325 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5325 gene encodes GR5325 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5325 precursor RNA folds spatially, forming GR5325 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5325 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5325 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5325 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8670 precursor RNA and GAM272115 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8670 RNA and GAM272115 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8670 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8670 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8670 target RNA into GAM8670 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM272115 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM272115 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM272115 target RNA into GAM272115 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly

utilities, of GR5325 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5325 gene: GAM8670 target protein and GAM272115 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8670 and GAM272115

GR5326 AI915130 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5326(GR5326) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5326 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5326 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5326 gene encodes GR5326 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5326 precursor RNA folds spatially, forming GR5326 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5326 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5326 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5326 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7066 precursor RNA and GAM58790 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7066 RNA and GAM58790 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7066 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7066 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig. 8, thereby inhibiting translation of GAM7066 target RNA into GAM7066 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM58790 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM58790 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM58790 target RNA into GAM58790 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5326 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5326 gene: GAM7066 target protein and GAM58790 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7066 and GAM58790

GR5327 BG682576 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5327(GR5327) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5327 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5327 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5327 gene encodes GR5327 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5327 precursor RNA folds spatially, forming GR5327 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5327 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5327 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5327 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM114921 precursor RNA and GAM184896 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin

shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM114921 RNA and GAM184896 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM114921 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM114921 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM114921 target RNA into GAM114921 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM184896 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM184896 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM184896 target RNA into GAM184896 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5327 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5327 gene: GAM114921 target protein and GAM184896 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM114921 and GAM184896

GR5328 BG201093 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5328(GR5328) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5328 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5328 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5328 gene encodes GR5328 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5328 precursor RNA folds spatially, forming GR5328 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5328 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5328 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5328 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4270 precursor RNA, GAM4582 precursor RNA and GAM191117 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4270 RNA, GAM4582 RNA and GAM191117 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4270 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4270 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4270 target RNA into GAM4270 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM4582 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4582 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4582 target RNA into GAM4582 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM191117 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM191117 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM191117 target RNA into GAM191117 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5328 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR5328 gene: GAM4270 target protein, GAM4582 target protein and GAM191117 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4270, GAM4582 and GAM191117

GR5329 T65609 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5329(GR5329) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5329 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5329 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5329 gene encodes GR5329 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5329 precursor RNA folds spatially, forming GR5329 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5329 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5329 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5329 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3838 precursor RNA, GAM124640 precursor RNA and GAM255600 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3838 RNA, GAM124640 RNA and GAM255600 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3838 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3838 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig. 8, thereby inhibiting translation of GAM3838 target RNA into GAM3838 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM124640 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM124640 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM124640 target RNA into GAM124640 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM255600 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM255600 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM255600 target RNA into GAM255600 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5329 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5329 gene: GAM3838 target protein, GAM124640 target protein and GAM255600 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3838, GAM124640 and GAM255600

GR5330 BM128676 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5330(GR5330) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5330 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5330 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5330 gene encodes GR5330 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5330 precursor RNA folds spatially, forming GR5330 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5330 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5330 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5330 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4526 precursor RNA, GAM272037 precursor RNA and GAM310510 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4526 RNA, GAM272037 RNA and GAM310510 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4526 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4526 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4526 target RNA into GAM4526 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM272037 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM272037 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM272037 target RNA into GAM272037 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM310510 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM310510 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM310510 target RNA into GAM310510 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5330 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5330 gene: GAM4526 target protein, GAM272037 target protein and GAM310510 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6,

hereby incorporated by reference, with references to GAM4526, GAM272037 and GAM310510

GR5331 AI685170 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5331 (GR5331) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5331 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5331 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5331 gene encodes GR5331 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5331 precursor RNA folds spatially, forming GR5331 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5331 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5331 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5331 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM100525 precursor RNA and GAM193641 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM100525 RNA and GAM193641 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM100525 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM100525 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM100525 target RNA into GAM100525 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM193641 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM193641 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM193641 target RNA into GAM193641 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5331 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5331 gene: GAM100525 target protein and GAM193641 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM100525 and GAM193641

GR5332 BF941879 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5332(GR5332) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5332 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5332 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5332 gene encodes GR5332 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5332 precursor RNA folds spatially, forming GR5332 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5332 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5332 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5332 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM8079 precursor RNA, GAM120700 precursor RNA and GAM191554 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM8079 RNA, GAM120700 RNA and GAM191554 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8079 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8079 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8079 target RNA into GAM8079 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM120700 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM120700 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM120700 target RNA into GAM120700 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM191554 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM191554 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM191554 target RNA into GAM191554 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5332 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5332 gene: GAM8079 target protein, GAM120700 target protein and GAM191554 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8079, GAM120700 and GAM191554

GR5333 BE613835 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5333(GR5333) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5333 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5333 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5333 gene encodes GR5333 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5333 precursor RNA folds spatially, forming GR5333 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5333 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5333 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5333 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3000 precursor RNA, GAM5899 precursor RNA and GAM118999 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3000 RNA, GAM5899 RNA and GAM118999 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3000 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3000 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3000 target RNA into GAM3000 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5899 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5899 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5899 target RNA into GAM5899 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM118999 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM118999 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM118999 target RNA into GAM118999 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5333 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5333 gene: GAM3000 target protein, GAM5899 target protein and GAM118999 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3000, GAM5899 and GAM118999

GR5334 BF215839 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5334(GR5334) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5334 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5334 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5334 gene encodes GR5334 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5334 precursor RNA folds spatially, forming GR5334 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5334 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5334 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5334 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM240440 precursor RNA and GAM307944 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM240440 RNA and GAM307944 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM240440 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM240440 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM240440 target RNA into GAM240440 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM307944 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM307944 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM307944 target RNA into GAM307944 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5334 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5334 gene: GAM240440 target protein and GAM307944 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM240440 and GAM307944

GR5335 AI084962 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5335(GR5335) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5335 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5335 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5335 gene encodes GR5335 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5335 precursor RNA folds spatially, forming GR5335 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5335 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5335 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5335 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM159 precursor RNA and GAM29400 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM159 RNA and GAM29400 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM159 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM159 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM159 target RNA into GAM159 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM29400 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM29400 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM29400 target RNA into GAM29400 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5335 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5335 gene: GAM159 target protein and GAM29400 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM159 and GAM29400

GR5336 AA776386 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5336(GR5336) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5336 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5336 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5336 gene encodes GR5336 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5336 precursor RNA folds spatially, forming GR5336 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5336 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5336 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5336 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM32078 precursor RNA, GAM115767 precursor RNA and GAM322448 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM32078 RNA, GAM115767 RNA and GAM322448 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM32078 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM32078 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM32078 target RNA into GAM32078 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM115767 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM115767 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM115767 target RNA into GAM115767 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM322448 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM322448 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM322448 target RNA into GAM322448 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5336 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5336 gene: GAM32078 target protein, GAM115767 target protein and GAM322448 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM32078, GAM115767 and GAM322448

GR5337 AU132826 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5337(GR5337) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5337 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5337 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5337 gene encodes GR5337 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5337 precursor RNA folds spatially, forming GR5337 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5337 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5337 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5337 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM72539 precursor RNA, GAM105226 precursor RNA and GAM189137 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM72539 RNA, GAM105226 RNA and GAM189137 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM72539 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM72539 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM72539 target RNA into GAM72539 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM105226 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM105226 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM105226 target RNA into GAM105226 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM189137 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM189137 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM189137 target RNA into GAM189137 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5337 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5337 gene: GAM72539 target protein, GAM105226 target protein and GAM189137 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM72539, GAM105226 and GAM189137

GR5338 BE908938 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5338(GR5338) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5338 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5338 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5338 gene encodes GR5338 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5338 precursor RNA folds spatially, forming GR5338 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5338 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5338 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5338 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM32734 precursor RNA, GAM48113 precursor RNA, GAM65513 precursor RNA and GAM288579 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM32734 RNA, GAM48113 RNA, GAM65513 RNA and GAM288579 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM32734 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM32734 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM32734 target RNA into GAM32734 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM48113 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM48113 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM48113 target RNA into GAM48113 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM65513 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM65513 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM65513 target RNA into GAM65513 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM288579 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM288579 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM288579 target RNA into GAM288579 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5338 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5338 gene: GAM32734 target protein, GAM48113 target protein, GAM65513 target protein and GAM288579 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM32734, GAM48113, GAM65513 and GAM288579

GR5339 BI520568 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5339(GR5339) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5339 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5339 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5339 gene encodes GR5339 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5339 precursor RNA folds spatially, forming GR5339 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5339 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5339 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5339 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3256 precursor RNA, GAM4606 precursor RNA and GAM194466 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3256 RNA, GAM4606 RNA and GAM194466 RNA, herein

schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3256 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3256 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3256 target RNA into GAM3256 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM4606 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4606 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4606 target RNA into GAM4606 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM194466 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM194466 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM194466 target RNA into GAM194466 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5339 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5339 gene: GAM3256 target protein, GAM4606 target protein and GAM194466 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3256, GAM4606 and GAM194466

GR5340 BM888337 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5340(GR5340) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5340 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5340 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5340 gene encodes GR5340 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5340 precursor RNA folds spatially, forming GR5340 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5340 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5340 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5340 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM31294 precursor RNA and GAM56216 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM31294 RNA and GAM56216 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM31294 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM31294 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM31294 target RNA into GAM31294 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM56216 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM56216 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM56216 target RNA into GAM56216 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5340 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5340 gene: GAM31294 target protein and GAM56216 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM31294 and GAM56216

GR5341 AA568397 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5341(GR5341) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5341 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5341 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5341 gene encodes GR5341 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5341 precursor RNA folds spatially, forming GR5341 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5341 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5341 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5341 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8044 precursor RNA and GAM15443 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8044 RNA and GAM15443 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8044 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8044 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8044 target RNA into GAM8044 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM15443 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM15443 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM15443 target RNA into GAM15443 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5341 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5341 gene: GAM8044 target protein and GAM15443 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8044 and GAM15443

GR5342 BG574096 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5342(GR5342) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5342 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5342 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5342 gene encodes GR5342 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5342 precursor RNA folds spatially, forming GR5342 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5342 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5342 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5342 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM260080 precursor RNA and GAM260932 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM260080 RNA and GAM260932 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM260080 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM260080 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM260080 target RNA into GAM260080 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM260932 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM260932 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM260932 target RNA into GAM260932 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5342 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5342 gene: GAM260080 target protein and GAM260932 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM260080 and GAM260932

GR5343 BE019701 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5343(GR5343) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5343 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5343 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5343 gene encodes GR5343 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5343 precursor RNA folds spatially, forming GR5343 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5343 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5343 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5343 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM80476 precursor RNA and GAM300825 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM80476 RNA and GAM300825 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM80476 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM80476 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM80476 target RNA into GAM80476 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM300825 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM300825 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM300825 target RNA into GAM300825 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5343 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5343 gene: GAM80476 target protein and GAM300825 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM80476 and GAM300825

GR5344 AW351745 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5344(GR5344) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5344 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5344 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5344 gene encodes GR5344 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5344 precursor RNA folds spatially, forming GR5344 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5344 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5344 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5344 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM47056 precursor RNA, GAM126504 precursor RNA and GAM257610 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM47056 RNA, GAM126504 RNA and GAM257610 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM47056 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM47056 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM47056 target RNA into GAM47056 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM126504 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM126504 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM126504 target RNA into GAM126504 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM257610 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM257610 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM257610

target RNA into GAM257610 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5344 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5344 gene: GAM47056 target protein, GAM126504 target protein and GAM257610 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM47056, GAM126504 and GAM257610

GR5345 AI681661 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5345(GR5345) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5345 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5345 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5345 gene encodes GR5345 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5345 precursor RNA folds spatially, forming GR5345 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5345 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5345 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5345 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM35638 precursor RNA and GAM272234 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM35638 RNA and GAM272234 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM35638 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM35638 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM35638 target RNA into GAM35638 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM272234 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM272234 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM272234 target RNA into GAM272234 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5345 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5345 gene: GAM35638 target protein and GAM272234 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM35638 and GAM272234

GR5346 BG026605 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5346(GR5346) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5346 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5346 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5346 gene encodes GR5346 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5346 precursor RNA folds spatially, forming GR5346 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5346 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5346 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5346 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4479 precursor RNA and GAM8074 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4479 RNA and GAM8074 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4479 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4479 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4479 target RNA into GAM4479 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8074 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8074 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8074 target RNA into GAM8074 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5346 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5346 gene: GAM4479 target protein and GAM8074 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4479 and GAM8074

GR5347 BF887564 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5347(GR5347) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5347 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5347 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5347 gene encodes GR5347 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5347 precursor RNA folds spatially, forming GR5347 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5347 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5347 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5347 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM21171 precursor RNA and GAM214321 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM21171 RNA and GAM214321 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM21171 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM21171 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM21171 target RNA into GAM21171 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM214321 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM214321 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM214321 target RNA into GAM214321 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5347 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5347 gene: GAM21171 target protein and GAM214321 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference,

with references to GAM21171 and GAM214321

GR5348 BG761042 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5348(GR5348) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5348 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5348 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5348 gene encodes GR5348 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5348 precursor RNA folds spatially, forming GR5348 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5348 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5348 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5348 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM67708 precursor RNA, GAM180019 precursor RNA and GAM317587 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM67708 RNA, GAM180019 RNA and GAM317587 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM67708 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM67708 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM67708 target RNA into GAM67708 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM180019 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM180019 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM180019 target RNA into GAM180019 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM317587 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM317587 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM317587 target RNA into GAM317587 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5348 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5348 gene: GAM67708 target protein, GAM180019 target protein and GAM317587 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM67708, GAM180019 and GAM317587

GR5349 AA601640 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5349(GR5349) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5349 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5349 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5349 gene encodes GR5349 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5349 precursor RNA folds spatially, forming GR5349 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5349 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5349 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5349 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM6741 precursor RNA, GAM239887 precursor RNA and GAM269002 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6741 RNA, GAM239887 RNA and GAM269002 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6741 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6741 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6741 target RNA into GAM6741 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM239887 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM239887 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM239887 target RNA into GAM239887 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM269002 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM269002 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM269002 target RNA into GAM269002 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5349 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5349 gene: GAM6741 target protein, GAM239887 target protein and GAM269002 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6741, GAM239887 and GAM269002

5350(GR5350) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5350 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5350 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5350 gene encodes GR5350 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5350 precursor RNA folds spatially, forming GR5350 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5350 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5350 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5350 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM233555 precursor RNA and GAM245911 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM233555 RNA and GAM245911 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM233555 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM233555 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM233555 target RNA into GAM233555 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM245911 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM245911 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM245911 target RNA into GAM245911 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5350 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5350 gene: GAM233555 target protein and GAM245911 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM233555 and GAM245911

GR5351 BM728428 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5351(GR5351) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5351 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5351 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5351 gene encodes GR5351 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5351 precursor RNA folds spatially, forming GR5351 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5351 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5351 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5351 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM61759 precursor RNA and GAM66698 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM61759 RNA and GAM66698 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM61759 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM61759 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM61759 target RNA into GAM61759 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM66698 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM66698 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM66698 target RNA into GAM66698 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5351 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5351 gene: GAM61759 target protein and GAM66698 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM61759 and GAM66698

GR5352 BG218244 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5352(GR5352) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5352 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5352 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5352 gene encodes GR5352 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5352 precursor RNA folds spatially, forming GR5352 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5352 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5352 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5352 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2

separate GAM precursor RNAs, GAM1113 precursor RNA and GAM128350 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1113 RNA and GAM128350 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1113 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1113 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1113 target RNA into GAM1113 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM128350 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM128350 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM128350 target RNA into GAM128350 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5352 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5352 gene: GAM1113 target protein and GAM128350 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1113 and GAM128350

GR5353 AI040290 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5353(GR5353) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5353 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5353 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5353 gene encodes GR5353 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR5353 precursor RNA folds spatially, forming GR5353 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5353 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5353 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5353 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM100305 precursor RNA, GAM152702 precursor RNA and GAM288069 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM100305 RNA, GAM152702 RNA and GAM288069 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM100305 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM100305 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM100305 target RNA into GAM100305 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM152702 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM152702 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM152702 target RNA into GAM152702 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM288069 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM288069 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM288069 target RNA into GAM288069 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5353 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5353 gene: GAM100305 target protein, GAM152702 target protein and GAM288069 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM100305, GAM152702 and GAM288069

GR5354 BF684321 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5354(GR5354) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5354 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5354 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5354 gene encodes GR5354 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5354 precursor RNA folds spatially, forming GR5354 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5354 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5354 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5354 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM53777 precursor RNA and GAM131469 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM53777 RNA and GAM131469 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM53777 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM53777 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM53777 target RNA into GAM53777 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM131469 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM131469 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM131469 target RNA into GAM131469 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5354 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5354 gene: GAM53777 target protein and GAM131469 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM53777 and GAM131469

GR5355 BI056853 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5355(GR5355) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5355 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5355 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5355 gene encodes GR5355 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5355 precursor RNA folds spatially, forming GR5355 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5355 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5355 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5355 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM44544 precursor RNA, GAM105082 precursor RNA

and GAM186264 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM44544 RNA, GAM105082 RNA and GAM186264 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM44544 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM44544 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM44544 target RNA into GAM44544 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM105082 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM105082 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM105082 target RNA into GAM105082 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM186264 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM186264 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM186264 target RNA into GAM186264 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5355 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5355 gene: GAM44544 target protein, GAM105082 target protein and GAM186264 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM44544, GAM105082 and GAM186264

GR5356 BM310385 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5356(GR5356) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR5356 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5356 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5356 gene encodes GR5356 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5356 precursor RNA folds spatially, forming GR5356 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5356 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5356 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5356 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM298863 precursor RNA and GAM303519 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM298863 RNA and GAM303519 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM298863 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM298863 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM298863 target RNA into GAM298863 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM303519 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM303519 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM303519 target RNA into GAM303519 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5356 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5356 gene: GAM298863 target protein and GAM303519 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM298863 and GAM303519

GR5357 BI494786 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5357(GR5357) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5357 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5357 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5357 gene encodes GR5357 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5357 precursor RNA folds spatially, forming GR5357 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5357 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5357 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5357 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1811 precursor RNA and GAM5661 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1811 RNA and GAM5661 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1811 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1811 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds

to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1811 target RNA into GAM1811 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5661 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5661 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5661 target RNA into GAM5661 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5357 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5357 gene: GAM1811 target protein and GAM5661 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1811 and GAM5661

GR5358 BF222361 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5358(GR5358) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5358 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5358 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5358 gene encodes GR5358 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5358 precursor RNA folds spatially, forming GR5358 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5358 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5358 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5358 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2193 precursor RNA, GAM3222 precursor RNA and GAM224017 precursor RNA, herein schematically represented by GAM1 FOLDED

PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2193 RNA, GAM3222 RNA and GAM224017 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2193 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2193 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2193 target RNA into GAM2193 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM3222 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3222 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3222 target RNA into GAM3222 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM224017 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM224017 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM224017 target RNA into GAM224017 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5358 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5358 gene: GAM2193 target protein, GAM3222 target protein and GAM224017 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2193, GAM3222 and GAM224017

GR5359 AV736254 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5359(GR5359) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR5359 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5359 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5359 gene encodes GR5359 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5359 precursor RNA folds spatially, forming GR5359 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5359 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5359 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5359 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3153 precursor RNA, GAM201596 precursor RNA and GAM250831 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3153 RNA, GAM201596 RNA and GAM250831 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3153 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3153 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3153 target RNA into GAM3153 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM201596 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM201596 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM201596 target RNA into GAM201596 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM250831 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM250831 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM250831 target RNA into GAM250831 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5359 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5359 gene: GAM3153 target protein, GAM201596 target protein and GAM250831 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3153, GAM201596 and GAM250831

GR5360 BF875808 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5360(GR5360) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5360 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5360 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5360 gene encodes GR5360 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5360 precursor RNA folds spatially, forming GR5360 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5360 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5360 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5360 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM485 precursor RNA and GAM2741 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM485 RNA and GAM2741 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM485 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM485 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM485 target RNA into GAM485 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM2741 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2741 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2741 target RNA into GAM2741 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5360 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5360 gene: GAM485 target protein and GAM2741 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM485 and GAM2741

GR5361 AV760230 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5361(GR5361) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5361 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5361 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5361 gene encodes GR5361 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5361 precursor RNA folds spatially, forming GR5361 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5361 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR5361 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5361 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM276 precursor RNA, GAM2622 precursor RNA and GAM31666 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM276 RNA, GAM2622 RNA and GAM31666 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM276 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM276 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM276 target RNA into GAM276 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM2622 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2622 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2622 target RNA into GAM2622 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM31666 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM31666 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM31666 target RNA into GAM31666 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5361 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5361 gene: GAM276 target protein, GAM2622 target protein and GAM31666 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN.

The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM276, GAM2622 and GAM31666

GR5362 AI391570 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5362 (GR5362) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5362 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5362 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5362 gene encodes GR5362 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5362 precursor RNA folds spatially, forming GR5362 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5362 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5362 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5362 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM149218 precursor RNA and GAM254039 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM149218 RNA and GAM254039 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM149218 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM149218 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM149218 target RNA into GAM149218 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM254039 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM254039 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM254039 target RNA into GAM254039 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5362 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5362 gene: GAM149218 target protein and GAM254039 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM149218 and GAM254039

GR5363 AA531596 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5363(GR5363) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5363 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5363 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5363 gene encodes GR5363 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5363 precursor RNA folds spatially, forming GR5363 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5363 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5363 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5363 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3961 precursor RNA, GAM244912 precursor RNA and GAM321527 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3961 RNA, GAM244912 RNA and GAM321527 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3961 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3961 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3961 target RNA into GAM3961 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM244912 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM244912 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM244912 target RNA into GAM244912 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM321527 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM321527 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM321527 target RNA into GAM321527 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5363 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5363 gene: GAM3961 target protein, GAM244912 target protein and GAM321527 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3961, GAM244912 and GAM321527

GR5364 AI903040 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5364(GR5364) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5364 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5364 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5364 gene encodes GR5364 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5364 precursor RNA folds spatially, forming GR5364 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5364 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5364 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5364 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5443 precursor RNA and GAM195920 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5443 RNA and GAM195920 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5443 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5443 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5443 target RNA into GAM5443 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM195920 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM195920 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM195920 target RNA into GAM195920 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5364 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5364 gene: GAM5443 target protein and GAM195920 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes

is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5443 and GAM195920

GR5365 AI431616 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5365(GR5365) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5365 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5365 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5365 gene encodes GR5365 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5365 precursor RNA folds spatially, forming GR5365 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5365 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5365 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5365 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM908 precursor RNA and GAM104186 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM908 RNA and GAM104186 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM908 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM908 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM908 target RNA into GAM908 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM104186 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM104186 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM104186 target RNA into GAM104186 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5365 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5365 gene: GAM908 target protein and GAM104186 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM908 and GAM104186

GR5366 AA365535 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5366(GR5366) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5366 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5366 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5366 gene encodes GR5366 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5366 precursor RNA folds spatially, forming GR5366 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5366 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5366 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5366 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8475 precursor RNA and GAM246133 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8475 RNA and GAM246133 RNA, herein schematically

represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8475 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8475 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8475 target RNA into GAM8475 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM246133 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM246133 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM246133 target RNA into GAM246133 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5366 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5366 gene: GAM8475 target protein and GAM246133 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8475 and GAM246133

GR5367 AA280805 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5367(GR5367) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5367 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5367 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5367 gene encodes GR5367 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5367 precursor RNA folds spatially, forming GR5367 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5367 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5367 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5367 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM218483 precursor RNA and GAM305792 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM218483 RNA and GAM305792 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM218483 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM218483 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM218483 target RNA into GAM218483 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM305792 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM305792 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM305792 target RNA into GAM305792 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5367 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5367 gene: GAM218483 target protein and GAM305792 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM218483 and GAM305792

GR5368 AW368024 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5368(GR5368) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5368 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR5368 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5368 gene encodes GR5368 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5368 precursor RNA folds spatially, forming GR5368 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5368 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5368 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5368 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM167813 precursor RNA and GAM258895 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM167813 RNA and GAM258895 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM167813 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM167813 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM167813 target RNA into GAM167813 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM258895 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM258895 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM258895 target RNA into GAM258895 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5368 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5368 gene: GAM167813 target

protein and GAM258895 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM167813 and GAM258895

GR5369 AW000749 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5369(GR5369) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5369 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5369 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5369 gene encodes GR5369 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5369 precursor RNA folds spatially, forming GR5369 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5369 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5369 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5369 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2809 precursor RNA and GAM233882 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2809 RNA and GAM233882 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2809 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2809 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2809 target RNA into GAM2809 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM233882 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM233882 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM233882 target RNA into GAM233882 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5369 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5369 gene: GAM2809 target protein and GAM233882 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2809 and GAM233882

GR5370 AA764889 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5370(GR5370) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5370 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5370 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5370 gene encodes GR5370 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5370 precursor RNA folds spatially, forming GR5370 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5370 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5370 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5370 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM6480 precursor RNA, GAM24228 precursor RNA, GAM151523 precursor RNA and GAM317926 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6480 RNA, GAM24228 RNA, GAM151523 RNA and GAM317926 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6480 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6480 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6480 target RNA into GAM6480 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM24228 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM24228 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM24228 target RNA into GAM24228 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM151523 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM151523 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM151523 target RNA into GAM151523 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM317926 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM317926 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM317926 target RNA into GAM317926 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5370 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5370 gene: GAM6480 target protein, GAM24228 target protein, GAM151523 target protein and GAM317926 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6480, GAM24228, GAM151523 and GAM317926

bioinformatically detected regulatory gene, referred to here as Genomic Record 5371 (GR5371) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5371 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5371 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5371 gene encodes GR5371 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5371 precursor RNA folds spatially, forming GR5371 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5371 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5371 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5371 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1138 precursor RNA, GAM198712 precursor RNA and GAM291151 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1138 RNA, GAM198712 RNA and GAM291151 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1138 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1138 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1138 target RNA into GAM1138 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM198712 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM198712 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM198712 target RNA into GAM198712 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM291151 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM291151 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM291151 target RNA into GAM291151 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5371 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5371 gene: GAM1138 target protein, GAM198712 target protein and GAM291151 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1138, GAM198712 and GAM291151

GR5372 AW609739 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5372(GR5372) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5372 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5372 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5372 gene encodes GR5372 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5372 precursor RNA folds spatially, forming GR5372 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5372 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5372 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5372 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM217509 precursor RNA and GAM321604 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3

FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM217509 RNA and GAM321604 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM217509 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM217509 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM217509 target RNA into GAM217509 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM321604 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM321604 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM321604 target RNA into GAM321604 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5372 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5372 gene: GAM217509 target protein and GAM321604 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM217509 and GAM321604

GR5373 BE867448 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5373(GR5373) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5373 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5373 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5373 gene encodes GR5373 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5373 precursor RNA folds spatially, forming GR5373 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5373 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5373 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5373 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM3553 precursor RNA, GAM5230 precursor RNA, GAM60922 precursor RNA and GAM72926 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3553 RNA, GAM5230 RNA, GAM60922 RNA and GAM72926 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3553 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3553 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3553 target RNA into GAM3553 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5230 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5230 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5230 target RNA into GAM5230 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM60922 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM60922 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM60922 target RNA into GAM60922 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM72926 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM72926 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM72926 target RNA into GAM72926 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5373 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5373 gene: GAM3553 target protein, GAM5230 target protein, GAM60922 target protein and GAM72926 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3553, GAM5230, GAM60922 and GAM72926

GR5374 AI934445 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5374(GR5374) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5374 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5374 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5374 gene encodes GR5374 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5374 precursor RNA folds spatially, forming GR5374 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5374 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5374 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5374 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1223 precursor RNA and GAM243375 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1223 RNA and GAM243375 RNA, herein schematically

represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1223 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1223 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1223 target RNA into GAM1223 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM243375 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM243375 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM243375 target RNA into GAM243375 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5374 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5374 gene: GAM1223 target protein and GAM243375 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1223 and GAM243375

GR5375 BE062112 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5375(GR5375) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5375 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5375 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5375 gene encodes GR5375 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5375 precursor RNA folds spatially, forming GR5375 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5375 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5375 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5375 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM262649 precursor RNA and GAM291649 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM262649 RNA and GAM291649 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM262649 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM262649 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM262649 target RNA into GAM262649 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM291649 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM291649 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM291649 target RNA into GAM291649 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5375 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5375 gene: GAM262649 target protein and GAM291649 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM262649 and GAM291649

GR5376 BM172251 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5376(GR5376) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5376 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR5376 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5376 gene encodes GR5376 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5376 precursor RNA folds spatially, forming GR5376 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5376 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5376 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5376 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM72345 precursor RNA and GAM99176 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM72345 RNA and GAM99176 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM72345 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM72345 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM72345 target RNA into GAM72345 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM99176 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM99176 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM99176 target RNA into GAM99176 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5376 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5376 gene: GAM72345 target

protein and GAM99176 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM72345 and GAM99176

GR5377 BE551676 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5377(GR5377) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5377 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5377 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5377 gene encodes GR5377 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5377 precursor RNA folds spatially, forming GR5377 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5377 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5377 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5377 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM7912 precursor RNA, GAM17921 precursor RNA and GAM316944 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7912 RNA, GAM17921 RNA and GAM316944 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7912 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7912 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7912 target RNA into GAM7912 target protein, herein schematically represented by GAM1 TARGET

PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM17921 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM17921 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM17921 target RNA into GAM17921 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM316944 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM316944 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM316944 target RNA into GAM316944 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5377 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5377 gene: GAM7912 target protein, GAM17921 target protein and GAM316944 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7912, GAM17921 and GAM316944

GR5378 AV728031 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5378(GR5378) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5378 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5378 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5378 gene encodes GR5378 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5378 precursor RNA folds spatially, forming GR5378 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5378 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5378 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR5378 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM55190 precursor RNA and GAM333754 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM55190 RNA and GAM333754 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM55190 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM55190 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM55190 target RNA into GAM55190 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM333754 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM333754 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM333754 target RNA into GAM333754 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5378 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5378 gene: GAM55190 target protein and GAM333754 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM55190 and GAM333754

GR5379 BE269186 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5379(GR5379) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5379 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5379

gene was detected is described hereinabove with reference to Figs. 8-18.

GR5379 gene encodes GR5379 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5379 precursor RNA folds spatially, forming GR5379 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5379 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5379 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5379 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5380 precursor RNA and GAM216015 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5380 RNA and GAM216015 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5380 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5380 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5380 target RNA into GAM5380 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM216015 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM216015 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM216015 target RNA into GAM216015 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5379 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5379 gene: GAM5380 target protein and GAM216015 target protein, herein schematically represented by GAM1

TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5380 and GAM216015

GR5380 AW250805 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5380(GR5380) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5380 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5380 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5380 gene encodes GR5380 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5380 precursor RNA folds spatially, forming GR5380 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5380 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5380 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5380 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6519 precursor RNA and GAM7475 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6519 RNA and GAM7475 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6519 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6519 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6519 target RNA into GAM6519 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7475 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7475 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7475 target RNA into GAM7475 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5380 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5380 gene: GAM6519 target protein and GAM7475 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6519 and GAM7475

GR5381 BF988693 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5381(GR5381) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5381 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5381 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5381 gene encodes GR5381 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5381 precursor RNA folds spatially, forming GR5381 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5381 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5381 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5381 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM220342 precursor RNA and GAM309923 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM220342 RNA and GAM309923 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM220342 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM220342 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM220342 target RNA into GAM220342 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM309923 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM309923 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM309923 target RNA into GAM309923 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5381 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5381 gene: GAM220342 target protein and GAM309923 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM220342 and GAM309923

GR5382 BI039438 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5382(GR5382) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5382 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5382 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5382 gene encodes GR5382 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5382 precursor RNA folds spatially, forming GR5382 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5382 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5382 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5382 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM6026 precursor RNA, GAM6884 precursor RNA and GAM8948 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6026 RNA, GAM6884 RNA and GAM8948 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6026 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6026 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6026 target RNA into GAM6026 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6884 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6884 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6884 target RNA into GAM6884 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8948 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8948 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8948 target RNA into GAM8948 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5382 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5382 gene: GAM6026 target protein, GAM6884 target protein and GAM8948 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6,

hereby incorporated by reference, with references to GAM6026, GAM6884 and GAM8948

GR5383 AI673405 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5383(GR5383) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5383 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5383 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5383 gene encodes GR5383 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5383 precursor RNA folds spatially, forming GR5383 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5383 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5383 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5383 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM398 precursor RNA and GAM105507 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM398 RNA and GAM105507 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM398 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM398 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM398 target RNA into GAM398 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM105507 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM105507 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM105507 target RNA into GAM105507 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5383 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5383 gene: GAM398 target protein and GAM105507 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM398 and GAM105507

GR5384 AA063420 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5384(GR5384) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5384 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5384 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5384 gene encodes GR5384 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5384 precursor RNA folds spatially, forming GR5384 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5384 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5384 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5384 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2281 precursor RNA, GAM164889 precursor RNA and GAM279158 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM2281 RNA, GAM164889 RNA and GAM279158 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2281 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2281 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2281 target RNA into GAM2281 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM164889 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM164889 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM164889 target RNA into GAM164889 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM279158 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM279158 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM279158 target RNA into GAM279158 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5384 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5384 gene: GAM2281 target protein, GAM164889 target protein and GAM279158 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2281, GAM164889 and GAM279158

GR5385 BG532947 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5385(GR5385) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5385 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5385 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5385 gene encodes GR5385 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5385 precursor RNA folds spatially, forming GR5385 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5385 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5385 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5385 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM817 precursor RNA, GAM145768 precursor RNA and GAM249698 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM817 RNA, GAM145768 RNA and GAM249698 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM817 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM817 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM817 target RNA into GAM817 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM145768 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM145768 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM145768 target RNA into GAM145768 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM249698 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM249698 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM249698 target RNA into GAM249698 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5385 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5385 gene: GAM817 target protein, GAM145768 target protein and GAM249698 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM817, GAM145768 and GAM249698

GR5386 BG106411 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5386(GR5386) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5386 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5386 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5386 gene encodes GR5386 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5386 precursor RNA folds spatially, forming GR5386 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5386 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5386 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5386 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM22652 precursor RNA and GAM239453 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM22652 RNA and GAM239453 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM22652 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM22652 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM22652 target RNA into GAM22652 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM239453 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM239453 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM239453 target RNA into GAM239453 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5386 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5386 gene: GAM22652 target protein and GAM239453 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM22652 and GAM239453

GR5387 AI298788 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5387(GR5387) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5387 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5387 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5387 gene encodes GR5387 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5387 precursor RNA folds spatially, forming GR5387 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5387 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5387 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5387 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6019 precursor RNA and GAM8587 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6019 RNA and GAM8587 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6019 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6019 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6019 target RNA into GAM6019 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8587 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8587 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8587 target RNA into GAM8587 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5387 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5387 gene: GAM6019 target protein and GAM8587 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6019 and GAM8587

GR5388 BE092454 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5388(GR5388) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5388 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5388 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5388 gene encodes GR5388 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5388 precursor RNA folds spatially, forming GR5388 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5388 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5388 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5388 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM46 precursor RNA, GAM393 precursor RNA and GAM135375 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM46 RNA, GAM393 RNA and GAM135375 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM46 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM46 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM46 target RNA into GAM46 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM393 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM393 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM393 target RNA into GAM393 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM135375 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM135375 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM135375 target RNA into GAM135375 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5388 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5388 gene: GAM46 target protein, GAM393 target protein and GAM135375 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM46, GAM393 and GAM135375

GR5389 AA403097 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5389(GR5389) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5389 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5389 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5389 gene encodes GR5389 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5389 precursor RNA folds spatially, forming GR5389 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5389 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5389 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5389 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1038 precursor RNA, GAM19579 precursor RNA and GAM287975 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1038 RNA, GAM19579 RNA and GAM287975 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1038 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1038 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1038 target RNA into GAM1038 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM19579 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM19579 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM19579 target RNA into GAM19579 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM287975 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM287975 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM287975 target RNA into GAM287975 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5389 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5389 gene: GAM1038 target protein, GAM19579 target protein and GAM287975 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1038, GAM19579 and GAM287975

GR5390 BE392059 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5390(GR5390) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5390 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5390 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5390 gene encodes GR5390 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5390 precursor RNA folds spatially, forming GR5390 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5390 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5390 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5390 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM855 precursor RNA, GAM8648 precursor RNA, GAM102836 precursor RNA and GAM171268 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM855 RNA, GAM8648 RNA, GAM102836 RNA and GAM171268 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM855 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM855 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM855 target RNA into GAM855 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8648 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8648 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8648 target RNA into GAM8648 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM102836 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM102836 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM102836 target RNA into GAM102836 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM171268 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM171268 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM171268 target RNA into GAM171268 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5390 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5390 gene: GAM855 target protein, GAM8648 target protein, GAM102836 target protein and GAM171268 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM855, GAM8648, GAM102836 and GAM171268

GR5391 BG620903 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5391 (GR5391) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5391 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5391 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5391 gene encodes GR5391 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5391 precursor RNA folds spatially, forming GR5391 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5391 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5391 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5391 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM56562 precursor RNA and GAM247622 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM56562 RNA and GAM247622 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding

to GAM RNA of Fig. 8.

GAM56562 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM56562 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM56562 target RNA into GAM56562 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM247622 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM247622 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM247622 target RNA into GAM247622 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5391 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5391 gene: GAM56562 target protein and GAM247622 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM56562 and GAM247622

GR5392 BM478141 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5392(GR5392) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5392 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5392 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5392 gene encodes GR5392 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5392 precursor RNA folds spatially, forming GR5392 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5392 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5392 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR5392 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3209 precursor RNA and GAM271961 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3209 RNA and GAM271961 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3209 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3209 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3209 target RNA into GAM3209 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM271961 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM271961 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM271961 target RNA into GAM271961 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5392 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5392 gene: GAM3209 target protein and GAM271961 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3209 and GAM271961

GR5393 AA082667 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5393(GR5393) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5393 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5393

gene was detected is described hereinabove with reference to Figs. 8-18.

GR5393 gene encodes GR5393 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5393 precursor RNA folds spatially, forming GR5393 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5393 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5393 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5393 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM819 precursor RNA, GAM235727 precursor RNA and GAM310106 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM819 RNA, GAM235727 RNA and GAM310106 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM819 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM819 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM819 target RNA into GAM819 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM235727 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM235727 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM235727 target RNA into GAM235727 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM310106 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM310106 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM310106 target RNA into GAM310106 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5393 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5393 gene: GAM819 target protein, GAM235727 target protein and GAM310106 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM819, GAM235727 and GAM310106

GR5394 AA737123 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5394(GR5394) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5394 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5394 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5394 gene encodes GR5394 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5394 precursor RNA folds spatially, forming GR5394 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5394 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5394 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5394 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3216 precursor RNA and GAM11262 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3216 RNA and GAM11262 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3216 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3216 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3216 target RNA into GAM3216 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM11262 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM11262 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM11262 target RNA into GAM11262 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5394 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5394 gene: GAM3216 target protein and GAM11262 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3216 and GAM11262

GR5395 AA513037 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5395(GR5395) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5395 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5395 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5395 gene encodes GR5395 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5395 precursor RNA folds spatially, forming GR5395 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5395 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5395 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5395 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM6015 precursor RNA, GAM35480 precursor RNA and GAM297250 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6015 RNA, GAM35480 RNA and GAM297250 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6015 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6015 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6015 target RNA into GAM6015 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM35480 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM35480 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM35480 target RNA into GAM35480 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM297250 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM297250 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM297250 target RNA into GAM297250 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5395 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5395 gene: GAM6015 target protein, GAM35480 target protein and GAM297250 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6015, GAM35480 and GAM297250

GR5396 BE262042 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5396 (GR5396) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5396 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5396 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5396 gene encodes GR5396 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5396 precursor RNA folds spatially, forming GR5396 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5396 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5396 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5396 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM87699 precursor RNA, GAM223730 precursor RNA and GAM329709 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM87699 RNA, GAM223730 RNA and GAM329709 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM87699 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM87699 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM87699 target RNA into GAM87699 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM223730 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM223730 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM223730 target RNA into GAM223730 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM329709 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM329709 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM329709 target RNA into GAM329709 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5396 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5396 gene: GAM87699 target protein, GAM223730 target protein and GAM329709 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM87699, GAM223730 and GAM329709

GR5397 BG396654 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5397(GR5397) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5397 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5397 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5397 gene encodes GR5397 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5397 precursor RNA folds spatially, forming GR5397 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5397 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5397 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5397 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6677 precursor RNA and GAM113887 precursor

RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6677 RNA and GAM113887 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6677 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6677 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6677 target RNA into GAM6677 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM113887 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM113887 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM113887 target RNA into GAM113887 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5397 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5397 gene: GAM6677 target protein and GAM113887 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6677 and GAM113887

GR5398 AA857819 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5398 (GR5398) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5398 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5398 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5398 gene encodes GR5398 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5398 precursor RNA folds spatially, forming GR5398 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5398 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5398 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5398 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM189888 precursor RNA and GAM273521 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM189888 RNA and GAM273521 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM189888 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM189888 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM189888 target RNA into GAM189888 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM273521 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM273521 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM273521 target RNA into GAM273521 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5398 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5398 gene: GAM189888 target protein and GAM273521 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM189888 and GAM273521

bioinformatically detected regulatory gene, referred to here as Genomic Record 5399(GR5399) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5399 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5399 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5399 gene encodes GR5399 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5399 precursor RNA folds spatially, forming GR5399 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5399 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5399 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5399 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4497 precursor RNA, GAM6966 precursor RNA and GAM142433 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4497 RNA, GAM6966 RNA and GAM142433 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4497 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4497 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4497 target RNA into GAM4497 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6966 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6966 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig. 8, thereby inhibiting translation of GAM6966 target RNA into GAM6966 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM142433 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM142433 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM142433 target RNA into GAM142433 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5399 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5399 gene: GAM4497 target protein, GAM6966 target protein and GAM142433 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4497, GAM6966 and GAM142433

GR5400 BE973578 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5400(GR5400) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5400 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5400 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5400 gene encodes GR5400 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5400 precursor RNA folds spatially, forming GR5400 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5400 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5400 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5400 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM139417 precursor RNA and GAM306077 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3

FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM139417 RNA and GAM306077 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM139417 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM139417 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM139417 target RNA into GAM139417 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM306077 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM306077 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM306077 target RNA into GAM306077 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5400 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5400 gene: GAM139417 target protein and GAM306077 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM139417 and GAM306077

GR5401 BF514234 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5401(GR5401) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5401 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5401 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5401 gene encodes GR5401 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5401 precursor RNA folds spatially, forming GR5401 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5401 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5401 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5401 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM6067 precursor RNA, GAM178214 precursor RNA and GAM197510 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6067 RNA, GAM178214 RNA and GAM197510 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6067 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6067 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6067 target RNA into GAM6067 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM178214 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM178214 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM178214 target RNA into GAM178214 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM197510 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM197510 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM197510 target RNA into GAM197510 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5401 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5401 gene: GAM6067 target protein, GAM178214 target protein and GAM197510 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6067, GAM178214 and GAM197510

GR5402 AW838712 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5402(GR5402) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5402 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5402 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5402 gene encodes GR5402 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5402 precursor RNA folds spatially, forming GR5402 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5402 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5402 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5402 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM13325 precursor RNA and GAM300226 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM13325 RNA and GAM300226 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM13325 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM13325 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM13325 target RNA into GAM13325 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM300226 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM300226 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM300226 target RNA into GAM300226 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5402 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5402 gene: GAM13325 target protein and GAM300226 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM13325 and GAM300226

GR5403 BM817601 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5403(GR5403) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5403 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5403 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5403 gene encodes GR5403 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5403 precursor RNA folds spatially, forming GR5403 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5403 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5403 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5403 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM177056 precursor RNA and GAM296200 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin

shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM177056 RNA and GAM296200 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM177056 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM177056 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM177056 target RNA into GAM177056 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM296200 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM296200 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM296200 target RNA into GAM296200 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5403 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5403 gene: GAM177056 target protein and GAM296200 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM177056 and GAM296200

GR5404 AI125608 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5404(GR5404) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5404 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5404 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5404 gene encodes GR5404 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5404 precursor RNA folds spatially, forming GR5404 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5404 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5404 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5404 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5316 precursor RNA and GAM16939 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5316 RNA and GAM16939 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5316 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5316 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5316 target RNA into GAM5316 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM16939 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM16939 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM16939 target RNA into GAM16939 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5404 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5404 gene: GAM5316 target protein and GAM16939 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5316 and GAM16939

GR5405 BG956006 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5405(GR5405) gene, which encodes an `operon-like` cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5405 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5405 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5405 gene encodes GR5405 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5405 precursor RNA folds spatially, forming GR5405 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5405 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5405 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5405 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6885 precursor RNA and GAM188103 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6885 RNA and GAM188103 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6885 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6885 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6885 target RNA into GAM6885 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM188103 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM188103 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM188103 target RNA into GAM188103 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5405 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5405 gene: GAM6885 target protein and GAM188103 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6885 and GAM188103

GR5406 BI871376 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5406(GR5406) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5406 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5406 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5406 gene encodes GR5406 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5406 precursor RNA folds spatially, forming GR5406 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5406 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5406 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5406 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM164772 precursor RNA and GAM256133 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM164772 RNA and GAM256133 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM164772 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM164772 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM164772 target RNA into GAM164772 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM256133 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM256133 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM256133 target RNA into GAM256133 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5406 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5406 gene: GAM164772 target protein and GAM256133 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM164772 and GAM256133

GR5407 AA426598 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5407(GR5407) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5407 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5407 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5407 gene encodes GR5407 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5407 precursor RNA folds spatially, forming GR5407 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5407 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5407 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5407 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3836 precursor RNA and GAM336012 precursor

RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3836 RNA and GAM336012 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3836 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3836 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3836 target RNA into GAM3836 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336012 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336012 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336012 target RNA into GAM336012 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5407 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5407 gene: GAM3836 target protein and GAM336012 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3836 and GAM336012

GR5408 AI025117 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5408(GR5408) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5408 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5408 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5408 gene encodes GR5408 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5408 precursor RNA folds spatially, forming GR5408 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5408 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5408 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5408 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM749 precursor RNA and GAM289990 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM749 RNA and GAM289990 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM749 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM749 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM749 target RNA into GAM749 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM289990 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM289990 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM289990 target RNA into GAM289990 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5408 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5408 gene: GAM749 target protein and GAM289990 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM749 and GAM289990

bioinformatically detected regulatory gene, referred to here as Genomic Record 5409(GR5409) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5409 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5409 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5409 gene encodes GR5409 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5409 precursor RNA folds spatially, forming GR5409 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5409 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5409 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5409 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM57661 precursor RNA, GAM145491 precursor RNA and GAM223893 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM57661 RNA, GAM145491 RNA and GAM223893 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM57661 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM57661 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM57661 target RNA into GAM57661 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM145491 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM145491 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM145491 target RNA into GAM145491 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM223893 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM223893 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM223893 target RNA into GAM223893 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5409 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5409 gene: GAM57661 target protein, GAM145491 target protein and GAM223893 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM57661, GAM145491 and GAM223893

GR5410 AL713342 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5410 (GR5410) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5410 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5410 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5410 gene encodes GR5410 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5410 precursor RNA folds spatially, forming GR5410 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5410 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5410 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5410 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM124262 precursor RNA, GAM161169 precursor RNA and GAM197373 precursor RNA, herein schematically represented by GAM1 FOLDED

PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM124262 RNA, GAM161169 RNA and GAM197373 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM124262 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM124262 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM124262 target RNA into GAM124262 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM161169 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM161169 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM161169 target RNA into GAM161169 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM197373 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM197373 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM197373 target RNA into GAM197373 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5410 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5410 gene: GAM124262 target protein, GAM161169 target protein and GAM197373 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM124262, GAM161169 and GAM197373

GR5411 BQ068484 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5411(GR5411) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR5411 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5411 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5411 gene encodes GR5411 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5411 precursor RNA folds spatially, forming GR5411 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5411 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5411 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5411 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2177 precursor RNA, GAM5914 precursor RNA and GAM213716 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2177 RNA, GAM5914 RNA and GAM213716 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2177 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2177 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2177 target RNA into GAM2177 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5914 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5914 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5914 target RNA into GAM5914 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM213716 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM213716 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM213716 target RNA into GAM213716 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5411 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5411 gene: GAM2177 target protein, GAM5914 target protein and GAM213716 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2177, GAM5914 and GAM213716

GR5412 AI473229 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5412(GR5412) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5412 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5412 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5412 gene encodes GR5412 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5412 precursor RNA folds spatially, forming GR5412 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5412 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5412 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5412 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM100112 precursor RNA and GAM192291 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM100112 RNA and GAM192291 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM100112 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM100112 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM100112 target RNA into GAM100112 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM192291 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM192291 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM192291 target RNA into GAM192291 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5412 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5412 gene: GAM100112 target protein and GAM192291 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM100112 and GAM192291

GR5413 AA112102 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5413(GR5413) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5413 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5413 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5413 gene encodes GR5413 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5413 precursor RNA folds spatially, forming GR5413 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5413 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR5413 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5413 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM898 precursor RNA, GAM4590 precursor RNA and GAM123918 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM898 RNA, GAM4590 RNA and GAM123918 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM898 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM898 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM898 target RNA into GAM898 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM4590 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4590 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4590 target RNA into GAM4590 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM123918 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM123918 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM123918 target RNA into GAM123918 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5413 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5413 gene: GAM898 target protein, GAM4590 target protein and GAM123918 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN.

The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM898, GAM4590 and GAM123918

GR5414 BG719831 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5414(GR5414) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5414 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5414 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5414 gene encodes GR5414 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5414 precursor RNA folds spatially, forming GR5414 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5414 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5414 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5414 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4760 precursor RNA, GAM6453 precursor RNA and GAM325960 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4760 RNA, GAM6453 RNA and GAM325960 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4760 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4760 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4760 target RNA into GAM4760 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6453 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6453 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6453 target RNA into GAM6453 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM325960 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM325960 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM325960 target RNA into GAM325960 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5414 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5414 gene: GAM4760 target protein, GAM6453 target protein and GAM325960 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4760, GAM6453 and GAM325960

GR5415 AA502351 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5415(GR5415) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5415 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5415 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5415 gene encodes GR5415 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5415 precursor RNA folds spatially, forming GR5415 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5415 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5415 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5415 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5181 precursor RNA and GAM184966 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5181 RNA and GAM184966 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5181 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5181 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5181 target RNA into GAM5181 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM184966 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM184966 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM184966 target RNA into GAM184966 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5415 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5415 gene: GAM5181 target protein and GAM184966 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5181 and GAM184966

GR5416 AW028260 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5416(GR5416) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5416 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5416 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5416 gene encodes GR5416 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5416 precursor RNA folds spatially, forming GR5416 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5416 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5416 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5416 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM58892 precursor RNA and GAM64308 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM58892 RNA and GAM64308 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM58892 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM58892 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM58892 target RNA into GAM58892 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM64308 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM64308 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM64308 target RNA into GAM64308 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5416 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5416 gene: GAM58892 target protein and GAM64308 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes

is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM58892 and GAM64308

GR5417 AI140319 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5417 (GR5417) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5417 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5417 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5417 gene encodes GR5417 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5417 precursor RNA folds spatially, forming GR5417 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5417 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5417 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5417 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6488 precursor RNA and GAM180803 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6488 RNA and GAM180803 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6488 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6488 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6488 target RNA into GAM6488 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM180803 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM180803 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM180803 target RNA into GAM180803 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5417 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5417 gene: GAM6488 target protein and GAM180803 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6488 and GAM180803

GR5418 BM920875 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5418(GR5418) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5418 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5418 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5418 gene encodes GR5418 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5418 precursor RNA folds spatially, forming GR5418 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5418 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5418 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5418 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2779 precursor RNA, GAM20461 precursor RNA and GAM64193 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM2779 RNA, GAM20461 RNA and GAM64193 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2779 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2779 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2779 target RNA into GAM2779 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM20461 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM20461 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM20461 target RNA into GAM20461 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM64193 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM64193 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM64193 target RNA into GAM64193 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5418 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5418 gene: GAM2779 target protein, GAM20461 target protein and GAM64193 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2779, GAM20461 and GAM64193

GR5419 BF699479 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5419 (GR5419) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5419 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5419 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5419 gene encodes GR5419 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5419 precursor RNA folds spatially, forming GR5419 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5419 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5419 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5419 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3915 precursor RNA and GAM7996 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3915 RNA and GAM7996 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3915 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3915 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3915 target RNA into GAM3915 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7996 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7996 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7996 target RNA into GAM7996 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5419 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5419 gene: GAM3915 target protein and GAM7996 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference,

with references to GAM3915 and GAM7996

GR5420 AI954277 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5420 (GR5420) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5420 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5420 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5420 gene encodes GR5420 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5420 precursor RNA folds spatially, forming GR5420 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5420 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5420 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5420 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM132036 precursor RNA and GAM228531 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM132036 RNA and GAM228531 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM132036 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM132036 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM132036 target RNA into GAM132036 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM228531 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM228531 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM228531 target RNA into GAM228531 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5420 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5420 gene: GAM132036 target protein and GAM228531 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM132036 and GAM228531

GR5421 BG183763 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5421(GR5421) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5421 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5421 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5421 gene encodes GR5421 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5421 precursor RNA folds spatially, forming GR5421 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5421 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5421 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5421 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM139080 precursor RNA, GAM149073 precursor RNA and GAM252470 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM139080 RNA, GAM149073 RNA and GAM252470 RNA, herein

schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM139080 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM139080 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM139080 target RNA into GAM139080 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM149073 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM149073 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM149073 target RNA into GAM149073 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM252470 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM252470 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM252470 target RNA into GAM252470 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5421 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5421 gene: GAM139080 target protein, GAM149073 target protein and GAM252470 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM139080, GAM149073 and GAM252470

GR5422 AA229240 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5422(GR5422) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5422 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5422 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5422 gene encodes GR5422 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5422 precursor RNA folds spatially, forming GR5422 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5422 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5422 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5422 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7737 precursor RNA and GAM274432 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7737 RNA and GAM274432 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7737 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7737 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7737 target RNA into GAM7737 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM274432 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM274432 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM274432 target RNA into GAM274432 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5422 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5422 gene: GAM7737 target protein and GAM274432 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7737 and GAM274432

GR5423 BF345590 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5423(GR5423) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5423 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5423 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5423 gene encodes GR5423 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5423 precursor RNA folds spatially, forming GR5423 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5423 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5423 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5423 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2445 precursor RNA, GAM273340 precursor RNA and GAM277265 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2445 RNA, GAM273340 RNA and GAM277265 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2445 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2445 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2445 target RNA into GAM2445 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM273340 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM273340 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM273340 target RNA into GAM273340 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM277265 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM277265 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM277265 target RNA into GAM277265 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5423 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5423 gene: GAM2445 target protein, GAM273340 target protein and GAM277265 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2445, GAM273340 and GAM277265

GR5424 AV705453 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5424(GR5424) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5424 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5424 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5424 gene encodes GR5424 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5424 precursor RNA folds spatially, forming GR5424 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5424 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5424 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5424 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3

separate GAM precursor RNAs, GAM122650 precursor RNA, GAM301773 precursor RNA and GAM327232 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM122650 RNA, GAM301773 RNA and GAM327232 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM122650 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM122650 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM122650 target RNA into GAM122650 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM301773 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM301773 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM301773 target RNA into GAM301773 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM327232 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM327232 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM327232 target RNA into GAM327232 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5424 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5424 gene: GAM122650 target protein, GAM301773 target protein and GAM327232 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM122650, GAM301773 and GAM327232

GR5425 AW592820 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5425(GR5425) gene, which encodes an `operon-like` cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5425 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5425 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5425 gene encodes GR5425 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5425 precursor RNA folds spatially, forming GR5425 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5425 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5425 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5425 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM7564 precursor RNA, GAM34849 precursor RNA and GAM160514 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7564 RNA, GAM34849 RNA and GAM160514 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7564 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7564 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7564 target RNA into GAM7564 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM34849 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM34849 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM34849 target RNA into GAM34849 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM160514 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM160514 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM160514 target RNA into GAM160514 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5425 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5425 gene: GAM7564 target protein, GAM34849 target protein and GAM160514 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7564, GAM34849 and GAM160514

GR5426 BG473047 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5426(GR5426) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5426 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5426 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5426 gene encodes GR5426 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5426 precursor RNA folds spatially, forming GR5426 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5426 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5426 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5426 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3935 precursor RNA and GAM65355 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3935 RNA and GAM65355 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3935 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3935 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3935 target RNA into GAM3935 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM65355 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM65355 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM65355 target RNA into GAM65355 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5426 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5426 gene: GAM3935 target protein and GAM65355 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3935 and GAM65355

GR5427 N57674 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5427(GR5427) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5427 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5427 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5427 gene encodes GR5427 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5427 precursor RNA folds spatially, forming GR5427 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated

that GR5427 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5427 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5427 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM20499 precursor RNA and GAM127244 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM20499 RNA and GAM127244 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM20499 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM20499 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM20499 target RNA into GAM20499 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM127244 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM127244 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM127244 target RNA into GAM127244 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5427 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5427 gene: GAM20499 target protein and GAM127244 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM20499 and GAM127244

GR5428 BG614149 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5428(GR5428) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR5428 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5428 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5428 gene encodes GR5428 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5428 precursor RNA folds spatially, forming GR5428 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5428 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5428 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5428 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM117973 precursor RNA, GAM140386 precursor RNA and GAM315568 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM117973 RNA, GAM140386 RNA and GAM315568 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM117973 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM117973 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM117973 target RNA into GAM117973 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM140386 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM140386 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM140386 target RNA into GAM140386 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM315568 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM315568 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM315568 target RNA into GAM315568 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5428 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5428 gene: GAM117973 target protein, GAM140386 target protein and GAM315568 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM117973, GAM140386 and GAM315568

GR5429 BM460321 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5429(GR5429) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5429 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5429 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5429 gene encodes GR5429 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5429 precursor RNA folds spatially, forming GR5429 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5429 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5429 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5429 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM64963 precursor RNA and GAM335726 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM64963 RNA and GAM335726 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM64963 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM64963 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM64963 target RNA into GAM64963 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM335726 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM335726 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM335726 target RNA into GAM335726 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5429 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5429 gene: GAM64963 target protein and GAM335726 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM64963 and GAM335726

GR5430 AW812949 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5430(GR5430) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5430 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5430 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5430 gene encodes GR5430 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5430 precursor RNA folds spatially, forming GR5430 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5430 folded precursor RNA comprises a plurality of what is known in the

art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5430 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5430 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM8482 precursor RNA, GAM29327 precursor RNA and GAM240988 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8482 RNA, GAM29327 RNA and GAM240988 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8482 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8482 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8482 target RNA into GAM8482 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM29327 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM29327 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM29327 target RNA into GAM29327 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM240988 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM240988 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM240988 target RNA into GAM240988 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5430 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5430 gene: GAM8482 target protein, GAM29327 target protein and GAM240988 target protein, herein

schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8482, GAM29327 and GAM240988

GR5431 BI260821 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5431 (GR5431) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5431 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5431 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5431 gene encodes GR5431 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5431 precursor RNA folds spatially, forming GR5431 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5431 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5431 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5431 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM162473 precursor RNA and GAM195961 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM162473 RNA and GAM195961 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM162473 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM162473 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM162473 target RNA into GAM162473 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM195961 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM195961 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM195961 target RNA into GAM195961 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5431 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5431 gene: GAM162473 target protein and GAM195961 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM162473 and GAM195961

GR5432 W49534 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5432(GR5432) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5432 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5432 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5432 gene encodes GR5432 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5432 precursor RNA folds spatially, forming GR5432 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5432 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5432 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5432 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM109141 precursor RNA and GAM289906 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM109141 RNA and GAM289906 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM109141 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM109141 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM109141 target RNA into GAM109141 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM289906 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM289906 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM289906 target RNA into GAM289906 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5432 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5432 gene: GAM109141 target protein and GAM289906 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM109141 and GAM289906

GR5433 BM747745 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5433(GR5433) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5433 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5433 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5433 gene encodes GR5433 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5433 precursor RNA folds spatially, forming GR5433 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5433 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR5433 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5433 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM47638 precursor RNA and GAM199250 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM47638 RNA and GAM199250 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM47638 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM47638 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM47638 target RNA into GAM47638 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM199250 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM199250 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM199250 target RNA into GAM199250 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5433 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5433 gene: GAM47638 target protein and GAM199250 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM47638 and GAM199250

GR5434 BG774461 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5434(GR5434) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5434 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5434 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5434 gene encodes GR5434 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5434 precursor RNA folds spatially, forming GR5434 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5434 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5434 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5434 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM7417 precursor RNA, GAM64979 precursor RNA and GAM317609 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7417 RNA, GAM64979 RNA and GAM317609 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7417 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7417 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7417 target RNA into GAM7417 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM64979 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM64979 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM64979 target RNA into GAM64979 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM317609 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM317609 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM317609 target RNA into GAM317609 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5434 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5434 gene: GAM7417 target protein, GAM64979 target protein and GAM317609 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7417, GAM64979 and GAM317609

GR5435 H28949 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5435(GR5435) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5435 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5435 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5435 gene encodes GR5435 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5435 precursor RNA folds spatially, forming GR5435 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5435 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5435 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5435 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7055 precursor RNA and GAM233792 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM7055 RNA and GAM233792 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7055 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7055 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7055 target RNA into GAM7055 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM233792 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM233792 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM233792 target RNA into GAM233792 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5435 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5435 gene: GAM7055 target protein and GAM233792 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7055 and GAM233792

GR5436 BF510718 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5436(GR5436) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5436 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5436 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5436 gene encodes GR5436 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5436 precursor RNA folds spatially, forming GR5436 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5436 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5436 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5436 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1156 precursor RNA and GAM6866 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1156 RNA and GAM6866 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1156 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1156 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1156 target RNA into GAM1156 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6866 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6866 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6866 target RNA into GAM6866 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5436 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5436 gene: GAM1156 target protein and GAM6866 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1156 and GAM6866

GR5437 BG938672 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5437(GR5437) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5437 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5437 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5437 gene encodes GR5437 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5437 precursor RNA folds spatially, forming GR5437 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5437 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5437 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5437 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4204 precursor RNA and GAM131346 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4204 RNA and GAM131346 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4204 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4204 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4204 target RNA into GAM4204 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM131346 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM131346 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM131346 target RNA into GAM131346 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5437 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR5437 gene: GAM4204 target protein and GAM131346 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4204 and GAM131346

GR5438 BE794797 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5438(GR5438) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5438 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5438 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5438 gene encodes GR5438 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5438 precursor RNA folds spatially, forming GR5438 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5438 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5438 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5438 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM160820 precursor RNA and GAM239207 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM160820 RNA and GAM239207 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM160820 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM160820 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM160820 target RNA into GAM160820 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM239207 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM239207 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM239207 target RNA into GAM239207 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5438 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5438 gene: GAM160820 target protein and GAM239207 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM160820 and GAM239207

GR5439 BF976598 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5439(GR5439) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5439 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5439 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5439 gene encodes GR5439 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5439 precursor RNA folds spatially, forming GR5439 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5439 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5439 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5439 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3054 precursor RNA and GAM118867 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3054 RNA and GAM118867 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3054 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3054 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3054 target RNA into GAM3054 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM118867 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM118867 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM118867 target RNA into GAM118867 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5439 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5439 gene: GAM3054 target protein and GAM118867 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3054 and GAM118867

GR5440 BI085119 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5440(GR5440) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5440 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5440 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5440 gene encodes GR5440 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5440 precursor RNA folds spatially, forming GR5440 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5440 folded precursor RNA comprises a plurality of what is known in the

art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5440 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5440 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM35713 precursor RNA and GAM63599 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM35713 RNA and GAM63599 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM35713 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM35713 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM35713 target RNA into GAM35713 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM63599 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM63599 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM63599 target RNA into GAM63599 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5440 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5440 gene: GAM35713 target protein and GAM63599 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM35713 and GAM63599

GR5441 R38932 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5441 (GR5441) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR5441 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5441 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5441 gene encodes GR5441 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5441 precursor RNA folds spatially, forming GR5441 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5441 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5441 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5441 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1805 precursor RNA, GAM144112 precursor RNA and GAM248779 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1805 RNA, GAM144112 RNA and GAM248779 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1805 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1805 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1805 target RNA into GAM1805 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM144112 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM144112 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM144112 target RNA into GAM144112 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM248779 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM248779 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM248779 target RNA into GAM248779 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5441 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5441 gene: GAM1805 target protein, GAM144112 target protein and GAM248779 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1805, GAM144112 and GAM248779

GR5442 BE074770 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5442(GR5442) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5442 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5442 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5442 gene encodes GR5442 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5442 precursor RNA folds spatially, forming GR5442 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5442 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5442 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5442 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM120991 precursor RNA and GAM138219 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM120991 RNA and GAM138219 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM120991 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM120991 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM120991 target RNA into GAM120991 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM138219 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM138219 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM138219 target RNA into GAM138219 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5442 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5442 gene: GAM120991 target protein and GAM138219 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM120991 and GAM138219

GR5443 BQ003476 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5443(GR5443) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5443 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5443 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5443 gene encodes GR5443 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5443 precursor RNA folds spatially, forming GR5443 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5443 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR5443 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5443 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6167 precursor RNA and GAM7518 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6167 RNA and GAM7518 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6167 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6167 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6167 target RNA into GAM6167 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7518 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7518 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7518 target RNA into GAM7518 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5443 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5443 gene: GAM6167 target protein and GAM7518 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6167 and GAM7518

GR5444 AW014411 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5444(GR5444) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5444 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5444 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5444 gene encodes GR5444 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5444 precursor RNA folds spatially, forming GR5444 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5444 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5444 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5444 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM25592 precursor RNA and GAM193988 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM25592 RNA and GAM193988 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM25592 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM25592 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM25592 target RNA into GAM25592 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM193988 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM193988 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM193988 target RNA into GAM193988 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5444 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5444 gene: GAM25592 target protein and GAM193988 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM25592 and GAM193988

GR5445 N42421 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5445(GR5445) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5445 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5445 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5445 gene encodes GR5445 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5445 precursor RNA folds spatially, forming GR5445 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5445 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5445 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5445 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7747 precursor RNA and GAM53049 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7747 RNA and GAM53049 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7747 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7747 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7747 target RNA into

GAM7747 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM53049 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM53049 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM53049 target RNA into GAM53049 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5445 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5445 gene: GAM7747 target protein and GAM53049 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7747 and GAM53049

GR5446 AI860471 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5446(GR5446) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5446 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5446 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5446 gene encodes GR5446 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5446 precursor RNA folds spatially, forming GR5446 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5446 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5446 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5446 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2069 precursor RNA and GAM8087 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2069 RNA and GAM8087 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2069 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2069 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2069 target RNA into GAM2069 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8087 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8087 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8087 target RNA into GAM8087 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5446 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5446 gene: GAM2069 target protein and GAM8087 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2069 and GAM8087

GR5447 BM907982 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5447(GR5447) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5447 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5447 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5447 gene encodes GR5447 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5447 precursor RNA folds spatially, forming GR5447 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated

that GR5447 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5447 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5447 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM214001 precursor RNA and GAM266017 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM214001 RNA and GAM266017 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM214001 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM214001 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM214001 target RNA into GAM214001 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM266017 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM266017 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM266017 target RNA into GAM266017 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5447 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5447 gene: GAM214001 target protein and GAM266017 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM214001 and GAM266017

GR5448 BF240248 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5448(GR5448) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR5448 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5448 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5448 gene encodes GR5448 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5448 precursor RNA folds spatially, forming GR5448 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5448 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5448 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5448 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM568 precursor RNA and GAM166978 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM568 RNA and GAM166978 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM568 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM568 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM568 target RNA into GAM568 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM166978 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM166978 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM166978 target RNA into GAM166978 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5448 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5448 gene: GAM568 target protein and GAM166978 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM568 and GAM166978

GR5449 BM677834 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5449(GR5449) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5449 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5449 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5449 gene encodes GR5449 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5449 precursor RNA folds spatially, forming GR5449 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5449 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5449 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5449 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3583 precursor RNA and GAM252984 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3583 RNA and GAM252984 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3583 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3583 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds

to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3583 target RNA into GAM3583 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM252984 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM252984 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM252984 target RNA into GAM252984 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5449 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5449 gene: GAM3583 target protein and GAM252984 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3583 and GAM252984

GR5450 BG056457 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5450(GR5450) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5450 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5450 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5450 gene encodes GR5450 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5450 precursor RNA folds spatially, forming GR5450 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5450 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5450 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5450 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM13371 precursor RNA and GAM241093 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3

FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM13371 RNA and GAM241093 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM13371 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM13371 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM13371 target RNA into GAM13371 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM241093 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM241093 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM241093 target RNA into GAM241093 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5450 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5450 gene: GAM13371 target protein and GAM241093 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM13371 and GAM241093

GR5451 BF669050 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5451(GR5451) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5451 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5451 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5451 gene encodes GR5451 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5451 precursor RNA folds spatially, forming GR5451 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5451 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5451 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5451 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1399 precursor RNA and GAM5590 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1399 RNA and GAM5590 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1399 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1399 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1399 target RNA into GAM1399 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5590 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5590 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5590 target RNA into GAM5590 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5451 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5451 gene: GAM1399 target protein and GAM5590 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1399 and GAM5590

5452(GR5452) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5452 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5452 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5452 gene encodes GR5452 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5452 precursor RNA folds spatially, forming GR5452 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5452 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5452 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5452 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3273 precursor RNA and GAM178188 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3273 RNA and GAM178188 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3273 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3273 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3273 target RNA into GAM3273 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM178188 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM178188 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM178188 target RNA into GAM178188 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5452 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5452 gene: GAM3273 target protein and GAM178188 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3273 and GAM178188

GR5453 BM806263 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5453(GR5453) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5453 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5453 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5453 gene encodes GR5453 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5453 precursor RNA folds spatially, forming GR5453 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5453 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5453 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5453 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM53435 precursor RNA and GAM199633 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM53435 RNA and GAM199633 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM53435 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM53435 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM53435 target RNA into GAM53435 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM199633 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM199633 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM199633 target RNA into GAM199633 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5453 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5453 gene: GAM53435 target protein and GAM199633 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM53435 and GAM199633

GR5454 BF895204 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5454(GR5454) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5454 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5454 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5454 gene encodes GR5454 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5454 precursor RNA folds spatially, forming GR5454 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5454 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5454 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5454 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2

separate GAM precursor RNAs, GAM5133 precursor RNA and GAM6449 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5133 RNA and GAM6449 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5133 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5133 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5133 target RNA into GAM5133 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6449 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6449 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6449 target RNA into GAM6449 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5454 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5454 gene: GAM5133 target protein and GAM6449 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5133 and GAM6449

GR5455 AI005152 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5455 (GR5455) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5455 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5455 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5455 gene encodes GR5455 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR5455 precursor RNA folds spatially, forming GR5455 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5455 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5455 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5455 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM8541 precursor RNA, GAM235909 precursor RNA, GAM256284 precursor RNA and GAM330464 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8541 RNA, GAM235909 RNA, GAM256284 RNA and GAM330464 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8541 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8541 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8541 target RNA into GAM8541 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM235909 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM235909 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM235909 target RNA into GAM235909 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM256284 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM256284 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM256284 target RNA into GAM256284 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM330464 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM330464 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM330464 target RNA into GAM330464 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5455 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5455 gene: GAM8541 target protein, GAM235909 target protein, GAM256284 target protein and GAM330464 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8541, GAM235909, GAM256284 and GAM330464

GR5456 BI860310 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5456(GR5456) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5456 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5456 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5456 gene encodes GR5456 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5456 precursor RNA folds spatially, forming GR5456 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5456 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5456 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5456 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1821 precursor RNA, GAM7368 precursor RNA and GAM71916 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1821 RNA, GAM7368 RNA and GAM71916 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1821 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1821 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1821 target RNA into GAM1821 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7368 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7368 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7368 target RNA into GAM7368 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM71916 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM71916 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM71916 target RNA into GAM71916 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5456 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5456 gene: GAM1821 target protein, GAM7368 target protein and GAM71916 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1821, GAM7368 and GAM71916

GR5457 AL708470 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5457(GR5457) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5457 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5457

gene was detected is described hereinabove with reference to Figs. 8-18.

GR5457 gene encodes GR5457 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5457 precursor RNA folds spatially, forming GR5457 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5457 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5457 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5457 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2147 precursor RNA and GAM2169 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2147 RNA and GAM2169 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2147 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2147 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2147 target RNA into GAM2147 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM2169 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2169 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2169 target RNA into GAM2169 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5457 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5457 gene: GAM2147 target protein and GAM2169 target protein, herein schematically represented by GAM1

TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2147 and GAM2169

GR5458 BQ059911 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5458(GR5458) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5458 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5458 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5458 gene encodes GR5458 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5458 precursor RNA folds spatially, forming GR5458 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5458 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5458 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5458 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM99357 precursor RNA, GAM128961 precursor RNA and GAM265093 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM99357 RNA, GAM128961 RNA and GAM265093 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM99357 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM99357 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM99357 target RNA into GAM99357 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM128961 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM128961 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM128961 target RNA into GAM128961 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM265093 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM265093 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM265093 target RNA into GAM265093 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5458 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5458 gene: GAM99357 target protein, GAM128961 target protein and GAM265093 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM99357, GAM128961 and GAM265093

GR5459 T05265 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5459(GR5459) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5459 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5459 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5459 gene encodes GR5459 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5459 precursor RNA folds spatially, forming GR5459 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5459 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5459 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5459 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1610 precursor RNA, GAM98580 precursor RNA and GAM208300 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1610 RNA, GAM98580 RNA and GAM208300 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1610 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1610 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1610 target RNA into GAM1610 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM98580 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM98580 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM98580 target RNA into GAM98580 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM208300 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM208300 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM208300 target RNA into GAM208300 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5459 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5459 gene: GAM1610 target protein, GAM98580 target protein and GAM208300 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1610, GAM98580 and GAM208300

GR5460 BF312915 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5460(GR5460) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5460 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5460 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5460 gene encodes GR5460 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5460 precursor RNA folds spatially, forming GR5460 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5460 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5460 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5460 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM56482 precursor RNA, GAM277393 precursor RNA, GAM285636 precursor RNA and GAM316976 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM56482 RNA, GAM277393 RNA, GAM285636 RNA and GAM316976 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM56482 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM56482 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM56482 target RNA into GAM56482 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM277393 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM277393 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM277393 target RNA into GAM277393 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM285636 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM285636 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM285636 target RNA into GAM285636 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM316976 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM316976 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM316976 target RNA into GAM316976 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5460 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5460 gene: GAM56482 target protein, GAM277393 target protein, GAM285636 target protein and GAM316976 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM56482, GAM277393, GAM285636 and GAM316976

GR5461 BE541866 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5461 (GR5461) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5461 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5461 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5461 gene encodes GR5461 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5461 precursor RNA folds spatially, forming GR5461 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5461 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR5461 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5461 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4458 precursor RNA and GAM125712 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4458 RNA and GAM125712 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4458 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4458 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4458 target RNA into GAM4458 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM125712 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM125712 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM125712 target RNA into GAM125712 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5461 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5461 gene: GAM4458 target protein and GAM125712 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4458 and GAM125712

GR5462 BG436913 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5462(GR5462) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5462 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5462 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5462 gene encodes GR5462 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5462 precursor RNA folds spatially, forming GR5462 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5462 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5462 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5462 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM148167 precursor RNA and GAM219827 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM148167 RNA and GAM219827 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM148167 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM148167 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM148167 target RNA into GAM148167 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM219827 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM219827 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM219827 target RNA into GAM219827 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5462 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5462 gene: GAM148167 target protein and GAM219827 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM148167 and GAM219827

GR5463 BG236326 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5463(GR5463) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5463 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5463 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5463 gene encodes GR5463 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5463 precursor RNA folds spatially, forming GR5463 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5463 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5463 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5463 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM42551 precursor RNA and GAM220993 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM42551 RNA and GAM220993 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM42551 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM42551 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM42551

target RNA into GAM42551 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM220993 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM220993 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM220993 target RNA into GAM220993 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5463 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5463 gene: GAM42551 target protein and GAM220993 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM42551 and GAM220993

GR5464 BM044666 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5464(GR5464) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5464 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5464 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5464 gene encodes GR5464 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5464 precursor RNA folds spatially, forming GR5464 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5464 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5464 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5464 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM337 precursor RNA, GAM121400 precursor RNA and GAM218789 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED

PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM337 RNA, GAM121400 RNA and GAM218789 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM337 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM337 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM337 target RNA into GAM337 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM121400 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM121400 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM121400 target RNA into GAM121400 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM218789 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM218789 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM218789 target RNA into GAM218789 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5464 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5464 gene: GAM337 target protein, GAM121400 target protein and GAM218789 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM337, GAM121400 and GAM218789

GR5465 AU131401 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5465(GR5465) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5465 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5465 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5465 gene encodes GR5465 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5465 precursor RNA folds spatially, forming GR5465 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5465 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5465 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5465 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1317 precursor RNA, GAM4241 precursor RNA and GAM88382 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1317 RNA, GAM4241 RNA and GAM88382 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1317 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1317 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1317 target RNA into GAM1317 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM4241 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4241 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4241 target RNA into GAM4241 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM88382 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM88382 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM88382 target RNA into GAM88382 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5465 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5465 gene: GAM1317 target protein, GAM4241 target protein and GAM88382 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1317, GAM4241 and GAM88382

GR5466 BF751266 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5466(GR5466) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5466 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5466 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5466 gene encodes GR5466 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5466 precursor RNA folds spatially, forming GR5466 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5466 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5466 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5466 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1562 precursor RNA and GAM2045 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1562 RNA and GAM2045 RNA, herein schematically

represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1562 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1562 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1562 target RNA into GAM1562 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM2045 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2045 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2045 target RNA into GAM2045 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5466 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5466 gene: GAM1562 target protein and GAM2045 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1562 and GAM2045

GR5467 BQ001363 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5467(GR5467) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5467 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5467 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5467 gene encodes GR5467 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5467 precursor RNA folds spatially, forming GR5467 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5467 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5467 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5467 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM75009 precursor RNA and GAM98482 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM75009 RNA and GAM98482 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM75009 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM75009 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM75009 target RNA into GAM75009 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM98482 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM98482 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM98482 target RNA into GAM98482 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5467 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5467 gene: GAM75009 target protein and GAM98482 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM75009 and GAM98482

GR5468 T84986 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5468(GR5468) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5468 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR5468 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5468 gene encodes GR5468 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5468 precursor RNA folds spatially, forming GR5468 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5468 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5468 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5468 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5051 precursor RNA and GAM143003 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5051 RNA and GAM143003 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5051 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5051 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5051 target RNA into GAM5051 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM143003 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM143003 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM143003 target RNA into GAM143003 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5468 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5468 gene: GAM5051 target

protein and GAM143003 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5051 and GAM143003

GR5469 AI432322 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5469(GR5469) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5469 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5469 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5469 gene encodes GR5469 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5469 precursor RNA folds spatially, forming GR5469 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5469 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5469 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5469 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM94319 precursor RNA and GAM280852 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM94319 RNA and GAM280852 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM94319 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM94319 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM94319 target RNA into GAM94319 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM280852 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM280852 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM280852 target RNA into GAM280852 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5469 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5469 gene: GAM94319 target protein and GAM280852 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM94319 and GAM280852

GR5470 AW276019 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5470(GR5470) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5470 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5470 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5470 gene encodes GR5470 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5470 precursor RNA folds spatially, forming GR5470 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5470 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5470 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5470 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4562 precursor RNA and GAM240262 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4562 RNA and GAM240262 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4562 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4562 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4562 target RNA into GAM4562 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM240262 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM240262 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM240262 target RNA into GAM240262 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5470 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5470 gene: GAM4562 target protein and GAM240262 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4562 and GAM240262

GR5471 BI818183 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5471(GR5471) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5471 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5471 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5471 gene encodes GR5471 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5471 precursor RNA folds spatially, forming GR5471 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5471 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR5471 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5471 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM212262 precursor RNA, GAM215854 precursor RNA and GAM287188 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM212262 RNA, GAM215854 RNA and GAM287188 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM212262 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM212262 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM212262 target RNA into GAM212262 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM215854 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM215854 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM215854 target RNA into GAM215854 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM287188 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM287188 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM287188 target RNA into GAM287188 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5471 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5471 gene: GAM212262 target protein, GAM215854 target protein and GAM287188 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN.

The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM212262, GAM215854 and GAM287188

GR5472 H16762 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5472(GR5472) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5472 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5472 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5472 gene encodes GR5472 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5472 precursor RNA folds spatially, forming GR5472 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5472 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5472 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5472 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1700 precursor RNA and GAM206973 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1700 RNA and GAM206973 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1700 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1700 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1700 target RNA into GAM1700 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM206973 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM206973 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM206973 target RNA into GAM206973 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5472 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5472 gene: GAM1700 target protein and GAM206973 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1700 and GAM206973

GR5473 BG574640 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5473(GR5473) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5473 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5473 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5473 gene encodes GR5473 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5473 precursor RNA folds spatially, forming GR5473 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5473 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5473 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5473 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM119812 precursor RNA and GAM276010 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM119812 RNA and GAM276010 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM119812 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM119812 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM119812 target RNA into GAM119812 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM276010 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM276010 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM276010 target RNA into GAM276010 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5473 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5473 gene: GAM119812 target protein and GAM276010 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM119812 and GAM276010

GR5474 BE260786 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5474(GR5474) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5474 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5474 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5474 gene encodes GR5474 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5474 precursor RNA folds spatially, forming GR5474 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5474 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5474 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5474 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM86847 precursor RNA and GAM104964 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM86847 RNA and GAM104964 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM86847 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM86847 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM86847 target RNA into GAM86847 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM104964 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM104964 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM104964 target RNA into GAM104964 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5474 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5474 gene: GAM86847 target protein and GAM104964 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM86847 and GAM104964

GR5475 BF735674 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5475(GR5475) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5475 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5475 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5475 gene encodes GR5475 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5475 precursor RNA folds spatially, forming GR5475 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5475 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5475 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5475 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM31716 precursor RNA and GAM224689 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM31716 RNA and GAM224689 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM31716 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM31716 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM31716 target RNA into GAM31716 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM224689 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM224689 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM224689 target RNA into GAM224689 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5475 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR5475 gene: GAM31716 target protein and GAM224689 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM31716 and GAM224689

GR5476 BF912366 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5476(GR5476) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5476 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5476 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5476 gene encodes GR5476 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5476 precursor RNA folds spatially, forming GR5476 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5476 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5476 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5476 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1031 precursor RNA and GAM63441 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1031 RNA and GAM63441 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1031 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1031 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1031 target RNA into GAM1031 target protein, herein schematically represented by GAM1 TARGET

PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM63441 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM63441 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM63441 target RNA into GAM63441 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5476 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5476 gene: GAM1031 target protein and GAM63441 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1031 and GAM63441

GR5477 BI011009 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5477(GR5477) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5477 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5477 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5477 gene encodes GR5477 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5477 precursor RNA folds spatially, forming GR5477 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5477 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5477 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5477 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM6285 precursor RNA, GAM6717 precursor RNA and GAM7517 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6285 RNA, GAM6717 RNA and GAM7517 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6285 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6285 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6285 target RNA into GAM6285 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6717 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6717 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6717 target RNA into GAM6717 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7517 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7517 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7517 target RNA into GAM7517 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5477 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5477 gene: GAM6285 target protein, GAM6717 target protein and GAM7517 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6285, GAM6717 and GAM7517

GR5478 BE778106 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5478(GR5478) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5478 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR5478 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5478 gene encodes GR5478 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5478 precursor RNA folds spatially, forming GR5478 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5478 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5478 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5478 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM172772 precursor RNA and GAM275245 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM172772 RNA and GAM275245 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM172772 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM172772 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM172772 target RNA into GAM172772 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM275245 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM275245 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM275245 target RNA into GAM275245 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5478 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5478 gene: GAM172772 target

protein and GAM275245 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM172772 and GAM275245

GR5479 AA456448 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5479(GR5479) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5479 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5479 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5479 gene encodes GR5479 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5479 precursor RNA folds spatially, forming GR5479 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5479 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5479 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5479 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3652 precursor RNA and GAM5156 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3652 RNA and GAM5156 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3652 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3652 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3652 target RNA into GAM3652 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5156 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5156 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5156 target RNA into GAM5156 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5479 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5479 gene: GAM3652 target protein and GAM5156 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3652 and GAM5156

GR5480 AA883866 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5480(GR5480) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5480 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5480 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5480 gene encodes GR5480 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5480 precursor RNA folds spatially, forming GR5480 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5480 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5480 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5480 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2451 precursor RNA, GAM8413 precursor RNA and GAM106305 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2451 RNA, GAM8413 RNA and GAM106305 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2451 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2451 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2451 target RNA into GAM2451 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8413 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8413 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8413 target RNA into GAM8413 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM106305 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM106305 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM106305 target RNA into GAM106305 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5480 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5480 gene: GAM2451 target protein, GAM8413 target protein and GAM106305 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2451, GAM8413 and GAM106305

GR5481 BE538051 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5481(GR5481) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5481 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5481

gene was detected is described hereinabove with reference to Figs. 8-18.

GR5481 gene encodes GR5481 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5481 precursor RNA folds spatially, forming GR5481 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5481 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5481 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5481 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM33458 precursor RNA and GAM66442 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM33458 RNA and GAM66442 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM33458 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM33458 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM33458 target RNA into GAM33458 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM66442 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM66442 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM66442 target RNA into GAM66442 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5481 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5481 gene: GAM33458 target protein and GAM66442 target protein, herein schematically represented by GAM1

TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM33458 and GAM66442

GR5482 AW594008 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5482(GR5482) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5482 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5482 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5482 gene encodes GR5482 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5482 precursor RNA folds spatially, forming GR5482 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5482 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5482 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5482 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8709 precursor RNA and GAM283377 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8709 RNA and GAM283377 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8709 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8709 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8709 target RNA into GAM8709 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM283377 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM283377 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM283377 target RNA into GAM283377 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5482 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5482 gene: GAM8709 target protein and GAM283377 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8709 and GAM283377

GR5483 BF572821 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5483(GR5483) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5483 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5483 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5483 gene encodes GR5483 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5483 precursor RNA folds spatially, forming GR5483 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5483 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5483 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5483 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM119027 precursor RNA, GAM219702 precursor RNA and GAM257377 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM119027 RNA, GAM219702 RNA and GAM257377 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM119027 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM119027 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM119027 target RNA into GAM119027 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM219702 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM219702 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM219702 target RNA into GAM219702 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM257377 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM257377 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM257377 target RNA into GAM257377 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5483 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5483 gene: GAM119027 target protein, GAM219702 target protein and GAM257377 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM119027, GAM219702 and GAM257377

GR5484 AW262838 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5484(GR5484) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5484 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5484 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5484 gene encodes GR5484 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5484 precursor RNA folds spatially, forming GR5484 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5484 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5484 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5484 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3307 precursor RNA and GAM134680 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3307 RNA and GAM134680 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3307 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3307 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3307 target RNA into GAM3307 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM134680 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM134680 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM134680 target RNA into GAM134680 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5484 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5484 gene: GAM3307 target protein and GAM134680 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes

is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3307 and GAM134680

GR5485 BI767235 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5485(GR5485) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5485 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5485 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5485 gene encodes GR5485 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5485 precursor RNA folds spatially, forming GR5485 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5485 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5485 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5485 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM149382 precursor RNA and GAM257938 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM149382 RNA and GAM257938 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM149382 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM149382 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM149382 target RNA into GAM149382 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM257938 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM257938 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM257938 target RNA into GAM257938 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5485 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5485 gene: GAM149382 target protein and GAM257938 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM149382 and GAM257938

GR5486 BG105409 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5486(GR5486) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5486 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5486 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5486 gene encodes GR5486 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5486 precursor RNA folds spatially, forming GR5486 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5486 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5486 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5486 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5129 precursor RNA and GAM187345 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5129 RNA and GAM187345 RNA, herein schematically

represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5129 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5129 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5129 target RNA into GAM5129 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM187345 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM187345 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM187345 target RNA into GAM187345 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5486 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5486 gene: GAM5129 target protein and GAM187345 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5129 and GAM187345

GR5487 BG034034 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5487(GR5487) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5487 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5487 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5487 gene encodes GR5487 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5487 precursor RNA folds spatially, forming GR5487 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5487 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5487 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5487 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM4639 precursor RNA, GAM26298 precursor RNA, GAM134373 precursor RNA and GAM209896 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4639 RNA, GAM26298 RNA, GAM134373 RNA and GAM209896 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4639 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4639 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4639 target RNA into GAM4639 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM26298 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM26298 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM26298 target RNA into GAM26298 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM134373 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM134373 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM134373 target RNA into GAM134373 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM209896 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM209896 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM209896 target RNA into GAM209896 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5487 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5487 gene: GAM4639 target protein, GAM26298 target protein, GAM134373 target protein and GAM209896 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4639, GAM26298, GAM134373 and GAM209896

GR5488 BF764373 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5488(GR5488) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5488 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5488 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5488 gene encodes GR5488 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5488 precursor RNA folds spatially, forming GR5488 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5488 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5488 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5488 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM165062 precursor RNA, GAM172095 precursor RNA and GAM263524 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM165062 RNA, GAM172095 RNA and GAM263524 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM165062 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM165062 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM165062 target RNA into GAM165062 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM172095 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM172095 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM172095 target RNA into GAM172095 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM263524 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM263524 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM263524 target RNA into GAM263524 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5488 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5488 gene: GAM165062 target protein, GAM172095 target protein and GAM263524 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM165062, GAM172095 and GAM263524

GR5489 BF896282 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5489(GR5489) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5489 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5489 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5489 gene encodes GR5489 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5489 precursor RNA folds spatially, forming GR5489 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated

that GR5489 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5489 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5489 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2083 precursor RNA, GAM62099 precursor RNA and GAM113411 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2083 RNA, GAM62099 RNA and GAM113411 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2083 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2083 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2083 target RNA into GAM2083 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM62099 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM62099 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM62099 target RNA into GAM62099 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM113411 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM113411 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM113411 target RNA into GAM113411 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5489 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5489 gene: GAM2083 target

protein, GAM62099 target protein and GAM113411 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2083, GAM62099 and GAM113411

GR5490 BM822968 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5490(GR5490) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5490 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5490 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5490 gene encodes GR5490 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5490 precursor RNA folds spatially, forming GR5490 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5490 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5490 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5490 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM3029 precursor RNA, GAM178432 precursor RNA, GAM256376 precursor RNA and GAM260045 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3029 RNA, GAM178432 RNA, GAM256376 RNA and GAM260045 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3029 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3029 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3029 target RNA into

GAM3029 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM178432 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM178432 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM178432 target RNA into GAM178432 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM256376 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM256376 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM256376 target RNA into GAM256376 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM260045 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM260045 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM260045 target RNA into GAM260045 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5490 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5490 gene: GAM3029 target protein, GAM178432 target protein, GAM256376 target protein and GAM260045 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3029, GAM178432, GAM256376 and GAM260045

GR5491 AA129800 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5491 (GR5491) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5491 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5491 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5491 gene encodes GR5491 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR5491 precursor RNA folds spatially, forming GR5491 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5491 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5491 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5491 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM65663 precursor RNA, GAM77505 precursor RNA and GAM290943 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM65663 RNA, GAM77505 RNA and GAM290943 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM65663 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM65663 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM65663 target RNA into GAM65663 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM77505 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM77505 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM77505 target RNA into GAM77505 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM290943 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM290943 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM290943 target RNA into GAM290943 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5491 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5491 gene: GAM65663 target protein, GAM77505 target protein and GAM290943 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM65663, GAM77505 and GAM290943

GR5492 AW959487 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5492(GR5492) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5492 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5492 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5492 gene encodes GR5492 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5492 precursor RNA folds spatially, forming GR5492 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5492 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5492 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5492 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM316 precursor RNA, GAM2385 precursor RNA and GAM63873 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM316 RNA, GAM2385 RNA and GAM63873 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM316 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM316 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM316 target RNA into GAM316 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM2385 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2385 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2385 target RNA into GAM2385 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM63873 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM63873 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM63873 target RNA into GAM63873 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5492 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5492 gene: GAM316 target protein, GAM2385 target protein and GAM63873 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM316, GAM2385 and GAM63873

GR5493 BG114529 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5493(GR5493) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5493 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5493 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5493 gene encodes GR5493 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5493 precursor RNA folds spatially, forming GR5493 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated

that GR5493 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5493 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5493 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM39735 precursor RNA and GAM285936 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM39735 RNA and GAM285936 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM39735 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM39735 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM39735 target RNA into GAM39735 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM285936 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM285936 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM285936 target RNA into GAM285936 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5493 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5493 gene: GAM39735 target protein and GAM285936 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM39735 and GAM285936

GR5494 BG432537 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5494(GR5494) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR5494 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5494 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5494 gene encodes GR5494 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5494 precursor RNA folds spatially, forming GR5494 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5494 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5494 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5494 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM85687 precursor RNA and GAM316576 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM85687 RNA and GAM316576 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM85687 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM85687 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM85687 target RNA into GAM85687 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM316576 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM316576 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM316576 target RNA into GAM316576 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5494 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5494 gene: GAM85687 target protein and GAM316576 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM85687 and GAM316576

GR5495 AW992912 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5495(GR5495) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5495 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5495 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5495 gene encodes GR5495 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5495 precursor RNA folds spatially, forming GR5495 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5495 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5495 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5495 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM274807 precursor RNA and GAM317493 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM274807 RNA and GAM317493 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM274807 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM274807 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM274807 target RNA into GAM274807 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM317493 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM317493 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM317493 target RNA into GAM317493 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5495 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5495 gene: GAM274807 target protein and GAM317493 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM274807 and GAM317493

GR5496 AW238078 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5496(GR5496) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5496 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5496 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5496 gene encodes GR5496 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5496 precursor RNA folds spatially, forming GR5496 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5496 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5496 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5496 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3253 precursor RNA and GAM221840 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3

FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3253 RNA and GAM221840 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3253 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3253 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3253 target RNA into GAM3253 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM221840 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM221840 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM221840 target RNA into GAM221840 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5496 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5496 gene: GAM3253 target protein and GAM221840 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3253 and GAM221840

GR5497 AW674293 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5497(GR5497) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5497 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5497 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5497 gene encodes GR5497 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5497 precursor RNA folds spatially, forming GR5497 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5497 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5497 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5497 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM97033 precursor RNA and GAM167212 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM97033 RNA and GAM167212 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM97033 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM97033 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM97033 target RNA into GAM97033 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM167212 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM167212 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM167212 target RNA into GAM167212 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5497 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5497 gene: GAM97033 target protein and GAM167212 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM97033 and GAM167212

5498(GR5498) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5498 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5498 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5498 gene encodes GR5498 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5498 precursor RNA folds spatially, forming GR5498 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5498 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5498 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5498 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM1254 precursor RNA, GAM14989 precursor RNA, GAM35336 precursor RNA and GAM81132 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1254 RNA, GAM14989 RNA, GAM35336 RNA and GAM81132 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1254 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1254 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1254 target RNA into GAM1254 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM14989 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM14989 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM14989

target RNA into GAM14989 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM35336 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM35336 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM35336 target RNA into GAM35336 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM81132 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM81132 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM81132 target RNA into GAM81132 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5498 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5498 gene: GAM1254 target protein, GAM14989 target protein, GAM35336 target protein and GAM81132 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1254, GAM14989, GAM35336 and GAM81132

GR5499 BM051608 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5499(GR5499) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5499 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5499 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5499 gene encodes GR5499 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5499 precursor RNA folds spatially, forming GR5499 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5499 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5499 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5499 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM207937 precursor RNA and GAM243612 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM207937 RNA and GAM243612 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM207937 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM207937 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM207937 target RNA into GAM207937 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM243612 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM243612 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM243612 target RNA into GAM243612 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5499 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5499 gene: GAM207937 target protein and GAM243612 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM207937 and GAM243612

GR5500 BM803032 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5500(GR5500) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5500 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR5500 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5500 gene encodes GR5500 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5500 precursor RNA folds spatially, forming GR5500 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5500 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5500 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5500 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM19710 precursor RNA and GAM109885 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM19710 RNA and GAM109885 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM19710 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM19710 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM19710 target RNA into GAM19710 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM109885 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM109885 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM109885 target RNA into GAM109885 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5500 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5500 gene: GAM19710 target

protein and GAM109885 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM19710 and GAM109885

GR5501 AA846850 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5501 (GR5501) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5501 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5501 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5501 gene encodes GR5501 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5501 precursor RNA folds spatially, forming GR5501 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5501 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5501 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5501 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6471 precursor RNA and GAM263996 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6471 RNA and GAM263996 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6471 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6471 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6471 target RNA into GAM6471 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM263996 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM263996 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM263996 target RNA into GAM263996 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5501 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5501 gene: GAM6471 target protein and GAM263996 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6471 and GAM263996

GR5502 AI908602 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5502(GR5502) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5502 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5502 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5502 gene encodes GR5502 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5502 precursor RNA folds spatially, forming GR5502 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5502 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5502 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5502 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1178 precursor RNA and GAM111884 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1178 RNA and GAM11884 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1178 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1178 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1178 target RNA into GAM1178 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM11884 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM11884 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM11884 target RNA into GAM11884 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5502 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5502 gene: GAM1178 target protein and GAM11884 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1178 and GAM11884

GR5503 AI682254 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5503(GR5503) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5503 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5503 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5503 gene encodes GR5503 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5503 precursor RNA folds spatially, forming GR5503 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5503 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR5503 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5503 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM61689 precursor RNA, GAM113512 precursor RNA and GAM118720 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM61689 RNA, GAM113512 RNA and GAM118720 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM61689 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM61689 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM61689 target RNA into GAM61689 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM113512 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM113512 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM113512 target RNA into GAM113512 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM118720 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM118720 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM118720 target RNA into GAM118720 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5503 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5503 gene: GAM61689 target protein, GAM113512 target protein and GAM118720 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN.

The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM61689, GAM113512 and GAM118720

GR5504 BI825034 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5504(GR5504) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5504 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5504 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5504 gene encodes GR5504 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5504 precursor RNA folds spatially, forming GR5504 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5504 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5504 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5504 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM191690 precursor RNA and GAM256845 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM191690 RNA and GAM256845 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM191690 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM191690 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM191690 target RNA into GAM191690 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM256845 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM256845 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM256845 target RNA into GAM256845 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5504 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5504 gene: GAM191690 target protein and GAM256845 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM191690 and GAM256845

GR5505 AV726476 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5505(GR5505) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5505 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5505 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5505 gene encodes GR5505 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5505 precursor RNA folds spatially, forming GR5505 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5505 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5505 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5505 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM65 precursor RNA and GAM4445 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM65 RNA and GAM4445 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM65 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM65 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM65 target RNA into GAM65 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM4445 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4445 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4445 target RNA into GAM4445 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5505 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5505 gene: GAM65 target protein and GAM4445 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM65 and GAM4445

GR5506 AU138709 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5506(GR5506) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5506 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5506 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5506 gene encodes GR5506 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5506 precursor RNA folds spatially, forming GR5506 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5506 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5506 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5506 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM865 precursor RNA and GAM158299 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM865 RNA and GAM158299 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM865 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM865 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM865 target RNA into GAM865 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM158299 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM158299 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM158299 target RNA into GAM158299 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5506 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5506 gene: GAM865 target protein and GAM158299 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM865 and GAM158299

GR5507 BI031884 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5507(GR5507) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5507 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5507 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5507 gene encodes GR5507 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5507 precursor RNA folds spatially, forming GR5507 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5507 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5507 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5507 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM19987 precursor RNA and GAM333549 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM19987 RNA and GAM333549 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM19987 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM19987 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM19987 target RNA into GAM19987 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM333549 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM333549 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM333549 target RNA into GAM333549 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5507 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR5507 gene: GAM19987 target protein and GAM333549 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM19987 and GAM333549

GR5508 BF526671 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5508(GR5508) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5508 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5508 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5508 gene encodes GR5508 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5508 precursor RNA folds spatially, forming GR5508 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5508 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5508 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5508 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM11259 precursor RNA and GAM294947 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM11259 RNA and GAM294947 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM11259 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM11259 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM11259 target RNA into GAM11259 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM294947 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM294947 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM294947 target RNA into GAM294947 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5508 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5508 gene: GAM11259 target protein and GAM294947 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM11259 and GAM294947

GR5509 BF947013 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5509(GR5509) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5509 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5509 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5509 gene encodes GR5509 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5509 precursor RNA folds spatially, forming GR5509 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5509 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5509 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5509 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM58477 precursor RNA and GAM314534 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM58477 RNA and GAM314534 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM58477 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM58477 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM58477 target RNA into GAM58477 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM314534 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM314534 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM314534 target RNA into GAM314534 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5509 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5509 gene: GAM58477 target protein and GAM314534 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM58477 and GAM314534

GR5510 BI493075 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5510(GR5510) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5510 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5510 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5510 gene encodes GR5510 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5510 precursor RNA folds spatially, forming GR5510 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5510 folded precursor RNA comprises a plurality of what is known in the

art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5510 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5510 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7149 precursor RNA and GAM85080 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7149 RNA and GAM85080 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7149 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7149 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7149 target RNA into GAM7149 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM85080 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM85080 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM85080 target RNA into GAM85080 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5510 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5510 gene: GAM7149 target protein and GAM85080 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7149 and GAM85080

GR5511 AA699873 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5511(GR5511) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR5511 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5511 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5511 gene encodes GR5511 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5511 precursor RNA folds spatially, forming GR5511 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5511 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5511 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5511 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM181270 precursor RNA and GAM286419 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM181270 RNA and GAM286419 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM181270 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM181270 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM181270 target RNA into GAM181270 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM286419 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM286419 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM286419 target RNA into GAM286419 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly

utilities, of GR5511 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5511 gene: GAM181270 target protein and GAM286419 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM181270 and GAM286419

GR5512 AU117726 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5512(GR5512) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5512 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5512 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5512 gene encodes GR5512 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5512 precursor RNA folds spatially, forming GR5512 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5512 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5512 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5512 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM153729 precursor RNA and GAM248284 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM153729 RNA and GAM248284 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM153729 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM153729 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM153729 target RNA into GAM153729 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM248284 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM248284 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM248284 target RNA into GAM248284 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5512 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5512 gene: GAM153729 target protein and GAM248284 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM153729 and GAM248284

GR5513 BI836973 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5513(GR5513) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5513 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5513 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5513 gene encodes GR5513 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5513 precursor RNA folds spatially, forming GR5513 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5513 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5513 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5513 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3765 precursor RNA, GAM129433 precursor RNA and GAM23887 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded

precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3765 RNA, GAM129433 RNA and GAM238887 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3765 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3765 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3765 target RNA into GAM3765 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM129433 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM129433 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM129433 target RNA into GAM129433 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM238887 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM238887 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM238887 target RNA into GAM238887 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5513 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5513 gene: GAM3765 target protein, GAM129433 target protein and GAM238887 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3765, GAM129433 and GAM238887

GR5514 AV718145 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5514(GR5514) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5514 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5514 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5514 gene encodes GR5514 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5514 precursor RNA folds spatially, forming GR5514 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5514 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5514 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5514 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM163716 precursor RNA and GAM247274 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM163716 RNA and GAM247274 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM163716 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM163716 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM163716 target RNA into GAM163716 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM247274 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM247274 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM247274 target RNA into GAM247274 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5514 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5514 gene: GAM163716 target protein and GAM247274 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM163716 and GAM247274

GR5515 BM785509 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5515(GR5515) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5515 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5515 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5515 gene encodes GR5515 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5515 precursor RNA folds spatially, forming GR5515 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5515 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5515 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5515 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM78800 precursor RNA and GAM217728 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM78800 RNA and GAM217728 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM78800 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM78800 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM78800

target RNA into GAM78800 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM217728 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM217728 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM217728 target RNA into GAM217728 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5515 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5515 gene: GAM78800 target protein and GAM217728 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM78800 and GAM217728

GR5516 BE281643 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5516(GR5516) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5516 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5516 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5516 gene encodes GR5516 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5516 precursor RNA folds spatially, forming GR5516 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5516 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5516 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5516 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4196 precursor RNA and GAM211714 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4196 RNA and GAM211714 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4196 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4196 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4196 target RNA into GAM4196 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM211714 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM211714 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM211714 target RNA into GAM211714 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5516 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5516 gene: GAM4196 target protein and GAM211714 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4196 and GAM211714

GR5517 BM263470 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5517(GR5517) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5517 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5517 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5517 gene encodes GR5517 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5517 precursor RNA folds spatially, forming GR5517 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated

that GR5517 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5517 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5517 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM37360 precursor RNA and GAM263346 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM37360 RNA and GAM263346 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM37360 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM37360 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM37360 target RNA into GAM37360 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM263346 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM263346 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM263346 target RNA into GAM263346 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5517 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5517 gene: GAM37360 target protein and GAM263346 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM37360 and GAM263346

GR5518 AI763167 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5518(GR5518) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR5518 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5518 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5518 gene encodes GR5518 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5518 precursor RNA folds spatially, forming GR5518 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5518 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5518 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5518 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1890 precursor RNA and GAM220973 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1890 RNA and GAM220973 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1890 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1890 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1890 target RNA into GAM1890 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM220973 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM220973 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM220973 target RNA into GAM220973 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5518 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5518 gene: GAM1890 target protein and GAM220973 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1890 and GAM220973

GR5519 AW188463 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5519 (GR5519) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5519 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5519 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5519 gene encodes GR5519 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5519 precursor RNA folds spatially, forming GR5519 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5519 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5519 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5519 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM20488 precursor RNA and GAM44062 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM20488 RNA and GAM44062 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM20488 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM20488 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM20488 target RNA into GAM20488 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM44062 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM44062 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM44062 target RNA into GAM44062 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5519 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5519 gene: GAM20488 target protein and GAM44062 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM20488 and GAM44062

GR5520 BI335062 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5520(GR5520) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5520 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5520 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5520 gene encodes GR5520 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5520 precursor RNA folds spatially, forming GR5520 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5520 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5520 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5520 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5739 precursor RNA and GAM264138 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3

FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5739 RNA and GAM264138 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5739 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5739 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5739 target RNA into GAM5739 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM264138 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM264138 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM264138 target RNA into GAM264138 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5520 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5520 gene: GAM5739 target protein and GAM264138 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5739 and GAM264138

GR5521 BE222715 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5521 (GR5521) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5521 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5521 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5521 gene encodes GR5521 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5521 precursor RNA folds spatially, forming GR5521 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5521 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5521 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5521 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM187375 precursor RNA and GAM248567 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM187375 RNA and GAM248567 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM187375 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM187375 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM187375 target RNA into GAM187375 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM248567 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM248567 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM248567 target RNA into GAM248567 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5521 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5521 gene: GAM187375 target protein and GAM248567 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM187375 and GAM248567

5522(GR5522) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5522 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5522 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5522 gene encodes GR5522 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5522 precursor RNA folds spatially, forming GR5522 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5522 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5522 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5522 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM6084 precursor RNA, GAM127619 precursor RNA and GAM171035 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6084 RNA, GAM127619 RNA and GAM171035 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6084 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6084 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6084 target RNA into GAM6084 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM127619 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM127619 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM127619

target RNA into GAM127619 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM171035 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM171035 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM171035 target RNA into GAM171035 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5522 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5522 gene: GAM6084 target protein, GAM127619 target protein and GAM171035 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6084, GAM127619 and GAM171035

GR5523 BI758979 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5523(GR5523) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5523 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5523 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5523 gene encodes GR5523 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5523 precursor RNA folds spatially, forming GR5523 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5523 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5523 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5523 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM14163 precursor RNA, GAM115382 precursor RNA and GAM131960 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded

precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM14163 RNA, GAM115382 RNA and GAM131960 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM14163 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM14163 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM14163 target RNA into GAM14163 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM115382 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM115382 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM115382 target RNA into GAM115382 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM131960 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM131960 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM131960 target RNA into GAM131960 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5523 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5523 gene: GAM14163 target protein, GAM115382 target protein and GAM131960 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM14163, GAM115382 and GAM131960

GR5524 N76626 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5524(GR5524) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5524 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5524 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5524 gene encodes GR5524 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5524 precursor RNA folds spatially, forming GR5524 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5524 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5524 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5524 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2245 precursor RNA and GAM11901 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2245 RNA and GAM11901 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2245 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2245 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2245 target RNA into GAM2245 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM11901 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM11901 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM11901 target RNA into GAM11901 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5524 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5524 gene: GAM2245 target protein and GAM11901 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2245 and GAM11901

GR5525 AI524199 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5525(GR5525) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5525 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5525 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5525 gene encodes GR5525 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5525 precursor RNA folds spatially, forming GR5525 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5525 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5525 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5525 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM17082 precursor RNA and GAM272168 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM17082 RNA and GAM272168 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM17082 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM17082 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM17082

target RNA into GAM17082 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM272168 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM272168 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM272168 target RNA into GAM272168 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5525 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5525 gene: GAM17082 target protein and GAM272168 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM17082 and GAM272168

GR5526 BM977669 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5526(GR5526) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5526 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5526 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5526 gene encodes GR5526 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5526 precursor RNA folds spatially, forming GR5526 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5526 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5526 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5526 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2816 precursor RNA and GAM333307 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2816 RNA and GAM333307 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2816 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2816 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2816 target RNA into GAM2816 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM333307 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM333307 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM333307 target RNA into GAM333307 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5526 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5526 gene: GAM2816 target protein and GAM333307 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2816 and GAM333307

GR5527 BM705061 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5527(GR5527) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5527 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5527 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5527 gene encodes GR5527 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5527 precursor RNA folds spatially, forming GR5527 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated

that GR5527 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5527 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5527 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM120745 precursor RNA and GAM234133 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM120745 RNA and GAM234133 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM120745 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM120745 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM120745 target RNA into GAM120745 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM234133 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM234133 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM234133 target RNA into GAM234133 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5527 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5527 gene: GAM120745 target protein and GAM234133 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM120745 and GAM234133

GR5528 BG477202 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5528(GR5528) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR5528 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5528 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5528 gene encodes GR5528 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5528 precursor RNA folds spatially, forming GR5528 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5528 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5528 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5528 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1734 precursor RNA and GAM84658 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1734 RNA and GAM84658 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1734 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1734 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1734 target RNA into GAM1734 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM84658 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM84658 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM84658 target RNA into GAM84658 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5528 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5528 gene: GAM1734 target protein and GAM84658 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1734 and GAM84658

GR5529 BM014968 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5529(GR5529) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5529 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5529 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5529 gene encodes GR5529 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5529 precursor RNA folds spatially, forming GR5529 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5529 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5529 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5529 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM75387 precursor RNA and GAM247374 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM75387 RNA and GAM247374 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM75387 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM75387 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM75387 target RNA into GAM75387 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM247374 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM247374 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM247374 target RNA into GAM247374 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5529 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5529 gene: GAM75387 target protein and GAM247374 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM75387 and GAM247374

GR5530 AI056638 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5530(GR5530) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5530 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5530 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5530 gene encodes GR5530 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5530 precursor RNA folds spatially, forming GR5530 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5530 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5530 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5530 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM10060 precursor RNA and GAM270319 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3

FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM10060 RNA and GAM270319 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM10060 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM10060 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM10060 target RNA into GAM10060 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM270319 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM270319 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM270319 target RNA into GAM270319 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5530 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5530 gene: GAM10060 target protein and GAM270319 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM10060 and GAM270319

GR5531 BM674204 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5531 (GR5531) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5531 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5531 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5531 gene encodes GR5531 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5531 precursor RNA folds spatially, forming GR5531 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5531 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5531 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5531 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM58947 precursor RNA and GAM278964 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM58947 RNA and GAM278964 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM58947 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM58947 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM58947 target RNA into GAM58947 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM278964 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM278964 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM278964 target RNA into GAM278964 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5531 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5531 gene: GAM58947 target protein and GAM278964 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM58947 and GAM278964

5532(GR5532) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5532 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5532 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5532 gene encodes GR5532 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5532 precursor RNA folds spatially, forming GR5532 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5532 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5532 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5532 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM179073 precursor RNA and GAM334515 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM179073 RNA and GAM334515 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM179073 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM179073 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM179073 target RNA into GAM179073 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM334515 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM334515 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM334515 target RNA into GAM334515 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5532 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5532 gene: GAM179073 target protein and GAM334515 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM179073 and GAM334515

GR5533 BG621502 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5533(GR5533) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5533 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5533 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5533 gene encodes GR5533 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5533 precursor RNA folds spatially, forming GR5533 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5533 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5533 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5533 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM47556 precursor RNA and GAM294472 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM47556 RNA and GAM294472 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM47556 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM47556 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM47556 target RNA into GAM47556 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM294472 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM294472 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM294472 target RNA into GAM294472 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5533 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5533 gene: GAM47556 target protein and GAM294472 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM47556 and GAM294472

GR5534 R52640 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5534(GR5534) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5534 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5534 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5534 gene encodes GR5534 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5534 precursor RNA folds spatially, forming GR5534 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5534 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5534 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5534 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2

separate GAM precursor RNAs, GAM205919 precursor RNA and GAM333419 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM205919 RNA and GAM333419 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM205919 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM205919 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM205919 target RNA into GAM205919 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM333419 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM333419 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM333419 target RNA into GAM333419 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5534 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5534 gene: GAM205919 target protein and GAM333419 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM205919 and GAM333419

GR5535 AI879236 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5535(GR5535) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5535 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5535 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5535 gene encodes GR5535 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR5535 precursor RNA folds spatially, forming GR5535 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5535 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5535 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5535 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM41765 precursor RNA and GAM91978 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM41765 RNA and GAM91978 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM41765 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM41765 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM41765 target RNA into GAM41765 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM91978 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM91978 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM91978 target RNA into GAM91978 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5535 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5535 gene: GAM41765 target protein and GAM91978 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM41765 and GAM91978

GR5536 AV704114 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5536(GR5536) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5536 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5536 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5536 gene encodes GR5536 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5536 precursor RNA folds spatially, forming GR5536 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5536 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5536 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5536 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM249064 precursor RNA and GAM278850 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM249064 RNA and GAM278850 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM249064 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM249064 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM249064 target RNA into GAM249064 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM278850 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM278850 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM278850 target RNA into GAM278850 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5536 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5536 gene: GAM249064 target protein and GAM278850 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM249064 and GAM278850

GR5537 AW363157 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5537(GR5537) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5537 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5537 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5537 gene encodes GR5537 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5537 precursor RNA folds spatially, forming GR5537 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5537 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5537 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5537 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM625 precursor RNA and GAM270129 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM625 RNA and GAM270129 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM625 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM625 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM625 target RNA into GAM625 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM270129 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM270129 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM270129 target RNA into GAM270129 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5537 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5537 gene: GAM625 target protein and GAM270129 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM625 and GAM270129

GR5538 BF087110 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5538(GR5538) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5538 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5538 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5538 gene encodes GR5538 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5538 precursor RNA folds spatially, forming GR5538 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5538 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5538 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5538 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM75666 precursor RNA and GAM106584 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM75666 RNA and GAM106584 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM75666 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM75666 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM75666 target RNA into GAM75666 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM106584 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM106584 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM106584 target RNA into GAM106584 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5538 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5538 gene: GAM75666 target protein and GAM106584 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM75666 and GAM106584

GR5539 BI063815 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5539 (GR5539) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5539 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5539 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5539 gene encodes GR5539 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5539 precursor RNA folds spatially, forming GR5539 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5539 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5539 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5539 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM42285 precursor RNA, GAM81464 precursor RNA and GAM257114 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM42285 RNA, GAM81464 RNA and GAM257114 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM42285 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM42285 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM42285 target RNA into GAM42285 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM81464 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM81464 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM81464 target RNA into GAM81464 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM257114 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM257114 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM257114 target RNA into GAM257114 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5539 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5539 gene: GAM42285 target protein, GAM81464 target protein and GAM257114 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM42285, GAM81464 and GAM257114

GR5540 BI830472 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5540(GR5540) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5540 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5540 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5540 gene encodes GR5540 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5540 precursor RNA folds spatially, forming GR5540 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5540 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5540 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5540 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3854 precursor RNA and GAM45464 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3854 RNA and GAM45464 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3854 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3854 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3854 target RNA into GAM3854 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM45464 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM45464 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM45464 target RNA into GAM45464 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5540 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5540 gene: GAM3854 target protein and GAM45464 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3854 and GAM45464

GR5541 BM987696 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5541 (GR5541) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5541 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5541 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5541 gene encodes GR5541 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5541 precursor RNA folds spatially, forming GR5541 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5541 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5541 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5541 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM59093 precursor RNA and GAM320077 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM59093 RNA and GAM320077 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM59093 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM59093 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM59093 target RNA into GAM59093 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM320077 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM320077 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM320077 target RNA into GAM320077 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5541 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5541 gene: GAM59093 target protein and GAM320077 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM59093 and GAM320077

GR5542 AW753471 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5542(GR5542) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5542 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5542 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5542 gene encodes GR5542 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5542 precursor RNA folds spatially, forming GR5542 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5542 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5542 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5542 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM18497 precursor RNA, GAM36191 precursor RNA and GAM161981 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM18497 RNA, GAM36191 RNA and GAM161981 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM18497 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM18497 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM18497 target RNA into GAM18497 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM36191 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM36191 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM36191 target RNA into GAM36191 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM161981 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM161981 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM161981 target RNA into GAM161981 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5542 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5542 gene: GAM18497 target protein, GAM36191 target protein and GAM161981 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM18497, GAM36191 and GAM161981

GR5543 BG775881 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5543(GR5543) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5543 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5543 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5543 gene encodes GR5543 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5543 precursor RNA folds spatially, forming GR5543 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5543 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5543 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5543 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM6558 precursor RNA, GAM243971 precursor RNA and GAM324242 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6558 RNA, GAM243971 RNA and GAM324242 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6558 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6558 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6558 target RNA into GAM6558 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM243971 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM243971 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM243971 target RNA into GAM243971 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM324242 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM324242 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM324242 target RNA into GAM324242 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5543 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5543 gene: GAM6558 target protein, GAM243971 target protein and GAM324242 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6558, GAM243971 and GAM324242

GR5544 AA910666 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5544(GR5544) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5544 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5544 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5544 gene encodes GR5544 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5544 precursor RNA folds spatially, forming GR5544 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5544 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5544 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5544 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM110305 precursor RNA and GAM186289 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM110305 RNA and GAM186289 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM110305 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM110305 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM110305 target RNA into GAM110305 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM186289 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM186289 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM186289 target RNA into GAM186289 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5544 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5544 gene: GAM110305 target protein and GAM186289 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM110305 and GAM186289

GR5545 H64865 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5545(GR5545) gene, which encodes an `operon-like` cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5545 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5545 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5545 gene encodes GR5545 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5545 precursor RNA folds spatially, forming GR5545 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5545 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5545 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5545 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4623 precursor RNA and GAM157836 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4623 RNA and GAM157836 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4623 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4623 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4623 target RNA into GAM4623 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM157836 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM157836 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM157836 target RNA into GAM157836 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5545 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5545 gene: GAM4623 target protein and GAM157836 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4623 and GAM157836

GR5546 R62652 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5546(GR5546) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5546 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5546 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5546 gene encodes GR5546 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5546 precursor RNA folds spatially, forming GR5546 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5546 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5546 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5546 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM166749 precursor RNA, GAM280833 precursor RNA and GAM311815 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM166749 RNA, GAM280833 RNA and GAM311815 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM166749 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM166749 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM166749 target RNA into GAM166749 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM280833 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM280833 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM280833 target RNA into GAM280833 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM311815 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM311815 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM311815 target RNA into GAM311815 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5546 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5546 gene: GAM166749 target protein, GAM280833 target protein and GAM311815 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM166749, GAM280833 and GAM311815

GR5547 BE615626 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5547(GR5547) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5547 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5547 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5547 gene encodes GR5547 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5547 precursor RNA folds spatially, forming GR5547 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated

that GR5547 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5547 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5547 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM28433 precursor RNA and GAM60428 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM28433 RNA and GAM60428 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM28433 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM28433 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM28433 target RNA into GAM28433 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM60428 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM60428 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM60428 target RNA into GAM60428 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5547 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5547 gene: GAM28433 target protein and GAM60428 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM28433 and GAM60428

GR5548 AL706409 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5548(GR5548) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR5548 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5548 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5548 gene encodes GR5548 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5548 precursor RNA folds spatially, forming GR5548 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5548 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5548 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5548 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1858 precursor RNA, GAM79750 precursor RNA and GAM235372 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1858 RNA, GAM79750 RNA and GAM235372 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1858 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1858 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1858 target RNA into GAM1858 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM79750 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM79750 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM79750 target RNA into GAM79750 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM235372 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM235372 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM235372 target RNA into GAM235372 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5548 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5548 gene: GAM1858 target protein, GAM79750 target protein and GAM235372 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1858, GAM79750 and GAM235372

GR5549 BI519905 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5549(GR5549) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5549 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5549 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5549 gene encodes GR5549 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5549 precursor RNA folds spatially, forming GR5549 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5549 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5549 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5549 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM224763 precursor RNA and GAM307629 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM224763 RNA and GAM307629 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM224763 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM224763 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM224763 target RNA into GAM224763 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM307629 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM307629 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM307629 target RNA into GAM307629 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5549 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5549 gene: GAM224763 target protein and GAM307629 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM224763 and GAM307629

GR5550 F32275 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5550(GR5550) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5550 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5550 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5550 gene encodes GR5550 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5550 precursor RNA folds spatially, forming GR5550 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5550 folded precursor RNA comprises a plurality of what is known in the

art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5550 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5550 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2084 precursor RNA and GAM94549 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2084 RNA and GAM94549 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2084 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2084 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2084 target RNA into GAM2084 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM94549 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM94549 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM94549 target RNA into GAM94549 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5550 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5550 gene: GAM2084 target protein and GAM94549 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2084 and GAM94549

GR5551 AI168792 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5551 (GR5551) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR5551 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5551 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5551 gene encodes GR5551 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5551 precursor RNA folds spatially, forming GR5551 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5551 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5551 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5551 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM858 precursor RNA and GAM28242 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM858 RNA and GAM28242 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM858 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM858 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM858 target RNA into GAM858 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM28242 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM28242 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM28242 target RNA into GAM28242 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly

utilities, of GR5551 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5551 gene: GAM858 target protein and GAM28242 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM858 and GAM28242

GR5552 BG720511 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5552(GR5552) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5552 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5552 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5552 gene encodes GR5552 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5552 precursor RNA folds spatially, forming GR5552 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5552 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5552 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5552 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1463 precursor RNA and GAM271744 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1463 RNA and GAM271744 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1463 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1463 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig. 8, thereby inhibiting translation of GAM1463 target RNA into GAM1463 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM271744 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM271744 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM271744 target RNA into GAM271744 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5552 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5552 gene: GAM1463 target protein and GAM271744 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1463 and GAM271744

GR5553 BF308023 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5553(GR5553) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5553 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5553 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5553 gene encodes GR5553 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5553 precursor RNA folds spatially, forming GR5553 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5553 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5553 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5553 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4295 precursor RNA and GAM162343 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin

shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4295 RNA and GAM162343 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4295 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4295 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4295 target RNA into GAM4295 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM162343 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM162343 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM162343 target RNA into GAM162343 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5553 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5553 gene: GAM4295 target protein and GAM162343 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4295 and GAM162343

GR5554 BE744188 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5554(GR5554) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5554 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5554 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5554 gene encodes GR5554 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5554 precursor RNA folds spatially, forming GR5554 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5554 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5554 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5554 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM140195 precursor RNA and GAM157607 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM140195 RNA and GAM157607 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM140195 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM140195 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM140195 target RNA into GAM140195 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM157607 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM157607 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM157607 target RNA into GAM157607 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5554 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5554 gene: GAM140195 target protein and GAM157607 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM140195 and GAM157607

GR5555 BF568746 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5555(GR5555) gene, which encodes an `operon-like` cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5555 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5555 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5555 gene encodes GR5555 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5555 precursor RNA folds spatially, forming GR5555 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5555 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5555 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5555 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM376 precursor RNA, GAM89178 precursor RNA and GAM256475 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM376 RNA, GAM89178 RNA and GAM256475 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM376 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM376 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM376 target RNA into GAM376 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM89178 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM89178 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM89178 target RNA into GAM89178 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM256475 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM256475 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM256475 target RNA into GAM256475 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5555 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5555 gene: GAM376 target protein, GAM89178 target protein and GAM256475 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM376, GAM89178 and GAM256475

GR5556 BG942474 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5556(GR5556) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5556 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5556 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5556 gene encodes GR5556 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5556 precursor RNA folds spatially, forming GR5556 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5556 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5556 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5556 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM72346 precursor RNA and GAM210523 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM72346 RNA and GAM210523 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM72346 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM72346 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM72346 target RNA into GAM72346 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM210523 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM210523 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM210523 target RNA into GAM210523 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5556 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5556 gene: GAM72346 target protein and GAM210523 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM72346 and GAM210523

GR5557 AI656918 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5557(GR5557) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5557 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5557 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5557 gene encodes GR5557 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5557 precursor RNA folds spatially, forming GR5557 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated

that GR5557 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5557 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5557 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM522 precursor RNA and GAM224952 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM522 RNA and GAM224952 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM522 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM522 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM522 target RNA into GAM522 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM224952 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM224952 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM224952 target RNA into GAM224952 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5557 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5557 gene: GAM522 target protein and GAM224952 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM522 and GAM224952

GR5558 BE513337 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5558(GR5558) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR5558 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5558 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5558 gene encodes GR5558 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5558 precursor RNA folds spatially, forming GR5558 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5558 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5558 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5558 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM97050 precursor RNA and GAM265532 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM97050 RNA and GAM265532 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM97050 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM97050 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM97050 target RNA into GAM97050 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM265532 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM265532 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM265532 target RNA into GAM265532 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5558 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5558 gene: GAM97050 target protein and GAM265532 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM97050 and GAM265532

GR5559 BI048569 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5559(GR5559) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5559 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5559 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5559 gene encodes GR5559 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5559 precursor RNA folds spatially, forming GR5559 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5559 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5559 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5559 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM189400 precursor RNA and GAM213674 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM189400 RNA and GAM213674 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM189400 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM189400 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM189400 target RNA into GAM189400 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM213674 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM213674 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM213674 target RNA into GAM213674 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5559 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5559 gene: GAM189400 target protein and GAM213674 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM189400 and GAM213674

GR5560 BG252878 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5560(GR5560) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5560 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5560 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5560 gene encodes GR5560 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5560 precursor RNA folds spatially, forming GR5560 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5560 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5560 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5560 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM502 precursor RNA and GAM182366 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3

FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM502 RNA and GAM182366 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM502 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM502 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM502 target RNA into GAM502 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM182366 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM182366 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM182366 target RNA into GAM182366 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5560 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5560 gene: GAM502 target protein and GAM182366 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM502 and GAM182366

GR5561 BI669942 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5561 (GR5561) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5561 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5561 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5561 gene encodes GR5561 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5561 precursor RNA folds spatially, forming GR5561 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5561 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5561 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5561 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM180853 precursor RNA and GAM293776 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM180853 RNA and GAM293776 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM180853 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM180853 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM180853 target RNA into GAM180853 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM293776 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM293776 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM293776 target RNA into GAM293776 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5561 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5561 gene: GAM180853 target protein and GAM293776 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM180853 and GAM293776

5562(GR5562) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5562 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5562 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5562 gene encodes GR5562 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5562 precursor RNA folds spatially, forming GR5562 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5562 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5562 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5562 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8296 precursor RNA and GAM335789 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8296 RNA and GAM335789 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8296 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8296 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8296 target RNA into GAM8296 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM335789 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM335789 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM335789 target RNA into GAM335789 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5562 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5562 gene: GAM8296 target protein and GAM335789 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8296 and GAM335789

GR5563 BF205036 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5563(GR5563) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5563 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5563 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5563 gene encodes GR5563 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5563 precursor RNA folds spatially, forming GR5563 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5563 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5563 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5563 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM274818 precursor RNA and GAM278632 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM274818 RNA and GAM278632 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM274818 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM274818 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM274818 target RNA into GAM274818 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM278632 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM278632 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM278632 target RNA into GAM278632 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5563 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5563 gene: GAM274818 target protein and GAM278632 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM274818 and GAM278632

GR5564 AI968003 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5564(GR5564) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5564 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5564 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5564 gene encodes GR5564 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5564 precursor RNA folds spatially, forming GR5564 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5564 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5564 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5564 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2

separate GAM precursor RNAs, GAM7547 precursor RNA and GAM75777 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7547 RNA and GAM75777 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7547 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7547 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7547 target RNA into GAM7547 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM75777 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM75777 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM75777 target RNA into GAM75777 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5564 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5564 gene: GAM7547 target protein and GAM75777 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7547 and GAM75777

GR5565 BE048851 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5565(GR5565) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5565 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5565 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5565 gene encodes GR5565 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR5565 precursor RNA folds spatially, forming GR5565 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5565 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5565 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5565 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM139864 precursor RNA and GAM155199 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM139864 RNA and GAM155199 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM139864 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM139864 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM139864 target RNA into GAM139864 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM155199 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM155199 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM155199 target RNA into GAM155199 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5565 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5565 gene: GAM139864 target protein and GAM155199 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM139864 and GAM155199

GR5566 BG614896 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5566(GR5566) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5566 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5566 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5566 gene encodes GR5566 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5566 precursor RNA folds spatially, forming GR5566 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5566 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5566 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5566 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM27667 precursor RNA, GAM134708 precursor RNA and GAM321492 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM27667 RNA, GAM134708 RNA and GAM321492 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM27667 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM27667 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM27667 target RNA into GAM27667 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM134708 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM134708 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM134708 target RNA into GAM134708 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM321492 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM321492 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM321492 target RNA into GAM321492 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5566 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5566 gene: GAM27667 target protein, GAM134708 target protein and GAM321492 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM27667, GAM134708 and GAM321492

GR5567 BM665295 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5567(GR5567) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5567 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5567 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5567 gene encodes GR5567 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5567 precursor RNA folds spatially, forming GR5567 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5567 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5567 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5567 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2443 precursor RNA and GAM106668 precursor

RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2443 RNA and GAM106668 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2443 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2443 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2443 target RNA into GAM2443 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM106668 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM106668 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM106668 target RNA into GAM106668 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5567 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5567 gene: GAM2443 target protein and GAM106668 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2443 and GAM106668

GR5568 AI033218 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5568 (GR5568) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5568 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5568 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5568 gene encodes GR5568 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5568 precursor RNA folds spatially, forming GR5568 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5568 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5568 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5568 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6753 precursor RNA and GAM8166 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6753 RNA and GAM8166 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6753 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6753 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6753 target RNA into GAM6753 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8166 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8166 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8166 target RNA into GAM8166 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5568 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5568 gene: GAM6753 target protein and GAM8166 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6753 and GAM8166

bioinformatically detected regulatory gene, referred to here as Genomic Record 5569 (GR5569) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5569 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5569 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5569 gene encodes GR5569 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5569 precursor RNA folds spatially, forming GR5569 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5569 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5569 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5569 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM169008 precursor RNA and GAM287314 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM169008 RNA and GAM287314 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM169008 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM169008 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM169008 target RNA into GAM169008 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM287314 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM287314 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM287314

target RNA into GAM287314 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5569 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5569 gene: GAM169008 target protein and GAM287314 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM169008 and GAM287314

GR5570 BE302358 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5570(GR5570) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5570 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5570 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5570 gene encodes GR5570 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5570 precursor RNA folds spatially, forming GR5570 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5570 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5570 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5570 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM42063 precursor RNA and GAM228633 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM42063 RNA and GAM228633 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM42063 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM42063 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM42063 target RNA into GAM42063 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM228633 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM228633 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM228633 target RNA into GAM228633 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5570 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5570 gene: GAM42063 target protein and GAM228633 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM42063 and GAM228633

GR5571 BF991998 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5571(GR5571) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5571 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5571 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5571 gene encodes GR5571 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5571 precursor RNA folds spatially, forming GR5571 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5571 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5571 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5571 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM16141 precursor RNA, GAM243997 precursor RNA and GAM268243 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM16141 RNA, GAM243997 RNA and GAM268243 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM16141 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM16141 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM16141 target RNA into GAM16141 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM243997 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM243997 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM243997 target RNA into GAM243997 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM268243 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM268243 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM268243 target RNA into GAM268243 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5571 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5571 gene: GAM16141 target protein, GAM243997 target protein and GAM268243 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM16141, GAM243997 and GAM268243

5572(GR5572) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5572 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5572 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5572 gene encodes GR5572 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5572 precursor RNA folds spatially, forming GR5572 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5572 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5572 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5572 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM198891 precursor RNA and GAM324764 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM198891 RNA and GAM324764 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM198891 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM198891 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM198891 target RNA into GAM198891 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM324764 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM324764 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM324764 target RNA into GAM324764 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5572 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5572 gene: GAM198891 target protein and GAM324764 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM198891 and GAM324764

GR5573 AI279373 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5573(GR5573) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5573 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5573 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5573 gene encodes GR5573 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5573 precursor RNA folds spatially, forming GR5573 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5573 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5573 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5573 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM164017 precursor RNA and GAM230338 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM164017 RNA and GAM230338 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM164017 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM164017 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM164017 target RNA into GAM164017 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM230338 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM230338 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM230338 target RNA into GAM230338 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5573 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5573 gene: GAM164017 target protein and GAM230338 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM164017 and GAM230338

GR5574 BI560558 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5574(GR5574) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5574 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5574 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5574 gene encodes GR5574 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5574 precursor RNA folds spatially, forming GR5574 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5574 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5574 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5574 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2

separate GAM precursor RNAs, GAM162208 precursor RNA and GAM191750 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM162208 RNA and GAM191750 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM162208 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM162208 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM162208 target RNA into GAM162208 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM191750 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM191750 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM191750 target RNA into GAM191750 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5574 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5574 gene: GAM162208 target protein and GAM191750 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM162208 and GAM191750

GR5575 BQ058691 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5575 (GR5575) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5575 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5575 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5575 gene encodes GR5575 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR5575 precursor RNA folds spatially, forming GR5575 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5575 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5575 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5575 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM103134 precursor RNA, GAM163114 precursor RNA and GAM189293 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM103134 RNA, GAM163114 RNA and GAM189293 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM103134 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM103134 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM103134 target RNA into GAM103134 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM163114 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM163114 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM163114 target RNA into GAM163114 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM189293 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM189293 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM189293 target RNA into GAM189293 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5575 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5575 gene: GAM103134 target protein, GAM163114 target protein and GAM189293 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM103134, GAM163114 and GAM189293

GR5576 AW862575 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5576(GR5576) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5576 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5576 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5576 gene encodes GR5576 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5576 precursor RNA folds spatially, forming GR5576 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5576 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5576 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5576 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM110105 precursor RNA and GAM311737 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM110105 RNA and GAM311737 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM110105 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM110105 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM110105 target RNA into GAM110105 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM311737 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM311737 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM311737 target RNA into GAM311737 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5576 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5576 gene: GAM110105 target protein and GAM311737 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM110105 and GAM311737

GR5577 BF827058 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5577(GR5577) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5577 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5577 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5577 gene encodes GR5577 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5577 precursor RNA folds spatially, forming GR5577 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5577 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5577 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5577 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM16743 precursor RNA, GAM269498 precursor RNA

and GAM292285 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM16743 RNA, GAM269498 RNA and GAM292285 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM16743 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM16743 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM16743 target RNA into GAM16743 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM269498 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM269498 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM269498 target RNA into GAM269498 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM292285 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM292285 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM292285 target RNA into GAM292285 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5577 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5577 gene: GAM16743 target protein, GAM269498 target protein and GAM292285 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM16743, GAM269498 and GAM292285

GR5578 BG179277 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5578(GR5578) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR5578 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5578 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5578 gene encodes GR5578 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5578 precursor RNA folds spatially, forming GR5578 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5578 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5578 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5578 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM178 precursor RNA and GAM224614 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM178 RNA and GAM224614 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM178 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM178 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM178 target RNA into GAM178 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM224614 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM224614 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM224614 target RNA into GAM224614 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5578 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5578 gene: GAM178 target protein and GAM224614 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM178 and GAM224614

GR5579 BM907383 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5579(GR5579) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5579 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5579 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5579 gene encodes GR5579 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5579 precursor RNA folds spatially, forming GR5579 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5579 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5579 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5579 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM106735 precursor RNA and GAM131247 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM106735 RNA and GAM131247 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM106735 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM106735 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM106735 target RNA into GAM106735 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM131247 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM131247 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM131247 target RNA into GAM131247 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5579 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5579 gene: GAM106735 target protein and GAM131247 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM106735 and GAM131247

GR5580 BM748772 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5580 (GR5580) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5580 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5580 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5580 gene encodes GR5580 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5580 precursor RNA folds spatially, forming GR5580 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5580 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5580 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5580 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM69801 precursor RNA and GAM250247 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3

FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM69801 RNA and GAM250247 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM69801 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM69801 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM69801 target RNA into GAM69801 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM250247 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM250247 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM250247 target RNA into GAM250247 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5580 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5580 gene: GAM69801 target protein and GAM250247 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM69801 and GAM250247

GR5581 AI823496 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5581 (GR5581) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5581 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5581 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5581 gene encodes GR5581 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5581 precursor RNA folds spatially, forming GR5581 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5581 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5581 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5581 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM73782 precursor RNA and GAM106845 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM73782 RNA and GAM106845 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM73782 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM73782 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM73782 target RNA into GAM73782 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM106845 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM106845 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM106845 target RNA into GAM106845 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5581 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5581 gene: GAM73782 target protein and GAM106845 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM73782 and GAM106845

5582(GR5582) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5582 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5582 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5582 gene encodes GR5582 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5582 precursor RNA folds spatially, forming GR5582 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5582 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5582 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5582 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM133387 precursor RNA and GAM200764 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM133387 RNA and GAM200764 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM133387 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM133387 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM133387 target RNA into GAM133387 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM200764 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM200764 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM200764 target RNA into GAM200764 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5582 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5582 gene: GAM133387 target protein and GAM200764 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM133387 and GAM200764

GR5583 BF211945 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5583(GR5583) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5583 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5583 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5583 gene encodes GR5583 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5583 precursor RNA folds spatially, forming GR5583 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5583 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5583 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5583 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM239202 precursor RNA and GAM326328 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM239202 RNA and GAM326328 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM239202 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM239202 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM239202 target RNA into GAM239202 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM326328 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM326328 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM326328 target RNA into GAM326328 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5583 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5583 gene: GAM239202 target protein and GAM326328 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM239202 and GAM326328

GR5584 BE391085 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5584(GR5584) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5584 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5584 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5584 gene encodes GR5584 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5584 precursor RNA folds spatially, forming GR5584 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5584 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5584 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5584 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2

separate GAM precursor RNAs, GAM6751 precursor RNA and GAM7189 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6751 RNA and GAM7189 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6751 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6751 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6751 target RNA into GAM6751 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7189 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7189 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7189 target RNA into GAM7189 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5584 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5584 gene: GAM6751 target protein and GAM7189 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6751 and GAM7189

GR5585 BE933316 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5585(GR5585) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5585 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5585 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5585 gene encodes GR5585 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR5585 precursor RNA folds spatially, forming GR5585 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5585 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5585 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5585 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM134146 precursor RNA, GAM306601 precursor RNA and GAM320673 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM134146 RNA, GAM306601 RNA and GAM320673 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM134146 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM134146 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM134146 target RNA into GAM134146 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM306601 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM306601 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM306601 target RNA into GAM306601 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM320673 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM320673 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM320673 target RNA into GAM320673 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5585 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5585 gene: GAM134146 target protein, GAM306601 target protein and GAM320673 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM134146, GAM306601 and GAM320673

GR5586 BG496736 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5586(GR5586) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5586 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5586 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5586 gene encodes GR5586 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5586 precursor RNA folds spatially, forming GR5586 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5586 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5586 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5586 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1996 precursor RNA and GAM317159 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1996 RNA and GAM317159 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1996 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1996 target RNA, herein schematically represented by

GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1996 target RNA into GAM1996 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM317159 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM317159 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM317159 target RNA into GAM317159 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5586 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5586 gene: GAM1996 target protein and GAM317159 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1996 and GAM317159

GR5587 AA318669 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5587(GR5587) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5587 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5587 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5587 gene encodes GR5587 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5587 precursor RNA folds spatially, forming GR5587 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5587 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5587 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5587 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5771 precursor RNA and GAM182883 precursor

RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5771 RNA and GAM182883 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5771 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5771 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5771 target RNA into GAM5771 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM182883 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM182883 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM182883 target RNA into GAM182883 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5587 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5587 gene: GAM5771 target protein and GAM182883 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5771 and GAM182883

GR5588 AL600016 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5588(GR5588) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5588 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5588 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5588 gene encodes GR5588 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5588 precursor RNA folds spatially, forming GR5588 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5588 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5588 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5588 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM97365 precursor RNA and GAM314805 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM97365 RNA and GAM314805 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM97365 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM97365 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM97365 target RNA into GAM97365 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM314805 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM314805 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM314805 target RNA into GAM314805 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5588 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5588 gene: GAM97365 target protein and GAM314805 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM97365 and GAM314805

bioinformatically detected regulatory gene, referred to here as Genomic Record 5589(GR5589) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5589 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5589 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5589 gene encodes GR5589 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5589 precursor RNA folds spatially, forming GR5589 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5589 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5589 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5589 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7109 precursor RNA and GAM20063 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7109 RNA and GAM20063 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7109 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7109 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7109 target RNA into GAM7109 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM20063 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM20063 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM20063

target RNA into GAM20063 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5589 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5589 gene: GAM7109 target protein and GAM20063 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7109 and GAM20063

GR5590 BM503308 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5590(GR5590) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5590 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5590 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5590 gene encodes GR5590 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5590 precursor RNA folds spatially, forming GR5590 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5590 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5590 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5590 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1261 precursor RNA and GAM6688 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1261 RNA and GAM6688 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1261 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1261 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1261 target RNA into GAM1261 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6688 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6688 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6688 target RNA into GAM6688 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5590 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5590 gene: GAM1261 target protein and GAM6688 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1261 and GAM6688

GR5591 BE670794 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5591(GR5591) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5591 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5591 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5591 gene encodes GR5591 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5591 precursor RNA folds spatially, forming GR5591 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5591 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5591 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5591 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM43330 precursor RNA and GAM251884 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM43330 RNA and GAM251884 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM43330 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM43330 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM43330 target RNA into GAM43330 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM251884 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM251884 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM251884 target RNA into GAM251884 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5591 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5591 gene: GAM43330 target protein and GAM251884 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM43330 and GAM251884

GR5592 AV682704 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5592(GR5592) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5592 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5592 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5592 gene encodes GR5592 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5592 precursor RNA folds spatially, forming GR5592 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5592 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5592 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5592 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM125826 precursor RNA and GAM176521 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM125826 RNA and GAM176521 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM125826 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM125826 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM125826 target RNA into GAM125826 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM176521 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM176521 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM176521 target RNA into GAM176521 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5592 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5592 gene: GAM125826 target protein and GAM176521 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM125826 and GAM176521

GR5593 N27711 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5593(GR5593) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5593 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5593 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5593 gene encodes GR5593 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5593 precursor RNA folds spatially, forming GR5593 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5593 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5593 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5593 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM65807 precursor RNA and GAM84265 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM65807 RNA and GAM84265 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM65807 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM65807 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM65807 target RNA into GAM65807 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM84265 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM84265 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM84265 target RNA into GAM84265 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5593 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5593 gene: GAM65807 target protein and GAM84265 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM65807 and GAM84265

GR5594 AI625111 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5594(GR5594) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5594 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5594 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5594 gene encodes GR5594 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5594 precursor RNA folds spatially, forming GR5594 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5594 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5594 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5594 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM947 precursor RNA, GAM5460 precursor RNA and GAM8338 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM947 RNA, GAM5460 RNA and GAM8338 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs

corresponding to GAM RNA of Fig. 8.

GAM947 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM947 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM947 target RNA into GAM947 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5460 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5460 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5460 target RNA into GAM5460 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8338 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8338 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8338 target RNA into GAM8338 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5594 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5594 gene: GAM947 target protein, GAM5460 target protein and GAM8338 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM947, GAM5460 and GAM8338

GR5595 AW440631 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5595 (GR5595) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5595 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5595 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5595 gene encodes GR5595 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR5595 precursor RNA folds spatially, forming GR5595 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5595 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5595 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5595 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6325 precursor RNA and GAM170548 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6325 RNA and GAM170548 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6325 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6325 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6325 target RNA into GAM6325 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM170548 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM170548 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM170548 target RNA into GAM170548 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5595 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5595 gene: GAM6325 target protein and GAM170548 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6325 and GAM170548

GR5596 BE618572 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5596(GR5596) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5596 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5596 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5596 gene encodes GR5596 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5596 precursor RNA folds spatially, forming GR5596 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5596 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5596 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5596 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM149615 precursor RNA, GAM151508 precursor RNA and GAM224159 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM149615 RNA, GAM151508 RNA and GAM224159 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM149615 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM149615 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM149615 target RNA into GAM149615 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM151508 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM151508 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM151508 target RNA into GAM151508 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM224159 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM224159 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM224159 target RNA into GAM224159 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5596 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5596 gene: GAM149615 target protein, GAM151508 target protein and GAM224159 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM149615, GAM151508 and GAM224159

GR5597 BF679550 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5597(GR5597) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5597 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5597 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5597 gene encodes GR5597 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5597 precursor RNA folds spatially, forming GR5597 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5597 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5597 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5597 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1784 precursor RNA and GAM8254 precursor

RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1784 RNA and GAM8254 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1784 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1784 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1784 target RNA into GAM1784 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8254 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8254 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8254 target RNA into GAM8254 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5597 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5597 gene: GAM1784 target protein and GAM8254 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1784 and GAM8254

GR5598 BF995283 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5598 (GR5598) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5598 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5598 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5598 gene encodes GR5598 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5598 precursor RNA folds spatially, forming GR5598 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5598 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5598 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5598 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM43183 precursor RNA and GAM309507 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM43183 RNA and GAM309507 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM43183 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM43183 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM43183 target RNA into GAM43183 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM309507 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM309507 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM309507 target RNA into GAM309507 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5598 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5598 gene: GAM43183 target protein and GAM309507 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM43183 and GAM309507

bioinformatically detected regulatory gene, referred to here as Genomic Record 5599(GR5599) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5599 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5599 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5599 gene encodes GR5599 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5599 precursor RNA folds spatially, forming GR5599 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5599 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5599 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5599 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM6236 precursor RNA, GAM8081 precursor RNA and GAM291038 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6236 RNA, GAM8081 RNA and GAM291038 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6236 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6236 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6236 target RNA into GAM6236 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8081 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8081 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig. 8, thereby inhibiting translation of GAM8081 target RNA into GAM8081 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM291038 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM291038 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM291038 target RNA into GAM291038 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5599 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5599 gene: GAM6236 target protein, GAM8081 target protein and GAM291038 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6236, GAM8081 and GAM291038

GR5600 BI914012 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5600(GR5600) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5600 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5600 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5600 gene encodes GR5600 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5600 precursor RNA folds spatially, forming GR5600 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5600 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5600 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5600 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1590 precursor RNA and GAM3333 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3

FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1590 RNA and GAM3333 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1590 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1590 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1590 target RNA into GAM1590 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM3333 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3333 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3333 target RNA into GAM3333 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5600 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5600 gene: GAM1590 target protein and GAM3333 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1590 and GAM3333

GR5601 AA534953 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5601(GR5601) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5601 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5601 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5601 gene encodes GR5601 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5601 precursor RNA folds spatially, forming GR5601 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5601 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5601 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5601 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM53830 precursor RNA and GAM266746 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM53830 RNA and GAM266746 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM53830 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM53830 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM53830 target RNA into GAM53830 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM266746 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM266746 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM266746 target RNA into GAM266746 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5601 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5601 gene: GAM53830 target protein and GAM266746 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM53830 and GAM266746

5602(GR5602) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5602 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5602 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5602 gene encodes GR5602 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5602 precursor RNA folds spatially, forming GR5602 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5602 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5602 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5602 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM6748 precursor RNA, GAM7740 precursor RNA and GAM217543 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6748 RNA, GAM7740 RNA and GAM217543 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6748 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6748 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6748 target RNA into GAM6748 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7740 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7740 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7740 target RNA into

GAM7740 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM217543 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM217543 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM217543 target RNA into GAM217543 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5602 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5602 gene: GAM6748 target protein, GAM7740 target protein and GAM217543 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6748, GAM7740 and GAM217543

GR5603 AW889727 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5603(GR5603) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5603 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5603 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5603 gene encodes GR5603 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5603 precursor RNA folds spatially, forming GR5603 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5603 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5603 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5603 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4572 precursor RNA and GAM149260 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin

shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4572 RNA and GAM149260 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4572 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4572 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4572 target RNA into GAM4572 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM149260 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM149260 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM149260 target RNA into GAM149260 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5603 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5603 gene: GAM4572 target protein and GAM149260 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4572 and GAM149260

GR5604 BG505044 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5604(GR5604) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5604 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5604 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5604 gene encodes GR5604 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5604 precursor RNA folds spatially, forming GR5604 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5604 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5604 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5604 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3327 precursor RNA, GAM34025 precursor RNA and GAM248107 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3327 RNA, GAM34025 RNA and GAM248107 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3327 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3327 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3327 target RNA into GAM3327 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM34025 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM34025 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM34025 target RNA into GAM34025 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM248107 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM248107 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM248107 target RNA into GAM248107 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5604 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR5604 gene: GAM3327 target protein, GAM34025 target protein and GAM248107 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3327, GAM34025 and GAM248107

GR5605 BE963656 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5605(GR5605) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5605 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5605 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5605 gene encodes GR5605 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5605 precursor RNA folds spatially, forming GR5605 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5605 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5605 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5605 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM6013 precursor RNA, GAM84972 precursor RNA and GAM151080 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6013 RNA, GAM84972 RNA and GAM151080 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6013 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6013 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig. 8, thereby inhibiting translation of GAM6013 target RNA into GAM6013 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM84972 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM84972 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM84972 target RNA into GAM84972 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM151080 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM151080 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM151080 target RNA into GAM151080 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5605 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5605 gene: GAM6013 target protein, GAM84972 target protein and GAM151080 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6013, GAM84972 and GAM151080

GR5606 BF675048 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5606(GR5606) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5606 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5606 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5606 gene encodes GR5606 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5606 precursor RNA folds spatially, forming GR5606 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5606 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5606 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5606 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM1468 precursor RNA, GAM50552 precursor RNA, GAM113882 precursor RNA and GAM302414 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1468 RNA, GAM50552 RNA, GAM113882 RNA and GAM302414 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1468 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1468 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1468 target RNA into GAM1468 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM50552 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM50552 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM50552 target RNA into GAM50552 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM113882 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM113882 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM113882 target RNA into GAM113882 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM302414 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM302414 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM302414 target RNA into GAM302414 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5606 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5606 gene: GAM1468 target protein, GAM50552 target protein, GAM113882 target protein and GAM302414 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1468, GAM50552, GAM113882 and GAM302414

GR5607 AI857680 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5607(GR5607) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5607 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5607 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5607 gene encodes GR5607 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5607 precursor RNA folds spatially, forming GR5607 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5607 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5607 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5607 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM220611 precursor RNA, GAM251563 precursor RNA and GAM276215 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM220611 RNA, GAM251563 RNA and GAM276215 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM220611 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM220611 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM220611 target RNA into GAM220611 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM251563 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM251563 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM251563 target RNA into GAM251563 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM276215 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM276215 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM276215 target RNA into GAM276215 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5607 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5607 gene: GAM220611 target protein, GAM251563 target protein and GAM276215 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM220611, GAM251563 and GAM276215

GR5608 BI918396 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5608(GR5608) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5608 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5608 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5608 gene encodes GR5608 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5608 precursor RNA folds spatially, forming GR5608 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5608 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5608 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5608 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM97527 precursor RNA, GAM258132 precursor RNA and GAM260240 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM97527 RNA, GAM258132 RNA and GAM260240 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM97527 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM97527 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM97527 target RNA into GAM97527 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM258132 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM258132 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM258132 target RNA into GAM258132 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM260240 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM260240 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM260240 target RNA into GAM260240 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5608 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR5608 gene: GAM97527 target protein, GAM258132 target protein and GAM260240 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM97527, GAM258132 and GAM260240

GR5609 BM874543 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5609(GR5609) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5609 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5609 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5609 gene encodes GR5609 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5609 precursor RNA folds spatially, forming GR5609 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5609 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5609 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5609 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM31805 precursor RNA, GAM77476 precursor RNA and GAM327604 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM31805 RNA, GAM77476 RNA and GAM327604 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM31805 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM31805 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM31805 target RNA into GAM31805 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM77476 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM77476 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM77476 target RNA into GAM77476 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM327604 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM327604 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM327604 target RNA into GAM327604 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5609 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5609 gene: GAM31805 target protein, GAM77476 target protein and GAM327604 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM31805, GAM77476 and GAM327604

GR5610 AW070364 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5610 (GR5610) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5610 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5610 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5610 gene encodes GR5610 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5610 precursor RNA folds spatially, forming GR5610 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5610 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5610 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5610 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM208305 precursor RNA and GAM261602 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM208305 RNA and GAM261602 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM208305 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM208305 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM208305 target RNA into GAM208305 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM261602 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM261602 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM261602 target RNA into GAM261602 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5610 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5610 gene: GAM208305 target protein and GAM261602 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM208305 and GAM261602

GR5611 BM766749 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5611(GR5611) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5611 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5611 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5611 gene encodes GR5611 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5611 precursor RNA folds spatially, forming GR5611 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5611 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5611 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5611 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5725 precursor RNA and GAM275118 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5725 RNA and GAM275118 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5725 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5725 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5725 target RNA into GAM5725 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM275118 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM275118 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM275118 target RNA into GAM275118 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5611 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR5611 gene: GAM5725 target protein and GAM275118 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5725 and GAM275118

GR5612 BG194556 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5612(GR5612) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5612 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5612 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5612 gene encodes GR5612 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5612 precursor RNA folds spatially, forming GR5612 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5612 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5612 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5612 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM138441 precursor RNA and GAM191459 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM138441 RNA and GAM191459 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM138441 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM138441 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM138441 target RNA into GAM138441 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM191459 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM191459 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM191459 target RNA into GAM191459 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5612 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5612 gene: GAM138441 target protein and GAM191459 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM138441 and GAM191459

GR5613 BI599677 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5613(GR5613) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5613 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5613 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5613 gene encodes GR5613 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5613 precursor RNA folds spatially, forming GR5613 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5613 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5613 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5613 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4475 precursor RNA, GAM100045 precursor RNA and GAM277210 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4475 RNA, GAM100045 RNA and GAM277210 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4475 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4475 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4475 target RNA into GAM4475 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM100045 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM100045 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM100045 target RNA into GAM100045 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM277210 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM277210 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM277210 target RNA into GAM277210 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5613 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5613 gene: GAM4475 target protein, GAM100045 target protein and GAM277210 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4475, GAM100045 and GAM277210

GR5614 AI799591 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5614(GR5614) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5614 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR5614 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5614 gene encodes GR5614 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5614 precursor RNA folds spatially, forming GR5614 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5614 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5614 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5614 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2403 precursor RNA, GAM3034 precursor RNA and GAM320476 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2403 RNA, GAM3034 RNA and GAM320476 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2403 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2403 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2403 target RNA into GAM2403 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM3034 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3034 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3034 target RNA into GAM3034 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM320476 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM320476 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM320476 target RNA into GAM320476 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5614 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5614 gene: GAM2403 target protein, GAM3034 target protein and GAM320476 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2403, GAM3034 and GAM320476

GR5615 BI870156 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5615(GR5615) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5615 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5615 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5615 gene encodes GR5615 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5615 precursor RNA folds spatially, forming GR5615 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5615 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5615 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5615 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM15424 precursor RNA, GAM163435 precursor RNA and GAM323268 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM15424 RNA, GAM163435 RNA and GAM323268 RNA, herein

schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM15424 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM15424 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM15424 target RNA into GAM15424 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM163435 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM163435 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM163435 target RNA into GAM163435 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM323268 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM323268 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM323268 target RNA into GAM323268 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5615 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5615 gene: GAM15424 target protein, GAM163435 target protein and GAM323268 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM15424, GAM163435 and GAM323268

GR5616 BM927178 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5616(GR5616) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5616 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5616 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5616 gene encodes GR5616 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5616 precursor RNA folds spatially, forming GR5616 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5616 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5616 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5616 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM14540 precursor RNA and GAM115129 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM14540 RNA and GAM115129 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM14540 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM14540 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM14540 target RNA into GAM14540 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM115129 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM115129 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM115129 target RNA into GAM115129 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5616 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5616 gene: GAM14540 target protein and GAM115129 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM14540 and GAM115129

GR5617 BF854663 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5617(GR5617) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5617 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5617 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5617 gene encodes GR5617 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5617 precursor RNA folds spatially, forming GR5617 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5617 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5617 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5617 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2294 precursor RNA and GAM312546 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2294 RNA and GAM312546 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2294 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2294 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2294 target RNA into GAM2294 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM312546 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM312546 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM312546 target RNA into GAM312546 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5617 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5617 gene: GAM2294 target protein and GAM312546 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2294 and GAM312546

GR5618 AW134562 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5618(GR5618) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5618 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5618 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5618 gene encodes GR5618 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5618 precursor RNA folds spatially, forming GR5618 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5618 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5618 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5618 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM68310 precursor RNA, GAM158251 precursor RNA, GAM248354 precursor RNA and GAM259445 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM68310 RNA, GAM158251 RNA, GAM248354 RNA and GAM259445 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA,

each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM68310 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM68310 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM68310 target RNA into GAM68310 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM158251 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM158251 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM158251 target RNA into GAM158251 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM248354 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM248354 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM248354 target RNA into GAM248354 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM259445 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM259445 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM259445 target RNA into GAM259445 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5618 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5618 gene: GAM68310 target protein, GAM158251 target protein, GAM248354 target protein and GAM259445 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM68310, GAM158251, GAM248354 and GAM259445

GR5619 AA521383 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5619(GR5619) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR5619 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5619 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5619 gene encodes GR5619 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5619 precursor RNA folds spatially, forming GR5619 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5619 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5619 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5619 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5021 precursor RNA and GAM84079 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5021 RNA and GAM84079 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5021 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5021 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5021 target RNA into GAM5021 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM84079 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM84079 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM84079 target RNA into GAM84079 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly

utilities, of GR5619 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5619 gene: GAM5021 target protein and GAM84079 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5021 and GAM84079

GR5620 AA037196 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5620(GR5620) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5620 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5620 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5620 gene encodes GR5620 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5620 precursor RNA folds spatially, forming GR5620 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5620 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5620 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5620 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM162230 precursor RNA and GAM331909 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM162230 RNA and GAM331909 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM162230 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM162230 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM162230 target RNA into GAM162230 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM331909 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM331909 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM331909 target RNA into GAM331909 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5620 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5620 gene: GAM162230 target protein and GAM331909 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM162230 and GAM331909

GR5621 AA780835 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5621 (GR5621) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5621 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5621 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5621 gene encodes GR5621 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5621 precursor RNA folds spatially, forming GR5621 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5621 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5621 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5621 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4141 precursor RNA, GAM152318 precursor RNA and GAM295555 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded

precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4141 RNA, GAM152318 RNA and GAM295555 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4141 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4141 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4141 target RNA into GAM4141 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM152318 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM152318 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM152318 target RNA into GAM152318 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM295555 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM295555 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM295555 target RNA into GAM295555 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5621 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5621 gene: GAM4141 target protein, GAM152318 target protein and GAM295555 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4141, GAM152318 and GAM295555

GR5622 BG004209 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5622(GR5622) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5622 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5622 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5622 gene encodes GR5622 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5622 precursor RNA folds spatially, forming GR5622 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5622 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5622 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5622 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM9818 precursor RNA, GAM103934 precursor RNA and GAM301567 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM9818 RNA, GAM103934 RNA and GAM301567 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM9818 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM9818 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM9818 target RNA into GAM9818 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM103934 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM103934 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM103934 target RNA into GAM103934 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM301567 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM301567 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM301567 target RNA into GAM301567 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5622 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5622 gene: GAM9818 target protein, GAM103934 target protein and GAM301567 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM9818, GAM103934 and GAM301567

GR5623 BQ082797 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5623(GR5623) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5623 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5623 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5623 gene encodes GR5623 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5623 precursor RNA folds spatially, forming GR5623 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5623 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5623 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5623 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4498 precursor RNA and GAM287957 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM4498 RNA and GAM287957 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4498 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4498 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4498 target RNA into GAM4498 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM287957 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM287957 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM287957 target RNA into GAM287957 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5623 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5623 gene: GAM4498 target protein and GAM287957 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4498 and GAM287957

GR5624 BE072234 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5624(GR5624) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5624 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5624 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5624 gene encodes GR5624 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5624 precursor RNA folds spatially, forming GR5624 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5624 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5624 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5624 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2551 precursor RNA, GAM8683 precursor RNA and GAM53361 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2551 RNA, GAM8683 RNA and GAM53361 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2551 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2551 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2551 target RNA into GAM2551 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8683 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8683 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8683 target RNA into GAM8683 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM53361 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM53361 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM53361 target RNA into GAM53361 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5624 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5624 gene: GAM2551 target protein, GAM8683 target protein and GAM53361 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6,

hereby incorporated by reference, with references to GAM2551, GAM8683 and GAM53361

GR5625 AL699350 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5625(GR5625) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5625 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5625 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5625 gene encodes GR5625 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5625 precursor RNA folds spatially, forming GR5625 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5625 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5625 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5625 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM146579 precursor RNA and GAM206147 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM146579 RNA and GAM206147 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM146579 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM146579 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM146579 target RNA into GAM146579 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM206147 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM206147 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM206147 target RNA into GAM206147 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5625 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5625 gene: GAM146579 target protein and GAM206147 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM146579 and GAM206147

GR5626 H90006 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5626(GR5626) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5626 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5626 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5626 gene encodes GR5626 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5626 precursor RNA folds spatially, forming GR5626 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5626 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5626 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5626 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM9827 precursor RNA, GAM100277 precursor RNA and GAM206263 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM9827 RNA, GAM100277 RNA and GAM206263 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM9827 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM9827 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM9827 target RNA into GAM9827 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM100277 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM100277 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM100277 target RNA into GAM100277 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM206263 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM206263 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM206263 target RNA into GAM206263 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5626 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5626 gene: GAM9827 target protein, GAM100277 target protein and GAM206263 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM9827, GAM100277 and GAM206263

GR5627 AW382616 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5627 (GR5627) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5627 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5627 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5627 gene encodes GR5627 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5627 precursor RNA folds spatially, forming GR5627 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5627 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5627 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5627 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM19881 precursor RNA, GAM20399 precursor RNA, GAM197762 precursor RNA and GAM289970 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM19881 RNA, GAM20399 RNA, GAM197762 RNA and GAM289970 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM19881 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM19881 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM19881 target RNA into GAM19881 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM20399 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM20399 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM20399 target RNA into GAM20399 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM197762 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM197762 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM197762 target RNA into GAM197762 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM289970 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM289970 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM289970 target RNA into GAM289970 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5627 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5627 gene: GAM19881 target protein, GAM20399 target protein, GAM197762 target protein and GAM289970 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM19881, GAM20399, GAM197762 and GAM289970

GR5628 BG401578 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5628(GR5628) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5628 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5628 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5628 gene encodes GR5628 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5628 precursor RNA folds spatially, forming GR5628 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5628 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5628 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5628 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM156198 precursor RNA and GAM236095 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM156198 RNA and GAM236095 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM156198 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM156198 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM156198 target RNA into GAM156198 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM236095 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM236095 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM236095 target RNA into GAM236095 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5628 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5628 gene: GAM156198 target protein and GAM236095 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM156198 and GAM236095

GR5629 AA742774 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5629(GR5629) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5629 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5629 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5629 gene encodes GR5629 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5629 precursor RNA folds spatially, forming GR5629 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated

that GR5629 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5629 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5629 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6808 precursor RNA and GAM286392 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6808 RNA and GAM286392 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6808 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6808 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6808 target RNA into GAM6808 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM286392 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM286392 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM286392 target RNA into GAM286392 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5629 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5629 gene: GAM6808 target protein and GAM286392 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6808 and GAM286392

GR5630 BG705158 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5630(GR5630) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR5630 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5630 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5630 gene encodes GR5630 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5630 precursor RNA folds spatially, forming GR5630 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5630 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5630 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5630 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM60598 precursor RNA and GAM99973 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM60598 RNA and GAM99973 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM60598 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM60598 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM60598 target RNA into GAM60598 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM99973 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM99973 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM99973 target RNA into GAM99973 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5630 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5630 gene: GAM60598 target protein and GAM99973 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM60598 and GAM99973

GR5631 BE463445 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5631 (GR5631) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5631 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5631 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5631 gene encodes GR5631 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5631 precursor RNA folds spatially, forming GR5631 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5631 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5631 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5631 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM136037 precursor RNA and GAM239290 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM136037 RNA and GAM239290 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM136037 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM136037 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM136037 target RNA into GAM136037 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM239290 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM239290 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM239290 target RNA into GAM239290 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5631 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5631 gene: GAM136037 target protein and GAM239290 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM136037 and GAM239290

GR5632 BI547388 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5632(GR5632) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5632 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5632 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5632 gene encodes GR5632 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5632 precursor RNA folds spatially, forming GR5632 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5632 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5632 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5632 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM257295 precursor RNA and GAM303283 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3

FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM257295 RNA and GAM303283 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM257295 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM257295 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM257295 target RNA into GAM257295 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM303283 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM303283 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM303283 target RNA into GAM303283 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5632 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5632 gene: GAM257295 target protein and GAM303283 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM257295 and GAM303283

GR5633 N62063 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5633(GR5633) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5633 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5633 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5633 gene encodes GR5633 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5633 precursor RNA folds spatially, forming GR5633 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5633 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5633 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5633 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM44753 precursor RNA, GAM230677 precursor RNA and GAM332902 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM44753 RNA, GAM230677 RNA and GAM332902 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM44753 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM44753 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM44753 target RNA into GAM44753 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM230677 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM230677 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM230677 target RNA into GAM230677 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM332902 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM332902 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM332902 target RNA into GAM332902 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5633 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5633 gene: GAM44753 target protein, GAM230677 target protein and GAM332902 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM44753, GAM230677 and GAM332902

GR5634 BG169806 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5634(GR5634) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5634 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5634 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5634 gene encodes GR5634 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5634 precursor RNA folds spatially, forming GR5634 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5634 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5634 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5634 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2511 precursor RNA and GAM233304 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2511 RNA and GAM233304 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2511 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2511 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig. 8, thereby inhibiting translation of GAM2511 target RNA into GAM2511 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM233304 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM233304 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM233304 target RNA into GAM233304 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5634 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5634 gene: GAM2511 target protein and GAM233304 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2511 and GAM233304

GR5635 R80058 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5635(GR5635) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5635 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5635 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5635 gene encodes GR5635 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5635 precursor RNA folds spatially, forming GR5635 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5635 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5635 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5635 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM610 precursor RNA and GAM309276 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin

shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM610 RNA and GAM309276 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM610 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM610 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM610 target RNA into GAM610 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM309276 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM309276 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM309276 target RNA into GAM309276 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5635 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5635 gene: GAM610 target protein and GAM309276 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM610 and GAM309276

GR5636 BF690531 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5636(GR5636) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5636 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5636 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5636 gene encodes GR5636 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5636 precursor RNA folds spatially, forming GR5636 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5636 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5636 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5636 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM525 precursor RNA, GAM113551 precursor RNA and GAM216250 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM525 RNA, GAM113551 RNA and GAM216250 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM525 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM525 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM525 target RNA into GAM525 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM113551 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM113551 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM113551 target RNA into GAM113551 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM216250 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM216250 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM216250 target RNA into GAM216250 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5636 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR5636 gene: GAM525 target protein, GAM113551 target protein and GAM216250 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM525, GAM113551 and GAM216250

GR5637 BG539022 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5637 (GR5637) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5637 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5637 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5637 gene encodes GR5637 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5637 precursor RNA folds spatially, forming GR5637 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5637 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5637 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5637 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM9665 precursor RNA, GAM202768 precursor RNA and GAM270998 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM9665 RNA, GAM202768 RNA and GAM270998 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM9665 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM9665 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig. 8, thereby inhibiting translation of GAM9665 target RNA into GAM9665 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM202768 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM202768 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM202768 target RNA into GAM202768 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM270998 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM270998 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM270998 target RNA into GAM270998 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5637 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5637 gene: GAM9665 target protein, GAM202768 target protein and GAM270998 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM9665, GAM202768 and GAM270998

GR5638 BG484101 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5638(GR5638) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5638 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5638 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5638 gene encodes GR5638 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5638 precursor RNA folds spatially, forming GR5638 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5638 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5638 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5638 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3482 precursor RNA and GAM7826 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3482 RNA and GAM7826 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3482 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3482 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3482 target RNA into GAM3482 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7826 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7826 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7826 target RNA into GAM7826 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5638 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5638 gene: GAM3482 target protein and GAM7826 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3482 and GAM7826

GR5639 BF057432 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5639(GR5639) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5639 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5639 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5639 gene encodes GR5639 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5639 precursor RNA folds spatially, forming GR5639 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5639 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5639 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5639 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2811 precursor RNA and GAM2904 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2811 RNA and GAM2904 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2811 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2811 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2811 target RNA into GAM2811 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM2904 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2904 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2904 target RNA into GAM2904 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5639 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR5639 gene: GAM2811 target protein and GAM2904 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2811 and GAM2904

GR5640 BF184125 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5640(GR5640) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5640 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5640 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5640 gene encodes GR5640 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5640 precursor RNA folds spatially, forming GR5640 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5640 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5640 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5640 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3863 precursor RNA and GAM249072 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3863 RNA and GAM249072 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3863 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3863 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3863 target RNA into GAM3863 target protein, herein schematically represented by GAM1 TARGET

PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM249072 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM249072 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM249072 target RNA into GAM249072 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5640 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5640 gene: GAM3863 target protein and GAM249072 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3863 and GAM249072

GR5641 AI373154 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5641 (GR5641) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5641 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5641 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5641 gene encodes GR5641 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5641 precursor RNA folds spatially, forming GR5641 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5641 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5641 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5641 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM296638 precursor RNA and GAM310207 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM296638 RNA and GAM310207 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM296638 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM296638 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM296638 target RNA into GAM296638 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM310207 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM310207 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM310207 target RNA into GAM310207 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5641 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5641 gene: GAM296638 target protein and GAM310207 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM296638 and GAM310207

GR5642 BF238409 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5642(GR5642) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5642 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5642 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5642 gene encodes GR5642 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5642 precursor RNA folds spatially, forming GR5642 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5642 folded precursor RNA comprises a plurality of what is known in the

art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5642 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5642 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8480 precursor RNA and GAM255163 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8480 RNA and GAM255163 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8480 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8480 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8480 target RNA into GAM8480 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM255163 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM255163 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM255163 target RNA into GAM255163 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5642 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5642 gene: GAM8480 target protein and GAM255163 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8480 and GAM255163

GR5643 AA595985 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5643(GR5643) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR5643 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5643 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5643 gene encodes GR5643 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5643 precursor RNA folds spatially, forming GR5643 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5643 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5643 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5643 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM49607 precursor RNA and GAM217794 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM49607 RNA and GAM217794 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM49607 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM49607 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM49607 target RNA into GAM49607 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM217794 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM217794 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM217794 target RNA into GAM217794 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly

utilities, of GR5643 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5643 gene: GAM49607 target protein and GAM217794 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM49607 and GAM217794

GR5644 BE717798 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5644(GR5644) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5644 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5644 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5644 gene encodes GR5644 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5644 precursor RNA folds spatially, forming GR5644 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5644 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5644 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5644 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5167 precursor RNA and GAM182666 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5167 RNA and GAM182666 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5167 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5167 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig. 8, thereby inhibiting translation of GAM5167 target RNA into GAM5167 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM182666 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM182666 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM182666 target RNA into GAM182666 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5644 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5644 gene: GAM5167 target protein and GAM182666 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5167 and GAM182666

GR5645 BG821908 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5645(GR5645) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5645 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5645 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5645 gene encodes GR5645 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5645 precursor RNA folds spatially, forming GR5645 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5645 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5645 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5645 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2768 precursor RNA and GAM93256 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin

shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2768 RNA and GAM93256 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2768 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2768 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2768 target RNA into GAM2768 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM93256 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM93256 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM93256 target RNA into GAM93256 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5645 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5645 gene: GAM2768 target protein and GAM93256 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2768 and GAM93256

GR5646 BG328186 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5646(GR5646) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5646 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5646 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5646 gene encodes GR5646 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5646 precursor RNA folds spatially, forming GR5646 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5646 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5646 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5646 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2149 precursor RNA and GAM119206 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2149 RNA and GAM119206 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2149 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2149 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2149 target RNA into GAM2149 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM119206 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM119206 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM119206 target RNA into GAM119206 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5646 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5646 gene: GAM2149 target protein and GAM119206 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2149 and GAM119206

GR5647 AA483971 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5647(GR5647) gene, which encodes an `operon-like` cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5647 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5647 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5647 gene encodes GR5647 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5647 precursor RNA folds spatially, forming GR5647 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5647 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5647 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5647 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1747 precursor RNA and GAM304911 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1747 RNA and GAM304911 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1747 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1747 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1747 target RNA into GAM1747 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM304911 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM304911 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM304911 target RNA into GAM304911 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5647 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5647 gene: GAM1747 target protein and GAM304911 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1747 and GAM304911

GR5648 BG422375 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5648(GR5648) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5648 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5648 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5648 gene encodes GR5648 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5648 precursor RNA folds spatially, forming GR5648 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5648 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5648 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5648 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM125177 precursor RNA and GAM278778 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM125177 RNA and GAM278778 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM125177 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM125177 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM125177 target RNA into GAM125177 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM278778 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM278778 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM278778 target RNA into GAM278778 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5648 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5648 gene: GAM125177 target protein and GAM278778 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM125177 and GAM278778

GR5649 BI114496 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5649(GR5649) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5649 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5649 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5649 gene encodes GR5649 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5649 precursor RNA folds spatially, forming GR5649 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5649 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5649 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5649 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2983 precursor RNA, GAM243917 precursor RNA

and GAM315896 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2983 RNA, GAM243917 RNA and GAM315896 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2983 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2983 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2983 target RNA into GAM2983 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM243917 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM243917 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM243917 target RNA into GAM243917 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM315896 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM315896 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM315896 target RNA into GAM315896 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5649 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5649 gene: GAM2983 target protein, GAM243917 target protein and GAM315896 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2983, GAM243917 and GAM315896

GR5650 BF797295 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5650(GR5650) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR5650 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5650 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5650 gene encodes GR5650 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5650 precursor RNA folds spatially, forming GR5650 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5650 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5650 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5650 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2291 precursor RNA, GAM6192 precursor RNA and GAM184824 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2291 RNA, GAM6192 RNA and GAM184824 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2291 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2291 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2291 target RNA into GAM2291 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6192 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6192 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6192 target RNA into GAM6192 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM184824 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM184824 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM184824 target RNA into GAM184824 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5650 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5650 gene: GAM2291 target protein, GAM6192 target protein and GAM184824 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2291, GAM6192 and GAM184824

GR5651 R41307 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5651 (GR5651) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5651 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5651 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5651 gene encodes GR5651 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5651 precursor RNA folds spatially, forming GR5651 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5651 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5651 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5651 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM73430 precursor RNA, GAM142673 precursor RNA and GAM213724 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM73430 RNA, GAM142673 RNA and GAM213724 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM73430 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM73430 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM73430 target RNA into GAM73430 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM142673 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM142673 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM142673 target RNA into GAM142673 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM213724 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM213724 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM213724 target RNA into GAM213724 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5651 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5651 gene: GAM73430 target protein, GAM142673 target protein and GAM213724 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM73430, GAM142673 and GAM213724

GR5652 BE272233 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5652(GR5652) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5652 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR5652 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5652 gene encodes GR5652 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5652 precursor RNA folds spatially, forming GR5652 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5652 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5652 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5652 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM183035 precursor RNA and GAM239480 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM183035 RNA and GAM239480 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM183035 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM183035 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM183035 target RNA into GAM183035 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM239480 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM239480 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM239480 target RNA into GAM239480 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5652 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5652 gene: GAM183035 target

protein and GAM239480 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM183035 and GAM239480

GR5653 BF978080 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5653(GR5653) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5653 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5653 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5653 gene encodes GR5653 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5653 precursor RNA folds spatially, forming GR5653 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5653 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5653 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5653 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM14520 precursor RNA and GAM266684 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM14520 RNA and GAM266684 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM14520 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM14520 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM14520 target RNA into GAM14520 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM266684 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM266684 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM266684 target RNA into GAM266684 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5653 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5653 gene: GAM14520 target protein and GAM266684 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM14520 and GAM266684

GR5654 BG682350 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5654(GR5654) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5654 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5654 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5654 gene encodes GR5654 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5654 precursor RNA folds spatially, forming GR5654 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5654 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5654 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5654 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM243 precursor RNA, GAM3162 precursor RNA and GAM6991 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM243 RNA, GAM3162 RNA and GAM6991 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM243 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM243 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM243 target RNA into GAM243 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM3162 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3162 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3162 target RNA into GAM3162 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6991 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6991 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6991 target RNA into GAM6991 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5654 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5654 gene: GAM243 target protein, GAM3162 target protein and GAM6991 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM243, GAM3162 and GAM6991

GR5655 AA255871 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5655(GR5655) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5655 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5655

gene was detected is described hereinabove with reference to Figs. 8-18.

GR5655 gene encodes GR5655 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5655 precursor RNA folds spatially, forming GR5655 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5655 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5655 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5655 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM30056 precursor RNA and GAM154371 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM30056 RNA and GAM154371 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM30056 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM30056 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM30056 target RNA into GAM30056 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM154371 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM154371 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM154371 target RNA into GAM154371 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5655 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5655 gene: GAM30056 target protein and GAM154371 target protein, herein schematically represented by GAM1

TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM30056 and GAM154371

GR5656 BE835533 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5656(GR5656) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5656 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5656 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5656 gene encodes GR5656 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5656 precursor RNA folds spatially, forming GR5656 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5656 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5656 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5656 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3402 precursor RNA and GAM122205 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3402 RNA and GAM122205 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3402 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3402 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3402 target RNA into GAM3402 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM122205 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM122205 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM122205 target RNA into GAM122205 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5656 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5656 gene: GAM3402 target protein and GAM122205 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3402 and GAM122205

GR5657 AL521054 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5657(GR5657) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5657 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5657 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5657 gene encodes GR5657 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5657 precursor RNA folds spatially, forming GR5657 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5657 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5657 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5657 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4194 precursor RNA, GAM58527 precursor RNA and GAM105768 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4194 RNA, GAM58527 RNA and GAM105768 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4194 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4194 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4194 target RNA into GAM4194 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM58527 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM58527 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM58527 target RNA into GAM58527 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM105768 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM105768 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM105768 target RNA into GAM105768 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5657 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5657 gene: GAM4194 target protein, GAM58527 target protein and GAM105768 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4194, GAM58527 and GAM105768

GR5658 BG742070 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5658(GR5658) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5658 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5658 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5658 gene encodes GR5658 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5658 precursor RNA folds spatially, forming GR5658 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5658 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5658 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5658 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM5252 precursor RNA, GAM7878 precursor RNA, GAM118437 precursor RNA and GAM275997 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5252 RNA, GAM7878 RNA, GAM118437 RNA and GAM275997 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5252 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5252 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5252 target RNA into GAM5252 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7878 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7878 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7878 target RNA into GAM7878 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM118437 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM118437 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM118437

target RNA into GAM118437 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM275997 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM275997 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM275997 target RNA into GAM275997 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5658 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5658 gene: GAM5252 target protein, GAM7878 target protein, GAM118437 target protein and GAM275997 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5252, GAM7878, GAM118437 and GAM275997

GR5659 BF219297 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5659(GR5659) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5659 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5659 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5659 gene encodes GR5659 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5659 precursor RNA folds spatially, forming GR5659 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5659 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5659 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5659 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2737 precursor RNA and GAM14043 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin

shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2737 RNA and GAM14043 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2737 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2737 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2737 target RNA into GAM2737 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM14043 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM14043 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM14043 target RNA into GAM14043 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5659 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5659 gene: GAM2737 target protein and GAM14043 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2737 and GAM14043

GR5660 BF877949 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5660(GR5660) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5660 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5660 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5660 gene encodes GR5660 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5660 precursor RNA folds spatially, forming GR5660 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5660 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5660 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5660 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2581 precursor RNA and GAM148498 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2581 RNA and GAM148498 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2581 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2581 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2581 target RNA into GAM2581 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM148498 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM148498 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM148498 target RNA into GAM148498 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5660 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5660 gene: GAM2581 target protein and GAM148498 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2581 and GAM148498

GR5661 BG699075 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5661 (GR5661) gene, which encodes an `operon-like` cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5661 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5661 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5661 gene encodes GR5661 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5661 precursor RNA folds spatially, forming GR5661 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5661 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5661 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5661 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM333 precursor RNA and GAM229739 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM333 RNA and GAM229739 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM333 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM333 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM333 target RNA into GAM333 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM229739 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM229739 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM229739 target RNA into GAM229739 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5661 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5661 gene: GAM333 target protein and GAM229739 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM333 and GAM229739

GR5662 BF133083 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5662(GR5662) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5662 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5662 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5662 gene encodes GR5662 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5662 precursor RNA folds spatially, forming GR5662 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5662 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5662 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5662 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM64102 precursor RNA and GAM112673 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM64102 RNA and GAM112673 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM64102 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM64102 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM64102 target RNA into GAM64102 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM112673 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM112673 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM112673 target RNA into GAM112673 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5662 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5662 gene: GAM64102 target protein and GAM112673 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM64102 and GAM112673

GR5663 BG830639 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5663(GR5663) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5663 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5663 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5663 gene encodes GR5663 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5663 precursor RNA folds spatially, forming GR5663 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5663 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5663 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5663 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM89088 precursor RNA and GAM156356 precursor

RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM89088 RNA and GAM156356 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM89088 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM89088 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM89088 target RNA into GAM89088 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM156356 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM156356 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM156356 target RNA into GAM156356 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5663 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5663 gene: GAM89088 target protein and GAM156356 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM89088 and GAM156356

GR5664 BG491960 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5664(GR5664) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5664 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5664 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5664 gene encodes GR5664 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5664 precursor RNA folds spatially, forming GR5664 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5664 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5664 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5664 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM84554 precursor RNA and GAM269584 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM84554 RNA and GAM269584 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM84554 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM84554 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM84554 target RNA into GAM84554 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM269584 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM269584 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM269584 target RNA into GAM269584 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5664 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5664 gene: GAM84554 target protein and GAM269584 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM84554 and GAM269584

bioinformatically detected regulatory gene, referred to here as Genomic Record 5665(GR5665) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5665 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5665 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5665 gene encodes GR5665 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5665 precursor RNA folds spatially, forming GR5665 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5665 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5665 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5665 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3908 precursor RNA, GAM95615 precursor RNA and GAM134622 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3908 RNA, GAM95615 RNA and GAM134622 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3908 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3908 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3908 target RNA into GAM3908 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM95615 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM95615 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM95615 target RNA into GAM95615 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM134622 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM134622 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM134622 target RNA into GAM134622 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5665 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5665 gene: GAM3908 target protein, GAM95615 target protein and GAM134622 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3908, GAM95615 and GAM134622

GR5666 BG428138 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5666(GR5666) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5666 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5666 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5666 gene encodes GR5666 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5666 precursor RNA folds spatially, forming GR5666 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5666 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5666 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5666 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM289269 precursor RNA and GAM289397 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3

FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM289269 RNA and GAM289397 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM289269 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM289269 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM289269 target RNA into GAM289269 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM289397 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM289397 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM289397 target RNA into GAM289397 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5666 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5666 gene: GAM289269 target protein and GAM289397 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM289269 and GAM289397

GR5667 AA730532 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5667(GR5667) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5667 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5667 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5667 gene encodes GR5667 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5667 precursor RNA folds spatially, forming GR5667 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5667 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5667 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5667 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3439 precursor RNA and GAM139707 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3439 RNA and GAM139707 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3439 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3439 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3439 target RNA into GAM3439 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM139707 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM139707 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM139707 target RNA into GAM139707 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5667 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5667 gene: GAM3439 target protein and GAM139707 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3439 and GAM139707

5668(GR5668) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5668 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5668 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5668 gene encodes GR5668 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5668 precursor RNA folds spatially, forming GR5668 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5668 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5668 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5668 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7931 precursor RNA and GAM256347 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7931 RNA and GAM256347 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7931 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7931 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7931 target RNA into GAM7931 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM256347 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM256347 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM256347 target RNA into GAM256347 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5668 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5668 gene: GAM7931 target protein and GAM256347 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7931 and GAM256347

GR5669 BF028451 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5669(GR5669) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5669 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5669 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5669 gene encodes GR5669 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5669 precursor RNA folds spatially, forming GR5669 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5669 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5669 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5669 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM8521 precursor RNA, GAM14149 precursor RNA and GAM27486 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8521 RNA, GAM14149 RNA and GAM27486 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8521 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8521 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8521 target RNA into GAM8521 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM14149 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM14149 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM14149 target RNA into GAM14149 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM27486 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM27486 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM27486 target RNA into GAM27486 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5669 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5669 gene: GAM8521 target protein, GAM14149 target protein and GAM27486 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8521, GAM14149 and GAM27486

GR5670 BF509121 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5670(GR5670) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5670 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5670 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5670 gene encodes GR5670 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5670 precursor RNA folds spatially, forming GR5670 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5670 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5670 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5670 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM5795 precursor RNA, GAM188542 precursor RNA and GAM192315 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5795 RNA, GAM188542 RNA and GAM192315 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5795 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5795 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5795 target RNA into GAM5795 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM188542 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM188542 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM188542 target RNA into GAM188542 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM192315 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM192315 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM192315 target RNA into GAM192315 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5670 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR5670 gene: GAM5795 target protein, GAM188542 target protein and GAM192315 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5795, GAM188542 and GAM192315

GR5671 BE797905 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5671(GR5671) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5671 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5671 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5671 gene encodes GR5671 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5671 precursor RNA folds spatially, forming GR5671 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5671 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5671 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5671 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM161104 precursor RNA and GAM206705 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM161104 RNA and GAM206705 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM161104 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM161104 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM161104

target RNA into GAM161104 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM206705 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM206705 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM206705 target RNA into GAM206705 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5671 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5671 gene: GAM161104 target protein and GAM206705 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM161104 and GAM206705

GR5672 AI085403 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5672(GR5672) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5672 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5672 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5672 gene encodes GR5672 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5672 precursor RNA folds spatially, forming GR5672 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5672 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5672 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5672 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM52 precursor RNA, GAM41407 precursor RNA and GAM163577 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED

PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM52 RNA, GAM41407 RNA and GAM163577 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM52 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM52 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM52 target RNA into GAM52 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM41407 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM41407 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM41407 target RNA into GAM41407 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM163577 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM163577 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM163577 target RNA into GAM163577 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5672 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5672 gene: GAM52 target protein, GAM41407 target protein and GAM163577 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM52, GAM41407 and GAM163577

GR5673 BQ066172 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5673(GR5673) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5673 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5673 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5673 gene encodes GR5673 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5673 precursor RNA folds spatially, forming GR5673 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5673 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5673 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5673 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4095 precursor RNA and GAM20832 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4095 RNA and GAM20832 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4095 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4095 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4095 target RNA into GAM4095 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM20832 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM20832 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM20832 target RNA into GAM20832 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5673 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR5673 gene: GAM4095 target protein and GAM20832 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4095 and GAM20832

GR5674 R93903 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5674(GR5674) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5674 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5674 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5674 gene encodes GR5674 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5674 precursor RNA folds spatially, forming GR5674 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5674 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5674 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5674 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM188638 precursor RNA and GAM328544 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM188638 RNA and GAM328544 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM188638 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM188638 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM188638 target RNA into GAM188638 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM328544 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM328544 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM328544 target RNA into GAM328544 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5674 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5674 gene: GAM188638 target protein and GAM328544 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM188638 and GAM328544

GR5675 BI908742 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5675(GR5675) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5675 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5675 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5675 gene encodes GR5675 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5675 precursor RNA folds spatially, forming GR5675 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5675 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5675 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5675 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM17635 precursor RNA, GAM150936 precursor RNA and GAM220948 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM17635 RNA, GAM150936 RNA and GAM220948 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM17635 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM17635 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM17635 target RNA into GAM17635 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM150936 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM150936 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM150936 target RNA into GAM150936 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM220948 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM220948 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM220948 target RNA into GAM220948 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5675 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5675 gene: GAM17635 target protein, GAM150936 target protein and GAM220948 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM17635, GAM150936 and GAM220948

GR5676 BG746875 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5676(GR5676) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5676 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR5676 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5676 gene encodes GR5676 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5676 precursor RNA folds spatially, forming GR5676 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5676 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5676 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5676 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM97458 precursor RNA and GAM226427 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM97458 RNA and GAM226427 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM97458 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM97458 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM97458 target RNA into GAM97458 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM226427 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM226427 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM226427 target RNA into GAM226427 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5676 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5676 gene: GAM97458 target

protein and GAM226427 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM97458 and GAM226427

GR5677 BM918953 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5677(GR5677) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5677 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5677 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5677 gene encodes GR5677 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5677 precursor RNA folds spatially, forming GR5677 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5677 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5677 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5677 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM241451 precursor RNA and GAM251355 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM241451 RNA and GAM251355 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM241451 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM241451 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM241451 target RNA into GAM241451 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM251355 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM251355 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM251355 target RNA into GAM251355 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5677 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5677 gene: GAM241451 target protein and GAM251355 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM241451 and GAM251355

GR5678 BF339843 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5678(GR5678) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5678 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5678 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5678 gene encodes GR5678 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5678 precursor RNA folds spatially, forming GR5678 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5678 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5678 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5678 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1335 precursor RNA and GAM6393 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1335 RNA and GAM6393 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1335 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1335 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1335 target RNA into GAM1335 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6393 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6393 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6393 target RNA into GAM6393 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5678 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5678 gene: GAM1335 target protein and GAM6393 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1335 and GAM6393

GR5679 BF667996 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5679(GR5679) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5679 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5679 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5679 gene encodes GR5679 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5679 precursor RNA folds spatially, forming GR5679 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5679 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR5679 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5679 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1112 precursor RNA and GAM200231 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1112 RNA and GAM200231 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1112 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1112 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1112 target RNA into GAM1112 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM200231 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM200231 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM200231 target RNA into GAM200231 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5679 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5679 gene: GAM1112 target protein and GAM200231 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1112 and GAM200231

GR5680 AA984162 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5680 (GR5680) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5680 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5680 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5680 gene encodes GR5680 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5680 precursor RNA folds spatially, forming GR5680 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5680 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5680 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5680 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2853 precursor RNA, GAM82723 precursor RNA and GAM271341 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2853 RNA, GAM82723 RNA and GAM271341 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2853 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2853 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2853 target RNA into GAM2853 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM82723 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM82723 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM82723 target RNA into GAM82723 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM271341 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM271341 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM271341 target RNA into GAM271341 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5680 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5680 gene: GAM2853 target protein, GAM82723 target protein and GAM271341 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2853, GAM82723 and GAM271341

GR5681 AW613692 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5681(GR5681) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5681 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5681 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5681 gene encodes GR5681 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5681 precursor RNA folds spatially, forming GR5681 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5681 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5681 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5681 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM217513 precursor RNA, GAM232621 precursor RNA and GAM328776 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM217513 RNA, GAM232621 RNA and GAM328776 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM217513 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM217513 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM217513 target RNA into GAM217513 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM232621 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM232621 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM232621 target RNA into GAM232621 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM328776 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM328776 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM328776 target RNA into GAM328776 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5681 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5681 gene: GAM217513 target protein, GAM232621 target protein and GAM328776 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM217513, GAM232621 and GAM328776

GR5682 AA503449 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5682(GR5682) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5682 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5682 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5682 gene encodes GR5682 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5682 precursor RNA folds spatially, forming GR5682 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5682 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5682 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5682 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM103349 precursor RNA and GAM145333 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM103349 RNA and GAM145333 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM103349 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM103349 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM103349 target RNA into GAM103349 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM145333 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM145333 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM145333 target RNA into GAM145333 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5682 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5682 gene: GAM103349 target protein and GAM145333 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes

is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM103349 and GAM145333

GR5683 BI193427 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5683(GR5683) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5683 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5683 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5683 gene encodes GR5683 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5683 precursor RNA folds spatially, forming GR5683 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5683 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5683 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5683 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM58818 precursor RNA and GAM241352 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM58818 RNA and GAM241352 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM58818 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM58818 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM58818 target RNA into GAM58818 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM241352 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM241352 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM241352 target RNA into GAM241352 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5683 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5683 gene: GAM58818 target protein and GAM241352 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM58818 and GAM241352

GR5684 BE267874 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5684(GR5684) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5684 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5684 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5684 gene encodes GR5684 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5684 precursor RNA folds spatially, forming GR5684 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5684 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5684 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5684 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2076 precursor RNA, GAM216014 precursor RNA and GAM265335 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM2076 RNA, GAM216014 RNA and GAM265335 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2076 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2076 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2076 target RNA into GAM2076 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM216014 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM216014 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM216014 target RNA into GAM216014 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM265335 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM265335 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM265335 target RNA into GAM265335 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5684 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5684 gene: GAM2076 target protein, GAM216014 target protein and GAM265335 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2076, GAM216014 and GAM265335

GR5685 BF970954 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5685(GR5685) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5685 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5685 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5685 gene encodes GR5685 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5685 precursor RNA folds spatially, forming GR5685 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5685 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5685 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5685 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1548 precursor RNA and GAM106201 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1548 RNA and GAM106201 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1548 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1548 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1548 target RNA into GAM1548 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM106201 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM106201 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM106201 target RNA into GAM106201 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5685 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5685 gene: GAM1548 target protein and GAM106201 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference,

with references to GAM1548 and GAM106201

GR5686 AA613291 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5686(GR5686) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5686 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5686 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5686 gene encodes GR5686 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5686 precursor RNA folds spatially, forming GR5686 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5686 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5686 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5686 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1045 precursor RNA, GAM179523 precursor RNA and GAM302388 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1045 RNA, GAM179523 RNA and GAM302388 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1045 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1045 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1045 target RNA into GAM1045 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM179523 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM179523 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM179523 target RNA into GAM179523 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM302388 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM302388 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM302388 target RNA into GAM302388 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5686 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5686 gene: GAM1045 target protein, GAM179523 target protein and GAM302388 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1045, GAM179523 and GAM302388

GR5687 BG210094 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5687(GR5687) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5687 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5687 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5687 gene encodes GR5687 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5687 precursor RNA folds spatially, forming GR5687 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5687 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5687 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5687 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4779 precursor RNA and GAM7487 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4779 RNA and GAM7487 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4779 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4779 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4779 target RNA into GAM4779 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7487 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7487 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7487 target RNA into GAM7487 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5687 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5687 gene: GAM4779 target protein and GAM7487 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4779 and GAM7487

GR5688 BE696039 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5688(GR5688) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5688 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5688 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5688 gene encodes GR5688 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5688 precursor RNA folds spatially, forming GR5688 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5688 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5688 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5688 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM979 precursor RNA, GAM61601 precursor RNA and GAM68210 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM979 RNA, GAM61601 RNA and GAM68210 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM979 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM979 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM979 target RNA into GAM979 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM61601 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM61601 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM61601 target RNA into GAM61601 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM68210 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM68210 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM68210 target RNA into GAM68210 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5688 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5688 gene: GAM979 target protein, GAM61601 target protein and GAM68210 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM979, GAM61601 and GAM68210

GR5689 BM686977 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5689(GR5689) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5689 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5689 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5689 gene encodes GR5689 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5689 precursor RNA folds spatially, forming GR5689 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5689 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5689 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5689 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM509 precursor RNA, GAM161327 precursor RNA and GAM264217 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM509 RNA, GAM161327 RNA and GAM264217 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM509 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM509 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM509 target RNA into GAM509 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM161327 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM161327 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM161327 target RNA into GAM161327 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM264217 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM264217 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM264217 target RNA into GAM264217 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5689 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5689 gene: GAM509 target protein, GAM161327 target protein and GAM264217 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM509, GAM161327 and GAM264217

GR5690 BE538702 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5690(GR5690) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5690 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5690 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5690 gene encodes GR5690 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5690 precursor RNA folds spatially, forming GR5690 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5690 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5690 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5690 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2632 precursor RNA and GAM57553 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2632 RNA and GAM57553 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2632 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2632 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2632 target RNA into GAM2632 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM57553 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM57553 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM57553 target RNA into GAM57553 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5690 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5690 gene: GAM2632 target protein and GAM57553 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2632 and GAM57553

GR5691 BG471386 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5691 (GR5691) gene, which encodes an `operon-like` cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5691 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5691 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5691 gene encodes GR5691 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5691 precursor RNA folds spatially, forming GR5691 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5691 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5691 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5691 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM193142 precursor RNA and GAM265085 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM193142 RNA and GAM265085 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM193142 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM193142 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM193142 target RNA into GAM193142 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM265085 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM265085 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM265085 target RNA into GAM265085 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5691 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5691 gene: GAM193142 target protein and GAM265085 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM193142 and GAM265085

GR5692 BM681640 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5692(GR5692) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5692 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5692 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5692 gene encodes GR5692 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5692 precursor RNA folds spatially, forming GR5692 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5692 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5692 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5692 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM126925 precursor RNA and GAM266996 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM126925 RNA and GAM266996 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM126925 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM126925 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM126925 target RNA into GAM126925 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM266996 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM266996 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM266996 target RNA into GAM266996 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5692 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5692 gene: GAM126925 target protein and GAM266996 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM126925 and GAM266996

GR5693 AI936214 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5693(GR5693) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5693 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5693 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5693 gene encodes GR5693 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5693 precursor RNA folds spatially, forming GR5693 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5693 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5693 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5693 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5583 precursor RNA and GAM14352 precursor

RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5583 RNA and GAM14352 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5583 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5583 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5583 target RNA into GAM5583 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM14352 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM14352 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM14352 target RNA into GAM14352 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5693 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5693 gene: GAM5583 target protein and GAM14352 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5583 and GAM14352

GR5694 BF569589 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5694 (GR5694) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5694 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5694 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5694 gene encodes GR5694 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5694 precursor RNA folds spatially, forming GR5694 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5694 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5694 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5694 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM109 precursor RNA, GAM3301 precursor RNA, GAM118723 precursor RNA and GAM181019 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM109 RNA, GAM3301 RNA, GAM118723 RNA and GAM181019 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM109 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM109 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM109 target RNA into GAM109 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM3301 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3301 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3301 target RNA into GAM3301 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM118723 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM118723 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM118723 target RNA into GAM118723 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM181019 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM181019 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM181019 target RNA into GAM181019 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5694 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5694 gene: GAM109 target protein, GAM3301 target protein, GAM118723 target protein and GAM181019 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM109, GAM3301, GAM118723 and GAM181019

GR5695 AW970263 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5695(GR5695) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5695 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5695 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5695 gene encodes GR5695 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5695 precursor RNA folds spatially, forming GR5695 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5695 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5695 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5695 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM6316 precursor RNA, GAM7989 precursor RNA and GAM162107 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6316 RNA, GAM7989 RNA and GAM162107 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6316 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6316 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6316 target RNA into GAM6316 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7989 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7989 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7989 target RNA into GAM7989 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM162107 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM162107 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM162107 target RNA into GAM162107 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5695 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5695 gene: GAM6316 target protein, GAM7989 target protein and GAM162107 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6316, GAM7989 and GAM162107

GR5696 AA665452 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5696(GR5696) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5696 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5696 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5696 gene encodes GR5696 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5696 precursor RNA folds spatially, forming GR5696 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5696 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5696 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5696 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM78 precursor RNA, GAM3074 precursor RNA and GAM288771 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM78 RNA, GAM3074 RNA and GAM288771 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM78 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM78 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM78 target RNA into GAM78 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM3074 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3074 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3074 target RNA into GAM3074 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM288771 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM288771 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM288771

target RNA into GAM288771 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5696 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5696 gene: GAM78 target protein, GAM3074 target protein and GAM288771 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM78, GAM3074 and GAM288771

GR5697 AU124323 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5697(GR5697) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5697 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5697 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5697 gene encodes GR5697 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5697 precursor RNA folds spatially, forming GR5697 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5697 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5697 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5697 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1287 precursor RNA and GAM283615 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1287 RNA and GAM283615 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1287 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1287 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1287 target RNA into GAM1287 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM283615 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM283615 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM283615 target RNA into GAM283615 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5697 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5697 gene: GAM1287 target protein and GAM283615 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1287 and GAM283615

GR5698 BG756968 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5698(GR5698) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5698 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5698 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5698 gene encodes GR5698 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5698 precursor RNA folds spatially, forming GR5698 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5698 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5698 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5698 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1832 precursor RNA and GAM324274 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1832 RNA and GAM324274 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1832 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1832 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1832 target RNA into GAM1832 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM324274 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM324274 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM324274 target RNA into GAM324274 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5698 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5698 gene: GAM1832 target protein and GAM324274 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1832 and GAM324274

GR5699 AA907912 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5699(GR5699) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5699 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5699 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5699 gene encodes GR5699 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5699 precursor RNA folds spatially, forming GR5699 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5699 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5699 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5699 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5413 precursor RNA and GAM58128 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5413 RNA and GAM58128 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5413 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5413 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5413 target RNA into GAM5413 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM58128 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM58128 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM58128 target RNA into GAM58128 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5699 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5699 gene: GAM5413 target protein and GAM58128 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference,

with references to GAM5413 and GAM58128

GR5700 BI016564 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5700(GR5700) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5700 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5700 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5700 gene encodes GR5700 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5700 precursor RNA folds spatially, forming GR5700 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5700 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5700 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5700 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4306 precursor RNA, GAM6831 precursor RNA and GAM269865 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4306 RNA, GAM6831 RNA and GAM269865 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4306 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4306 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4306 target RNA into GAM4306 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6831 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM6831 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6831 target RNA into GAM6831 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM269865 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM269865 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM269865 target RNA into GAM269865 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5700 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5700 gene: GAM4306 target protein, GAM6831 target protein and GAM269865 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4306, GAM6831 and GAM269865

GR5701 BE794958 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5701(GR5701) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5701 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5701 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5701 gene encodes GR5701 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5701 precursor RNA folds spatially, forming GR5701 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5701 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5701 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5701 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8616 precursor RNA and GAM97004 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8616 RNA and GAM97004 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8616 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8616 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8616 target RNA into GAM8616 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM97004 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM97004 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM97004 target RNA into GAM97004 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5701 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5701 gene: GAM8616 target protein and GAM97004 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8616 and GAM97004

GR5702 AW610566 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5702(GR5702) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5702 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5702 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5702 gene encodes GR5702 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5702 precursor RNA folds spatially, forming GR5702 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5702 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5702 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5702 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM30497 precursor RNA and GAM116478 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM30497 RNA and GAM116478 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM30497 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM30497 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM30497 target RNA into GAM30497 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM116478 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM116478 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM116478 target RNA into GAM116478 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5702 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5702 gene: GAM30497 target protein and GAM116478 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM30497 and GAM116478

GR5703 H14915 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5703(GR5703) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5703 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5703 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5703 gene encodes GR5703 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5703 precursor RNA folds spatially, forming GR5703 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5703 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5703 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5703 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM26986 precursor RNA and GAM247922 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM26986 RNA and GAM247922 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM26986 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM26986 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM26986 target RNA into GAM26986 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM247922 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM247922 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM247922 target RNA into GAM247922 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5703 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5703 gene: GAM26986 target protein and GAM247922 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM26986 and GAM247922

GR5704 BG036206 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5704(GR5704) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5704 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5704 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5704 gene encodes GR5704 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5704 precursor RNA folds spatially, forming GR5704 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5704 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5704 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5704 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM123586 precursor RNA and GAM301020 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM123586 RNA and GAM301020 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM123586 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM123586 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM123586 target RNA into GAM123586 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM301020 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM301020 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM301020 target RNA into GAM301020 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5704 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5704 gene: GAM123586 target protein and GAM301020 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM123586 and GAM301020

GR5705 BI519097 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5705(GR5705) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5705 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5705 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5705 gene encodes GR5705 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5705 precursor RNA folds spatially, forming GR5705 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5705 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5705 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5705 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM5232 precursor RNA, GAM6334 precursor RNA and GAM179091 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5232 RNA, GAM6334 RNA and GAM179091 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5232 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5232 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5232 target RNA into GAM5232 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6334 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6334 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6334 target RNA into GAM6334 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM179091 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM179091 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM179091 target RNA into GAM179091 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5705 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5705 gene: GAM5232 target protein, GAM6334 target protein and GAM179091 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5232, GAM6334 and GAM179091

GR5706 AW242098 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5706(GR5706) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5706 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5706 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5706 gene encodes GR5706 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5706 precursor RNA folds spatially, forming GR5706 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5706 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5706 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5706 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM65871 precursor RNA and GAM104132 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM65871 RNA and GAM104132 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM65871 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM65871 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM65871 target RNA into GAM65871 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM104132 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM104132 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM104132 target RNA into GAM104132 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5706 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5706 gene: GAM65871 target protein and GAM104132 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM65871 and GAM104132

GR5707 BF126901 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5707(GR5707) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5707 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5707 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5707 gene encodes GR5707 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5707 precursor RNA folds spatially, forming GR5707 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5707 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5707 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5707 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM35862 precursor RNA, GAM221881 precursor RNA and GAM291729 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM35862 RNA, GAM221881 RNA and GAM291729 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM35862 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM35862 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM35862 target RNA into GAM35862 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM221881 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM221881 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM221881 target RNA into GAM221881 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM291729 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM291729 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM291729 target RNA into GAM291729 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5707 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5707 gene: GAM35862 target protein, GAM221881 target protein and GAM291729 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM35862, GAM221881 and GAM291729

GR5708 BF108286 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5708(GR5708) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5708 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5708 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5708 gene encodes GR5708 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5708 precursor RNA folds spatially, forming GR5708 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5708 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5708 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5708 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM93327 precursor RNA and GAM116528 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM93327 RNA and GAM116528 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM93327 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM93327 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM93327 target RNA into GAM93327 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM116528 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM116528 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM116528 target RNA into GAM116528 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5708 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5708 gene: GAM93327 target protein and GAM116528 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM93327 and GAM116528

bioinformatically detected regulatory gene, referred to here as Genomic Record 5709(GR5709) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5709 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5709 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5709 gene encodes GR5709 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5709 precursor RNA folds spatially, forming GR5709 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5709 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5709 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5709 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6669 precursor RNA and GAM40281 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6669 RNA and GAM40281 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6669 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6669 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6669 target RNA into GAM6669 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM40281 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM40281 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM40281

target RNA into GAM40281 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5709 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5709 gene: GAM6669 target protein and GAM40281 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6669 and GAM40281

GR5710 AI394648 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5710(GR5710) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5710 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5710 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5710 gene encodes GR5710 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5710 precursor RNA folds spatially, forming GR5710 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5710 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5710 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5710 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6613 precursor RNA and GAM7679 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6613 RNA and GAM7679 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6613 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6613 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6613 target RNA into GAM6613 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7679 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7679 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7679 target RNA into GAM7679 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5710 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5710 gene: GAM6613 target protein and GAM7679 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6613 and GAM7679

GR5711 AW665280 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5711(GR5711) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5711 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5711 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5711 gene encodes GR5711 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5711 precursor RNA folds spatially, forming GR5711 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5711 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5711 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5711 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4765 precursor RNA and GAM188355 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4765 RNA and GAM188355 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4765 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4765 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4765 target RNA into GAM4765 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM188355 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM188355 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM188355 target RNA into GAM188355 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5711 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5711 gene: GAM4765 target protein and GAM188355 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4765 and GAM188355

GR5712 BE783345 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5712(GR5712) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5712 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5712 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5712 gene encodes GR5712 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5712 precursor RNA folds spatially, forming GR5712 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5712 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5712 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5712 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM2895 precursor RNA, GAM4981 precursor RNA, GAM221872 precursor RNA and GAM300795 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2895 RNA, GAM4981 RNA, GAM221872 RNA and GAM300795 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2895 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2895 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2895 target RNA into GAM2895 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM4981 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4981 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4981 target RNA into GAM4981 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM221872 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM221872 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM221872 target RNA into GAM221872 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM300795 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM300795 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM300795 target RNA into GAM300795 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5712 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5712 gene: GAM2895 target protein, GAM4981 target protein, GAM221872 target protein and GAM300795 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2895, GAM4981, GAM221872 and GAM300795

GR5713 BF762270 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5713(GR5713) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5713 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5713 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5713 gene encodes GR5713 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5713 precursor RNA folds spatially, forming GR5713 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5713 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5713 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5713 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4040 precursor RNA and GAM17807 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4040 RNA and GAM17807 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4040 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4040 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4040 target RNA into GAM4040 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM17807 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM17807 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM17807 target RNA into GAM17807 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5713 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5713 gene: GAM4040 target protein and GAM17807 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4040 and GAM17807

GR5714 BM689228 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5714(GR5714) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5714 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5714 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5714 gene encodes GR5714 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5714 precursor RNA folds spatially, forming GR5714 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5714 folded precursor RNA comprises a plurality of what is known in the

art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5714 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5714 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM158690 precursor RNA and GAM198693 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM158690 RNA and GAM198693 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM158690 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM158690 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM158690 target RNA into GAM158690 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM198693 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM198693 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM198693 target RNA into GAM198693 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5714 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5714 gene: GAM158690 target protein and GAM198693 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM158690 and GAM198693

GR5715 BE542488 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5715(GR5715) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR5715 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5715 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5715 gene encodes GR5715 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5715 precursor RNA folds spatially, forming GR5715 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5715 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5715 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5715 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2349 precursor RNA, GAM3317 precursor RNA and GAM54485 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2349 RNA, GAM3317 RNA and GAM54485 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2349 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2349 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2349 target RNA into GAM2349 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM3317 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3317 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3317 target RNA into GAM3317 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM54485 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM54485 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM54485 target RNA into GAM54485 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5715 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5715 gene: GAM2349 target protein, GAM3317 target protein and GAM54485 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2349, GAM3317 and GAM54485

GR5716 AI962334 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5716(GR5716) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5716 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5716 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5716 gene encodes GR5716 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5716 precursor RNA folds spatially, forming GR5716 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5716 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5716 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5716 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM987 precursor RNA and GAM254536 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM987 RNA and GAM254536 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM987 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM987 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM987 target RNA into GAM987 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM254536 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM254536 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM254536 target RNA into GAM254536 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5716 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5716 gene: GAM987 target protein and GAM254536 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM987 and GAM254536

GR5717 BI822902 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5717(GR5717) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5717 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5717 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5717 gene encodes GR5717 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5717 precursor RNA folds spatially, forming GR5717 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5717 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR5717 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5717 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3699 precursor RNA and GAM296277 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3699 RNA and GAM296277 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3699 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3699 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3699 target RNA into GAM3699 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM296277 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM296277 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM296277 target RNA into GAM296277 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5717 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5717 gene: GAM3699 target protein and GAM296277 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3699 and GAM296277

GR5718 BF941803 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5718(GR5718) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5718 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5718 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5718 gene encodes GR5718 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5718 precursor RNA folds spatially, forming GR5718 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5718 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5718 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5718 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM65427 precursor RNA and GAM257954 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM65427 RNA and GAM257954 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM65427 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM65427 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM65427 target RNA into GAM65427 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM257954 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM257954 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM257954 target RNA into GAM257954 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5718 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5718 gene: GAM65427 target protein and GAM257954 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM65427 and GAM257954

GR5719 BM046157 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5719(GR5719) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5719 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5719 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5719 gene encodes GR5719 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5719 precursor RNA folds spatially, forming GR5719 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5719 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5719 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5719 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM5565 precursor RNA, GAM230490 precursor RNA and GAM291059 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5565 RNA, GAM230490 RNA and GAM291059 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5565 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5565 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig. 8, thereby inhibiting translation of GAM5565 target RNA into GAM5565 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM230490 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM230490 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM230490 target RNA into GAM230490 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM291059 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM291059 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM291059 target RNA into GAM291059 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5719 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5719 gene: GAM5565 target protein, GAM230490 target protein and GAM291059 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5565, GAM230490 and GAM291059

GR5720 AI749020 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5720 (GR5720) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5720 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5720 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5720 gene encodes GR5720 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5720 precursor RNA folds spatially, forming GR5720 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5720 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5720 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5720 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM87733 precursor RNA and GAM237712 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM87733 RNA and GAM237712 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM87733 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM87733 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM87733 target RNA into GAM87733 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM237712 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM237712 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM237712 target RNA into GAM237712 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5720 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5720 gene: GAM87733 target protein and GAM237712 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM87733 and GAM237712

GR5721 AW300887 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5721 (GR5721) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5721 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5721 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5721 gene encodes GR5721 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5721 precursor RNA folds spatially, forming GR5721 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5721 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5721 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5721 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM77486 precursor RNA and GAM151196 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM77486 RNA and GAM151196 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM77486 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM77486 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM77486 target RNA into GAM77486 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM151196 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM151196 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM151196 target RNA into GAM151196 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5721 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR5721 gene: GAM77486 target protein and GAM151196 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM77486 and GAM151196

GR5722 AA132579 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5722(GR5722) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5722 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5722 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5722 gene encodes GR5722 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5722 precursor RNA folds spatially, forming GR5722 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5722 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5722 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5722 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM16528 precursor RNA and GAM310015 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM16528 RNA and GAM310015 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM16528 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM16528 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM16528 target RNA into GAM16528 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM310015 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM310015 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM310015 target RNA into GAM310015 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5722 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5722 gene: GAM16528 target protein and GAM310015 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM16528 and GAM310015

GR5723 AI094357 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5723(GR5723) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5723 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5723 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5723 gene encodes GR5723 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5723 precursor RNA folds spatially, forming GR5723 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5723 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5723 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5723 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3960 precursor RNA, GAM42375 precursor RNA and GAM93166 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3960 RNA, GAM42375 RNA and GAM93166 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3960 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3960 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3960 target RNA into GAM3960 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM42375 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM42375 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM42375 target RNA into GAM42375 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM93166 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM93166 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM93166 target RNA into GAM93166 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5723 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5723 gene: GAM3960 target protein, GAM42375 target protein and GAM93166 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3960, GAM42375 and GAM93166

GR5724 BG613556 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5724(GR5724) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5724 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR5724 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5724 gene encodes GR5724 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5724 precursor RNA folds spatially, forming GR5724 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5724 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5724 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5724 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6781 precursor RNA and GAM75229 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6781 RNA and GAM75229 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6781 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6781 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6781 target RNA into GAM6781 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM75229 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM75229 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM75229 target RNA into GAM75229 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5724 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5724 gene: GAM6781 target

protein and GAM75229 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6781 and GAM75229

GR5725 BF528063 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5725(GR5725) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5725 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5725 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5725 gene encodes GR5725 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5725 precursor RNA folds spatially, forming GR5725 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5725 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5725 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5725 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2121 precursor RNA and GAM112520 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2121 RNA and GAM112520 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2121 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2121 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2121 target RNA into GAM2121 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM112520 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM112520 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM112520 target RNA into GAM112520 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5725 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5725 gene: GAM2121 target protein and GAM112520 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2121 and GAM112520

GR5726 BF790648 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5726(GR5726) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5726 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5726 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5726 gene encodes GR5726 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5726 precursor RNA folds spatially, forming GR5726 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5726 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5726 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5726 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM62193 precursor RNA, GAM147544 precursor RNA and GAM197771 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM62193 RNA, GAM147544 RNA and GAM197771 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM62193 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM62193 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM62193 target RNA into GAM62193 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM147544 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM147544 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM147544 target RNA into GAM147544 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM197771 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM197771 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM197771 target RNA into GAM197771 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5726 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5726 gene: GAM62193 target protein, GAM147544 target protein and GAM197771 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM62193, GAM147544 and GAM197771

GR5727 BI038187 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5727(GR5727) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5727 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5727

gene was detected is described hereinabove with reference to Figs. 8-18.

GR5727 gene encodes GR5727 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5727 precursor RNA folds spatially, forming GR5727 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5727 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5727 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5727 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM89012 precursor RNA and GAM206947 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM89012 RNA and GAM206947 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM89012 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM89012 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM89012 target RNA into GAM89012 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM206947 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM206947 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM206947 target RNA into GAM206947 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5727 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5727 gene: GAM89012 target protein and GAM206947 target protein, herein schematically represented by GAM1

TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM89012 and GAM206947

GR5728 BQ014312 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5728(GR5728) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5728 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5728 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5728 gene encodes GR5728 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5728 precursor RNA folds spatially, forming GR5728 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5728 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5728 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5728 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7194 precursor RNA and GAM334920 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7194 RNA and GAM334920 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7194 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7194 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7194 target RNA into GAM7194 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM334920 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM334920 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM334920 target RNA into GAM334920 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5728 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5728 gene: GAM7194 target protein and GAM334920 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7194 and GAM334920

GR5729 AA115212 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5729(GR5729) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5729 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5729 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5729 gene encodes GR5729 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5729 precursor RNA folds spatially, forming GR5729 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5729 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5729 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5729 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM154870 precursor RNA and GAM293645 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM154870 RNA and GAM293645 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM154870 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM154870 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM154870 target RNA into GAM154870 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM293645 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM293645 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM293645 target RNA into GAM293645 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5729 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5729 gene: GAM154870 target protein and GAM293645 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM154870 and GAM293645

GR5730 BF907842 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5730(GR5730) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5730 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5730 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5730 gene encodes GR5730 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5730 precursor RNA folds spatially, forming GR5730 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5730 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5730 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5730 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM228492 precursor RNA and GAM332189 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM228492 RNA and GAM332189 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM228492 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM228492 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM228492 target RNA into GAM228492 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM332189 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM332189 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM332189 target RNA into GAM332189 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5730 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5730 gene: GAM228492 target protein and GAM332189 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM228492 and GAM332189

GR5731 BF573272 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5731 (GR5731) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5731 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5731 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5731 gene encodes GR5731 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5731 precursor RNA folds spatially, forming GR5731 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5731 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5731 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5731 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3835 precursor RNA and GAM4905 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3835 RNA and GAM4905 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3835 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3835 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3835 target RNA into GAM3835 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM4905 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4905 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4905 target RNA into GAM4905 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5731 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR5731 gene: GAM3835 target protein and GAM4905 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3835 and GAM4905

GR5732 BG981142 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5732(GR5732) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5732 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5732 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5732 gene encodes GR5732 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5732 precursor RNA folds spatially, forming GR5732 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5732 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5732 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5732 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM17857 precursor RNA and GAM314303 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM17857 RNA and GAM314303 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM17857 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM17857 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM17857 target RNA into GAM17857 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM314303 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM314303 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM314303 target RNA into GAM314303 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5732 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5732 gene: GAM17857 target protein and GAM314303 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM17857 and GAM314303

GR5733 H05379 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5733(GR5733) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5733 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5733 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5733 gene encodes GR5733 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5733 precursor RNA folds spatially, forming GR5733 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5733 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5733 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5733 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM12717 precursor RNA, GAM169778 precursor RNA and GAM190476 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM12717 RNA, GAM169778 RNA and GAM190476 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM12717 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM12717 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM12717 target RNA into GAM12717 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM169778 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM169778 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM169778 target RNA into GAM169778 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM190476 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM190476 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM190476 target RNA into GAM190476 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5733 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5733 gene: GAM12717 target protein, GAM169778 target protein and GAM190476 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM12717, GAM169778 and GAM190476

GR5734 AA417809 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5734(GR5734) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5734 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR5734 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5734 gene encodes GR5734 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5734 precursor RNA folds spatially, forming GR5734 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5734 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5734 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5734 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM375 precursor RNA, GAM7544 precursor RNA and GAM7925 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM375 RNA, GAM7544 RNA and GAM7925 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM375 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM375 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM375 target RNA into GAM375 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7544 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7544 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7544 target RNA into GAM7544 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7925 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7925 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds

to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7925 target RNA into GAM7925 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5734 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5734 gene: GAM375 target protein, GAM7544 target protein and GAM7925 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM375, GAM7544 and GAM7925

GR5735 AU133440 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5735(GR5735) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5735 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5735 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5735 gene encodes GR5735 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5735 precursor RNA folds spatially, forming GR5735 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5735 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5735 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5735 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM120284 precursor RNA, GAM130229 precursor RNA and GAM219661 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM120284 RNA, GAM130229 RNA and GAM219661 RNA, herein

schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM120284 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM120284 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM120284 target RNA into GAM120284 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM130229 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM130229 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM130229 target RNA into GAM130229 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM219661 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM219661 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM219661 target RNA into GAM219661 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5735 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5735 gene: GAM120284 target protein, GAM130229 target protein and GAM219661 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM120284, GAM130229 and GAM219661

GR5736 BF514026 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5736(GR5736) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5736 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5736 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5736 gene encodes GR5736 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5736 precursor RNA folds spatially, forming GR5736 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5736 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5736 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5736 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2131 precursor RNA, GAM224280 precursor RNA and GAM276204 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2131 RNA, GAM224280 RNA and GAM276204 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2131 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2131 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2131 target RNA into GAM2131 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM224280 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM224280 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM224280 target RNA into GAM224280 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM276204 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM276204 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM276204 target RNA into GAM276204 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5736 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5736 gene: GAM2131 target protein, GAM224280 target protein and GAM276204 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2131, GAM224280 and GAM276204

GR5737 AV754883 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5737(GR5737) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5737 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5737 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5737 gene encodes GR5737 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5737 precursor RNA folds spatially, forming GR5737 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5737 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5737 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5737 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2661 precursor RNA and GAM272993 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2661 RNA and GAM272993 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2661 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM2661 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2661 target RNA into GAM2661 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM272993 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM272993 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM272993 target RNA into GAM272993 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5737 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5737 gene: GAM2661 target protein and GAM272993 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2661 and GAM272993

GR5738 BM083540 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5738(GR5738) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5738 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5738 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5738 gene encodes GR5738 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5738 precursor RNA folds spatially, forming GR5738 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5738 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5738 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5738 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2

separate GAM precursor RNAs, GAM1828 precursor RNA and GAM114633 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1828 RNA and GAM114633 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1828 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1828 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1828 target RNA into GAM1828 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM114633 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM114633 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM114633 target RNA into GAM114633 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5738 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5738 gene: GAM1828 target protein and GAM114633 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1828 and GAM114633

GR5739 BF243964 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5739(GR5739) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5739 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5739 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5739 gene encodes GR5739 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR5739 precursor RNA folds spatially, forming GR5739 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5739 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5739 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5739 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM8066 precursor RNA, GAM24825 precursor RNA and GAM192462 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8066 RNA, GAM24825 RNA and GAM192462 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8066 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8066 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8066 target RNA into GAM8066 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM24825 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM24825 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM24825 target RNA into GAM24825 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM192462 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM192462 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM192462 target RNA into GAM192462 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5739 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5739 gene: GAM8066 target protein, GAM24825 target protein and GAM192462 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8066, GAM24825 and GAM192462

GR5740 BG482538 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5740(GR5740) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5740 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5740 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5740 gene encodes GR5740 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5740 precursor RNA folds spatially, forming GR5740 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5740 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5740 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5740 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM7953 precursor RNA, GAM218298 precursor RNA and GAM257805 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7953 RNA, GAM218298 RNA and GAM257805 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7953 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM7953 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7953 target RNA into GAM7953 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM218298 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM218298 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM218298 target RNA into GAM218298 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM257805 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM257805 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM257805 target RNA into GAM257805 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5740 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5740 gene: GAM7953 target protein, GAM218298 target protein and GAM257805 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7953, GAM218298 and GAM257805

GR5741 BM017671 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5741(GR5741) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5741 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5741 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5741 gene encodes GR5741 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5741 precursor RNA folds spatially, forming GR5741 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated

that GR5741 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5741 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5741 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM34713 precursor RNA and GAM61770 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM34713 RNA and GAM61770 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM34713 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM34713 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM34713 target RNA into GAM34713 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM61770 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM61770 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM61770 target RNA into GAM61770 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5741 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5741 gene: GAM34713 target protein and GAM61770 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM34713 and GAM61770

GR5742 AI435525 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5742(GR5742) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR5742 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5742 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5742 gene encodes GR5742 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5742 precursor RNA folds spatially, forming GR5742 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5742 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5742 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5742 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM316488 precursor RNA and GAM334238 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM316488 RNA and GAM334238 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM316488 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM316488 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM316488 target RNA into GAM316488 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM334238 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM334238 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM334238 target RNA into GAM334238 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5742 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5742 gene: GAM316488 target protein and GAM334238 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM316488 and GAM334238

GR5743 AA648927 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5743(GR5743) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5743 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5743 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5743 gene encodes GR5743 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5743 precursor RNA folds spatially, forming GR5743 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5743 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5743 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5743 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM152652 precursor RNA, GAM173725 precursor RNA and GAM308923 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM152652 RNA, GAM173725 RNA and GAM308923 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM152652 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM152652 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM152652 target RNA into GAM152652 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM173725 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM173725 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM173725 target RNA into GAM173725 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM308923 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM308923 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM308923 target RNA into GAM308923 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5743 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5743 gene: GAM152652 target protein, GAM173725 target protein and GAM308923 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM152652, GAM173725 and GAM308923

GR5744 AA191047 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5744(GR5744) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5744 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5744 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5744 gene encodes GR5744 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5744 precursor RNA folds spatially, forming GR5744 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5744 folded precursor RNA comprises a plurality of what is known in the

art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5744 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5744 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM172663 precursor RNA and GAM302594 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM172663 RNA and GAM302594 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM172663 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM172663 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM172663 target RNA into GAM172663 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM302594 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM302594 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM302594 target RNA into GAM302594 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5744 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5744 gene: GAM172663 target protein and GAM302594 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM172663 and GAM302594

GR5745 AI677898 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5745(GR5745) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR5745 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5745 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5745 gene encodes GR5745 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5745 precursor RNA folds spatially, forming GR5745 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5745 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5745 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5745 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5320 precursor RNA and GAM135111 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5320 RNA and GAM135111 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5320 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5320 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5320 target RNA into GAM5320 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM135111 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM135111 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM135111 target RNA into GAM135111 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly

utilities, of GR5745 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5745 gene: GAM5320 target protein and GAM135111 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5320 and GAM135111

GR5746 BG674014 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5746(GR5746) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5746 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5746 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5746 gene encodes GR5746 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5746 precursor RNA folds spatially, forming GR5746 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5746 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5746 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5746 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4468 precursor RNA, GAM148226 precursor RNA and GAM229859 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4468 RNA, GAM148226 RNA and GAM229859 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4468 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4468 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds

to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4468 target RNA into GAM4468 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM148226 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM148226 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM148226 target RNA into GAM148226 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM229859 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM229859 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM229859 target RNA into GAM229859 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5746 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5746 gene: GAM4468 target protein, GAM148226 target protein and GAM229859 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4468, GAM148226 and GAM229859

GR5747 BI828837 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5747(GR5747) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5747 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5747 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5747 gene encodes GR5747 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5747 precursor RNA folds spatially, forming GR5747 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5747 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR5747 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5747 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM64332 precursor RNA and GAM159080 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM64332 RNA and GAM159080 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM64332 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM64332 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM64332 target RNA into GAM64332 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM159080 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM159080 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM159080 target RNA into GAM159080 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5747 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5747 gene: GAM64332 target protein and GAM159080 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM64332 and GAM159080

GR5748 BM700731 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5748(GR5748) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5748 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5748 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5748 gene encodes GR5748 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5748 precursor RNA folds spatially, forming GR5748 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5748 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5748 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5748 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2533 precursor RNA and GAM3886 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2533 RNA and GAM3886 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2533 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2533 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2533 target RNA into GAM2533 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM3886 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3886 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3886 target RNA into GAM3886 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5748 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5748 gene: GAM2533 target protein and GAM3886 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2533 and GAM3886

GR5749 BG435489 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5749(GR5749) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5749 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5749 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5749 gene encodes GR5749 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5749 precursor RNA folds spatially, forming GR5749 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5749 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5749 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5749 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7185 precursor RNA and GAM154205 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7185 RNA and GAM154205 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7185 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7185 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7185 target RNA into

GAM7185 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM154205 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM154205 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM154205 target RNA into GAM154205 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5749 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5749 gene: GAM7185 target protein and GAM154205 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7185 and GAM154205

GR5750 AW752814 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5750(GR5750) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5750 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5750 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5750 gene encodes GR5750 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5750 precursor RNA folds spatially, forming GR5750 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5750 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5750 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5750 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM108513 precursor RNA and GAM286522 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM108513 RNA and GAM286522 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM108513 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM108513 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM108513 target RNA into GAM108513 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM286522 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM286522 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM286522 target RNA into GAM286522 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5750 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5750 gene: GAM108513 target protein and GAM286522 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM108513 and GAM286522

GR5751 T74289 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5751(GR5751) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5751 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5751 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5751 gene encodes GR5751 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5751 precursor RNA folds spatially, forming GR5751 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated

that GR5751 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5751 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5751 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1604 precursor RNA and GAM299153 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1604 RNA and GAM299153 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1604 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1604 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1604 target RNA into GAM1604 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM299153 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM299153 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM299153 target RNA into GAM299153 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5751 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5751 gene: GAM1604 target protein and GAM299153 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1604 and GAM299153

GR5752 BI765533 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5752(GR5752) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR5752 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5752 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5752 gene encodes GR5752 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5752 precursor RNA folds spatially, forming GR5752 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5752 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5752 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5752 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM52627 precursor RNA, GAM91562 precursor RNA and GAM279436 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM52627 RNA, GAM91562 RNA and GAM279436 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM52627 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM52627 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM52627 target RNA into GAM52627 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM91562 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM91562 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM91562 target RNA into GAM91562 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM279436 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM279436 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM279436 target RNA into GAM279436 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5752 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5752 gene: GAM52627 target protein, GAM91562 target protein and GAM279436 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM52627, GAM91562 and GAM279436

GR5753 AI360445 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5753(GR5753) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5753 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5753 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5753 gene encodes GR5753 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5753 precursor RNA folds spatially, forming GR5753 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5753 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5753 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5753 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5440 precursor RNA and GAM10784 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5440 RNA and GAM10784 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5440 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5440 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5440 target RNA into GAM5440 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM10784 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM10784 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM10784 target RNA into GAM10784 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5753 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5753 gene: GAM5440 target protein and GAM10784 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5440 and GAM10784

GR5754 AW593249 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5754(GR5754) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5754 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5754 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5754 gene encodes GR5754 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5754 precursor RNA folds spatially, forming GR5754 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5754 folded precursor RNA comprises a plurality of what is known in the

art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5754 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5754 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8490 precursor RNA and GAM181844 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8490 RNA and GAM181844 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8490 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8490 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8490 target RNA into GAM8490 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM181844 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM181844 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM181844 target RNA into GAM181844 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5754 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5754 gene: GAM8490 target protein and GAM181844 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8490 and GAM181844

GR5755 AW995413 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5755(GR5755) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR5755 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5755 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5755 gene encodes GR5755 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5755 precursor RNA folds spatially, forming GR5755 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5755 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5755 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5755 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2653 precursor RNA, GAM8424 precursor RNA and GAM261127 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2653 RNA, GAM8424 RNA and GAM261127 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2653 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2653 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2653 target RNA into GAM2653 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8424 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8424 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8424 target RNA into GAM8424 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM261127 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM261127 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM261127 target RNA into GAM261127 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5755 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5755 gene: GAM2653 target protein, GAM8424 target protein and GAM261127 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2653, GAM8424 and GAM261127

GR5756 BI859038 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5756(GR5756) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5756 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5756 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5756 gene encodes GR5756 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5756 precursor RNA folds spatially, forming GR5756 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5756 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5756 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5756 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4343 precursor RNA and GAM321602 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4343 RNA and GAM321602 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4343 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4343 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4343 target RNA into GAM4343 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM321602 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM321602 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM321602 target RNA into GAM321602 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5756 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5756 gene: GAM4343 target protein and GAM321602 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4343 and GAM321602

GR5757 BG946112 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5757(GR5757) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5757 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5757 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5757 gene encodes GR5757 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5757 precursor RNA folds spatially, forming GR5757 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5757 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR5757 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5757 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3521 precursor RNA and GAM26838 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3521 RNA and GAM26838 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3521 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3521 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3521 target RNA into GAM3521 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM26838 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM26838 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM26838 target RNA into GAM26838 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5757 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5757 gene: GAM3521 target protein and GAM26838 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3521 and GAM26838

GR5758 BM768192 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5758(GR5758) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5758 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5758 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5758 gene encodes GR5758 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5758 precursor RNA folds spatially, forming GR5758 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5758 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5758 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5758 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3051 precursor RNA and GAM261448 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3051 RNA and GAM261448 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3051 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3051 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3051 target RNA into GAM3051 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM261448 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM261448 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM261448 target RNA into GAM261448 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5758 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5758 gene: GAM3051 target protein and GAM261448 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3051 and GAM261448

GR5759 AV705908 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5759(GR5759) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5759 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5759 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5759 gene encodes GR5759 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5759 precursor RNA folds spatially, forming GR5759 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5759 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5759 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5759 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM213071 precursor RNA and GAM317750 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM213071 RNA and GAM317750 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM213071 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM213071 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM213071

target RNA into GAM213071 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM317750 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM317750 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM317750 target RNA into GAM317750 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5759 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5759 gene: GAM213071 target protein and GAM317750 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM213071 and GAM317750

GR5760 BE275965 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5760(GR5760) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5760 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5760 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5760 gene encodes GR5760 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5760 precursor RNA folds spatially, forming GR5760 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5760 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5760 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5760 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM6256 precursor RNA, GAM14290 precursor RNA and GAM112984 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED

PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6256 RNA, GAM14290 RNA and GAM112984 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6256 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6256 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6256 target RNA into GAM6256 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM14290 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM14290 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM14290 target RNA into GAM14290 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM112984 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM112984 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM112984 target RNA into GAM112984 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5760 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5760 gene: GAM6256 target protein, GAM14290 target protein and GAM112984 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6256, GAM14290 and GAM112984

GR5761 BF082657 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5761(GR5761) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5761 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5761 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5761 gene encodes GR5761 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5761 precursor RNA folds spatially, forming GR5761 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5761 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5761 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5761 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1672 precursor RNA and GAM160771 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1672 RNA and GAM160771 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1672 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1672 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1672 target RNA into GAM1672 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM160771 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM160771 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM160771 target RNA into GAM160771 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5761 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR5761 gene: GAM1672 target protein and GAM160771 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1672 and GAM160771

GR5762 AI797880 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5762(GR5762) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5762 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5762 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5762 gene encodes GR5762 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5762 precursor RNA folds spatially, forming GR5762 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5762 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5762 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5762 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM59052 precursor RNA, GAM61002 precursor RNA and GAM79265 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM59052 RNA, GAM61002 RNA and GAM79265 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM59052 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM59052 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM59052

target RNA into GAM59052 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM61002 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM61002 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM61002 target RNA into GAM61002 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM79265 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM79265 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM79265 target RNA into GAM79265 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5762 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5762 gene: GAM59052 target protein, GAM61002 target protein and GAM79265 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM59052, GAM61002 and GAM79265

GR5763 AW163547 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5763(GR5763) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5763 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5763 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5763 gene encodes GR5763 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5763 precursor RNA folds spatially, forming GR5763 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5763 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5763 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5763 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1454 precursor RNA, GAM6088 precursor RNA and GAM246261 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1454 RNA, GAM6088 RNA and GAM246261 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1454 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1454 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1454 target RNA into GAM1454 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6088 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6088 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6088 target RNA into GAM6088 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM246261 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM246261 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM246261 target RNA into GAM246261 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5763 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5763 gene: GAM1454 target protein, GAM6088 target protein and GAM246261 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1454, GAM6088 and

GR5764 AW369106 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5764(GR5764) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5764 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5764 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5764 gene encodes GR5764 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5764 precursor RNA folds spatially, forming GR5764 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5764 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5764 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5764 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM6798 precursor RNA, GAM53601 precursor RNA and GAM87541 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6798 RNA, GAM53601 RNA and GAM87541 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6798 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6798 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6798 target RNA into GAM6798 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM53601 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM53601 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM53601 target RNA into GAM53601 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM87541 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM87541 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM87541 target RNA into GAM87541 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5764 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5764 gene: GAM6798 target protein, GAM53601 target protein and GAM87541 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6798, GAM53601 and GAM87541

GR5765 BI546779 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5765(GR5765) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5765 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5765 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5765 gene encodes GR5765 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5765 precursor RNA folds spatially, forming GR5765 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5765 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5765 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5765 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM7034 precursor RNA, GAM61860 precursor RNA and GAM275388 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7034 RNA, GAM61860 RNA and GAM275388 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7034 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7034 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7034 target RNA into GAM7034 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM61860 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM61860 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM61860 target RNA into GAM61860 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM275388 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM275388 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM275388 target RNA into GAM275388 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5765 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5765 gene: GAM7034 target protein, GAM61860 target protein and GAM275388 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7034, GAM61860 and GAM275388

5766(GR5766) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5766 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5766 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5766 gene encodes GR5766 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5766 precursor RNA folds spatially, forming GR5766 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5766 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5766 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5766 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM115359 precursor RNA, GAM222343 precursor RNA, GAM251202 precursor RNA and GAM284043 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM115359 RNA, GAM222343 RNA, GAM251202 RNA and GAM284043 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM115359 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM115359 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM115359 target RNA into GAM115359 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM222343 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM222343 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM222343

target RNA into GAM222343 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM251202 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM251202 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM251202 target RNA into GAM251202 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM284043 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM284043 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM284043 target RNA into GAM284043 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5766 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5766 gene: GAM115359 target protein, GAM222343 target protein, GAM251202 target protein and GAM284043 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM115359, GAM222343, GAM251202 and GAM284043

GR5767 H40907 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5767(GR5767) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5767 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5767 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5767 gene encodes GR5767 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5767 precursor RNA folds spatially, forming GR5767 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5767 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5767 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5767 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM131924 precursor RNA and GAM176601 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM131924 RNA and GAM176601 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM131924 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM131924 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM131924 target RNA into GAM131924 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM176601 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM176601 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM176601 target RNA into GAM176601 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5767 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5767 gene: GAM131924 target protein and GAM176601 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM131924 and GAM176601

GR5768 BM709967 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5768(GR5768) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5768 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR5768 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5768 gene encodes GR5768 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5768 precursor RNA folds spatially, forming GR5768 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5768 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5768 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5768 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM312099 precursor RNA and GAM324620 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM312099 RNA and GAM324620 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM312099 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM312099 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM312099 target RNA into GAM312099 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM324620 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM324620 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM324620 target RNA into GAM324620 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5768 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5768 gene: GAM312099 target

protein and GAM324620 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM312099 and GAM324620

GR5769 BG772745 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5769(GR5769) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5769 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5769 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5769 gene encodes GR5769 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5769 precursor RNA folds spatially, forming GR5769 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5769 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5769 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5769 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM68110 precursor RNA, GAM85139 precursor RNA and GAM255452 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM68110 RNA, GAM85139 RNA and GAM255452 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM68110 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM68110 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM68110 target RNA into GAM68110 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM85139 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM85139 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM85139 target RNA into GAM85139 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM255452 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM255452 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM255452 target RNA into GAM255452 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5769 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5769 gene: GAM68110 target protein, GAM85139 target protein and GAM255452 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM68110, GAM85139 and GAM255452

GR5770 AW797776 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5770(GR5770) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5770 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5770 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5770 gene encodes GR5770 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5770 precursor RNA folds spatially, forming GR5770 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5770 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5770 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR5770 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6720 precursor RNA and GAM16565 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6720 RNA and GAM16565 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6720 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6720 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6720 target RNA into GAM6720 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM16565 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM16565 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM16565 target RNA into GAM16565 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5770 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5770 gene: GAM6720 target protein and GAM16565 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6720 and GAM16565

GR5771 AW957365 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5771(GR5771) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5771 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5771

gene was detected is described hereinabove with reference to Figs. 8-18.

GR5771 gene encodes GR5771 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5771 precursor RNA folds spatially, forming GR5771 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5771 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5771 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5771 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM86455 precursor RNA, GAM132264 precursor RNA and GAM205818 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM86455 RNA, GAM132264 RNA and GAM205818 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM86455 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM86455 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM86455 target RNA into GAM86455 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM132264 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM132264 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM132264 target RNA into GAM132264 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM205818 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM205818 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM205818 target RNA into GAM205818 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5771 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5771 gene: GAM86455 target protein, GAM132264 target protein and GAM205818 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM86455, GAM132264 and GAM205818

GR5772 BE741716 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5772(GR5772) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5772 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5772 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5772 gene encodes GR5772 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5772 precursor RNA folds spatially, forming GR5772 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5772 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5772 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5772 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM97012 precursor RNA, GAM269446 precursor RNA and GAM325015 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM97012 RNA, GAM269446 RNA and GAM325015 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs

corresponding to GAM RNA of Fig. 8.

GAM97012 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM97012 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM97012 target RNA into GAM97012 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM269446 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM269446 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM269446 target RNA into GAM269446 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM325015 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM325015 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM325015 target RNA into GAM325015 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5772 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5772 gene: GAM97012 target protein, GAM269446 target protein and GAM325015 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM97012, GAM269446 and GAM325015

GR5773 AU139809 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5773(GR5773) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5773 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5773 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5773 gene encodes GR5773 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR5773 precursor RNA folds spatially, forming GR5773 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5773 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5773 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5773 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM851 precursor RNA and GAM47231 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM851 RNA and GAM47231 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM851 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM851 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM851 target RNA into GAM851 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM47231 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM47231 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM47231 target RNA into GAM47231 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5773 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5773 gene: GAM851 target protein and GAM47231 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM851 and GAM47231

GR5774 AW512809 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5774(GR5774) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5774 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5774 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5774 gene encodes GR5774 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5774 precursor RNA folds spatially, forming GR5774 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5774 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5774 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5774 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2520 precursor RNA and GAM2977 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2520 RNA and GAM2977 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2520 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2520 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2520 target RNA into GAM2520 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM2977 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2977 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig. 8, thereby inhibiting translation of GAM2977 target RNA into GAM2977 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5774 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5774 gene: GAM2520 target protein and GAM2977 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2520 and GAM2977

GR5775 AW380397 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5775(GR5775) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5775 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5775 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5775 gene encodes GR5775 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5775 precursor RNA folds spatially, forming GR5775 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5775 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5775 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5775 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM5533 precursor RNA, GAM195549 precursor RNA and GAM307432 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5533 RNA, GAM195549 RNA and GAM307432 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5533 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5533 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5533 target RNA into GAM5533 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM195549 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM195549 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM195549 target RNA into GAM195549 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM307432 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM307432 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM307432 target RNA into GAM307432 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5775 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5775 gene: GAM5533 target protein, GAM195549 target protein and GAM307432 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5533, GAM195549 and GAM307432

GR5776 W76439 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5776(GR5776) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5776 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5776 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5776 gene encodes GR5776 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5776 precursor RNA folds spatially, forming GR5776 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5776 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5776 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5776 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4428 precursor RNA, GAM49087 precursor RNA and GAM232629 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4428 RNA, GAM49087 RNA and GAM232629 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4428 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4428 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4428 target RNA into GAM4428 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM49087 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM49087 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM49087 target RNA into GAM49087 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM232629 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM232629 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM232629 target RNA into GAM232629 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly

utilities, of GR5776 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5776 gene: GAM4428 target protein, GAM49087 target protein and GAM232629 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4428, GAM49087 and GAM232629

GR5777 AV762064 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5777(GR5777) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5777 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5777 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5777 gene encodes GR5777 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5777 precursor RNA folds spatially, forming GR5777 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5777 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5777 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5777 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM179309 precursor RNA and GAM266977 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM179309 RNA and GAM266977 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM179309 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM179309 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM179309 target RNA into GAM179309 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM266977 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM266977 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM266977 target RNA into GAM266977 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5777 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5777 gene: GAM179309 target protein and GAM266977 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM179309 and GAM266977

GR5778 BI756229 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5778(GR5778) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5778 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5778 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5778 gene encodes GR5778 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5778 precursor RNA folds spatially, forming GR5778 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5778 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5778 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5778 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM100622 precursor RNA and GAM308431 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3

FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM100622 RNA and GAM308431 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM100622 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM100622 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM100622 target RNA into GAM100622 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM308431 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM308431 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM308431 target RNA into GAM308431 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5778 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5778 gene: GAM100622 target protein and GAM308431 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM100622 and GAM308431

GR5779 N80308 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5779(GR5779) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5779 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5779 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5779 gene encodes GR5779 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5779 precursor RNA folds spatially, forming GR5779 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5779 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5779 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5779 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1995 precursor RNA, GAM267168 precursor RNA and GAM324403 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1995 RNA, GAM267168 RNA and GAM324403 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1995 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1995 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1995 target RNA into GAM1995 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM267168 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM267168 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM267168 target RNA into GAM267168 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM324403 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM324403 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM324403 target RNA into GAM324403 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5779 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5779 gene: GAM1995 target protein, GAM267168 target protein and GAM324403 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1995, GAM267168 and GAM324403

GR5780 BE246226 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5780(GR5780) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5780 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5780 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5780 gene encodes GR5780 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5780 precursor RNA folds spatially, forming GR5780 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5780 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5780 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5780 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM148393 precursor RNA and GAM217570 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM148393 RNA and GAM217570 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM148393 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM148393 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM148393 target RNA into GAM148393 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM217570 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM217570 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM217570 target RNA into GAM217570 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5780 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5780 gene: GAM148393 target protein and GAM217570 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM148393 and GAM217570

GR5781 BG724338 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5781(GR5781) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5781 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5781 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5781 gene encodes GR5781 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5781 precursor RNA folds spatially, forming GR5781 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5781 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5781 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5781 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM271008 precursor RNA and GAM283292 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin

shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM271008 RNA and GAM283292 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM271008 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM271008 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM271008 target RNA into GAM271008 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM283292 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM283292 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM283292 target RNA into GAM283292 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5781 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5781 gene: GAM271008 target protein and GAM283292 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM271008 and GAM283292

GR5782 BE614110 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5782(GR5782) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5782 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5782 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5782 gene encodes GR5782 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5782 precursor RNA folds spatially, forming GR5782 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5782 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5782 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5782 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM8535 precursor RNA, GAM77969 precursor RNA and GAM289960 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8535 RNA, GAM77969 RNA and GAM289960 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8535 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8535 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8535 target RNA into GAM8535 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM77969 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM77969 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM77969 target RNA into GAM77969 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM289960 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM289960 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM289960 target RNA into GAM289960 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5782 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR5782 gene: GAM8535 target protein, GAM77969 target protein and GAM289960 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8535, GAM77969 and GAM289960

GR5783 BQ018544 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5783(GR5783) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5783 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5783 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5783 gene encodes GR5783 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5783 precursor RNA folds spatially, forming GR5783 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5783 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5783 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5783 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8017 precursor RNA and GAM115780 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8017 RNA and GAM115780 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8017 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8017 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8017 target RNA into

GAM8017 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM115780 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM115780 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM115780 target RNA into GAM115780 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5783 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5783 gene: GAM8017 target protein and GAM115780 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8017 and GAM115780

GR5784 BG254485 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5784(GR5784) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5784 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5784 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5784 gene encodes GR5784 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5784 precursor RNA folds spatially, forming GR5784 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5784 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5784 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5784 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM108062 precursor RNA and GAM173513 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM108062 RNA and GAM173513 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM108062 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM108062 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM108062 target RNA into GAM108062 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM173513 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM173513 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM173513 target RNA into GAM173513 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5784 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5784 gene: GAM108062 target protein and GAM173513 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM108062 and GAM173513

GR5785 AI184170 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5785(GR5785) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5785 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5785 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5785 gene encodes GR5785 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5785 precursor RNA folds spatially, forming GR5785 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated

that GR5785 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5785 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5785 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM5631 precursor RNA, GAM21365 precursor RNA, GAM58675 precursor RNA and GAM147739 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5631 RNA, GAM21365 RNA, GAM58675 RNA and GAM147739 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5631 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5631 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5631 target RNA into GAM5631 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM21365 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM21365 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM21365 target RNA into GAM21365 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM58675 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM58675 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM58675 target RNA into GAM58675 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM147739 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM147739 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM147739 target RNA into GAM147739 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5785 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5785 gene: GAM5631 target protein, GAM21365 target protein, GAM58675 target protein and GAM147739 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5631, GAM21365, GAM58675 and GAM147739

GR5786 AW948886 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5786(GR5786) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5786 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5786 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5786 gene encodes GR5786 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5786 precursor RNA folds spatially, forming GR5786 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5786 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5786 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5786 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM19279 precursor RNA and GAM265489 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM19279 RNA and GAM265489 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM19279 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM19279 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM19279 target RNA into GAM19279 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM265489 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM265489 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM265489 target RNA into GAM265489 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5786 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5786 gene: GAM19279 target protein and GAM265489 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM19279 and GAM265489

GR5787 BM720281 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5787(GR5787) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5787 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5787 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5787 gene encodes GR5787 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5787 precursor RNA folds spatially, forming GR5787 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5787 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5787 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5787 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM93958 precursor RNA, GAM185539 precursor RNA and GAM259327 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM93958 RNA, GAM185539 RNA and GAM259327 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM93958 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM93958 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM93958 target RNA into GAM93958 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM185539 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM185539 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM185539 target RNA into GAM185539 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM259327 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM259327 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM259327 target RNA into GAM259327 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5787 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5787 gene: GAM93958 target protein, GAM185539 target protein and GAM259327 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM93958, GAM185539 and GAM259327

GR5788 BE465052 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5788(GR5788) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5788 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5788 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5788 gene encodes GR5788 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5788 precursor RNA folds spatially, forming GR5788 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5788 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5788 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5788 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM7932 precursor RNA, GAM64369 precursor RNA and GAM251603 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7932 RNA, GAM64369 RNA and GAM251603 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7932 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7932 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7932 target RNA into GAM7932 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM64369 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM64369 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM64369 target RNA into GAM64369 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM251603 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM251603 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM251603 target RNA into GAM251603 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5788 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5788 gene: GAM7932 target protein, GAM64369 target protein and GAM251603 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7932, GAM64369 and GAM251603

GR5789 AA927222 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5789(GR5789) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5789 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5789 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5789 gene encodes GR5789 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5789 precursor RNA folds spatially, forming GR5789 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5789 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5789 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5789 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM951 precursor RNA, GAM3478 precursor RNA and

GAM166850 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM951 RNA, GAM3478 RNA and GAM166850 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM951 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM951 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM951 target RNA into GAM951 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM3478 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3478 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3478 target RNA into GAM3478 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM166850 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM166850 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM166850 target RNA into GAM166850 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5789 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5789 gene: GAM951 target protein, GAM3478 target protein and GAM166850 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM951, GAM3478 and GAM166850

GR5790 BE617857 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5790(GR5790) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR5790 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5790 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5790 gene encodes GR5790 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5790 precursor RNA folds spatially, forming GR5790 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5790 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5790 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5790 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4143 precursor RNA and GAM6222 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4143 RNA and GAM6222 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4143 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4143 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4143 target RNA into GAM4143 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6222 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6222 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6222 target RNA into GAM6222 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5790 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5790 gene: GAM4143 target protein and GAM6222 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4143 and GAM6222

GR5791 BM008028 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5791 (GR5791) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5791 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5791 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5791 gene encodes GR5791 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5791 precursor RNA folds spatially, forming GR5791 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5791 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5791 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5791 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM6822 precursor RNA, GAM7967 precursor RNA and GAM131264 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6822 RNA, GAM7967 RNA and GAM131264 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6822 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6822 target RNA, herein schematically represented by

GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6822 target RNA into GAM6822 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7967 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7967 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7967 target RNA into GAM7967 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM131264 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM131264 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM131264 target RNA into GAM131264 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5791 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5791 gene: GAM6822 target protein, GAM7967 target protein and GAM131264 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6822, GAM7967 and GAM131264

GR5792 AI873812 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5792(GR5792) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5792 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5792 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5792 gene encodes GR5792 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5792 precursor RNA folds spatially, forming GR5792 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5792 folded precursor RNA comprises a plurality of what is known in the

art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5792 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5792 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM304020 precursor RNA and GAM310124 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM304020 RNA and GAM310124 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM304020 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM304020 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM304020 target RNA into GAM304020 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM310124 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM310124 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM310124 target RNA into GAM310124 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5792 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5792 gene: GAM304020 target protein and GAM310124 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM304020 and GAM310124

GR5793 BE902698 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5793(GR5793) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR5793 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5793 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5793 gene encodes GR5793 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5793 precursor RNA folds spatially, forming GR5793 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5793 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5793 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5793 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3092 precursor RNA, GAM7728 precursor RNA and GAM135455 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3092 RNA, GAM7728 RNA and GAM135455 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3092 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3092 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3092 target RNA into GAM3092 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7728 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7728 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7728 target RNA into GAM7728 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM135455 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM135455 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM135455 target RNA into GAM135455 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5793 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5793 gene: GAM3092 target protein, GAM7728 target protein and GAM135455 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3092, GAM7728 and GAM135455

GR5794 BI667529 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5794(GR5794) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5794 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5794 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5794 gene encodes GR5794 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5794 precursor RNA folds spatially, forming GR5794 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5794 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5794 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5794 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6943 precursor RNA and GAM271893 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6943 RNA and GAM271893 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6943 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6943 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6943 target RNA into GAM6943 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM271893 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM271893 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM271893 target RNA into GAM271893 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5794 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5794 gene: GAM6943 target protein and GAM271893 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6943 and GAM271893

GR5795 BF093028 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5795(GR5795) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5795 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5795 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5795 gene encodes GR5795 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5795 precursor RNA folds spatially, forming GR5795 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5795 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR5795 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5795 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM816 precursor RNA, GAM17289 precursor RNA, GAM149742 precursor RNA and GAM249073 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM816 RNA, GAM17289 RNA, GAM149742 RNA and GAM249073 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM816 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM816 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM816 target RNA into GAM816 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM17289 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM17289 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM17289 target RNA into GAM17289 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM149742 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM149742 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM149742 target RNA into GAM149742 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM249073 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM249073 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM249073 target RNA into GAM249073 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5795 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5795 gene: GAM816 target protein, GAM17289 target protein, GAM149742 target protein and GAM249073 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM816, GAM17289, GAM149742 and GAM249073

GR5796 AI143306 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5796(GR5796) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5796 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5796 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5796 gene encodes GR5796 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5796 precursor RNA folds spatially, forming GR5796 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5796 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5796 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5796 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM5833 precursor RNA, GAM7606 precursor RNA and GAM27603 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5833 RNA, GAM7606 RNA and GAM27603 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5833 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5833 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5833 target RNA into GAM5833 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7606 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7606 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7606 target RNA into GAM7606 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM27603 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM27603 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM27603 target RNA into GAM27603 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5796 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5796 gene: GAM5833 target protein, GAM7606 target protein and GAM27603 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5833, GAM7606 and GAM27603

GR5797 BG476180 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5797(GR5797) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5797 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5797 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5797 gene encodes GR5797 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5797 precursor RNA folds spatially, forming GR5797 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5797 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5797 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5797 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM47250 precursor RNA, GAM128132 precursor RNA, GAM294782 precursor RNA and GAM310690 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM47250 RNA, GAM128132 RNA, GAM294782 RNA and GAM310690 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM47250 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM47250 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM47250 target RNA into GAM47250 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM128132 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM128132 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM128132 target RNA into GAM128132 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM294782 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM294782 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM294782 target RNA into GAM294782 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM310690 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM310690 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM310690 target RNA into GAM310690 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5797 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5797 gene: GAM47250 target protein, GAM128132 target protein, GAM294782 target protein and GAM310690 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM47250, GAM128132, GAM294782 and GAM310690

GR5798 BE041845 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5798(GR5798) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5798 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5798 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5798 gene encodes GR5798 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5798 precursor RNA folds spatially, forming GR5798 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5798 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5798 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5798 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM64351 precursor RNA, GAM69534 precursor RNA and GAM248738 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM64351 RNA, GAM69534 RNA and GAM248738 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM64351 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM64351 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM64351 target RNA into GAM64351 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM69534 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM69534 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM69534 target RNA into GAM69534 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM248738 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM248738 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM248738 target RNA into GAM248738 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5798 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5798 gene: GAM64351 target protein, GAM69534 target protein and GAM248738 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM64351, GAM69534 and GAM248738

GR5799 BG620579 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5799(GR5799) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5799 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5799 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5799 gene encodes GR5799 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5799 precursor RNA folds spatially, forming GR5799 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5799 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5799 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5799 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3338 precursor RNA and GAM106456 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3338 RNA and GAM106456 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3338 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3338 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3338 target RNA into GAM3338 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM106456 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM106456 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM106456 target RNA into GAM106456 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5799 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5799 gene: GAM3338 target protein and GAM106456 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference,

with references to GAM3338 and GAM106456

GR5800 AI458067 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5800 (GR5800) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5800 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5800 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5800 gene encodes GR5800 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5800 precursor RNA folds spatially, forming GR5800 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5800 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5800 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5800 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5341 precursor RNA and GAM66399 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5341 RNA and GAM66399 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5341 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5341 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5341 target RNA into GAM5341 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM66399 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM66399 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM66399 target RNA into GAM66399 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5800 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5800 gene: GAM5341 target protein and GAM66399 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5341 and GAM66399

GR5801 AA156659 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5801(GR5801) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5801 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5801 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5801 gene encodes GR5801 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5801 precursor RNA folds spatially, forming GR5801 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5801 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5801 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5801 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3832 precursor RNA and GAM8357 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3832 RNA and GAM8357 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding

to GAM RNA of Fig. 8.

GAM3832 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3832 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3832 target RNA into GAM3832 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8357 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8357 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8357 target RNA into GAM8357 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5801 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5801 gene: GAM3832 target protein and GAM8357 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3832 and GAM8357

GR5802 AI760284 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5802(GR5802) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5802 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5802 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5802 gene encodes GR5802 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5802 precursor RNA folds spatially, forming GR5802 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5802 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5802 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR5802 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM178222 precursor RNA and GAM217752 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM178222 RNA and GAM217752 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM178222 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM178222 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM178222 target RNA into GAM178222 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM217752 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM217752 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM217752 target RNA into GAM217752 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5802 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5802 gene: GAM178222 target protein and GAM217752 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM178222 and GAM217752

GR5803 BE294365 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5803(GR5803) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5803 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5803

gene was detected is described hereinabove with reference to Figs. 8-18.

GR5803 gene encodes GR5803 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5803 precursor RNA folds spatially, forming GR5803 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5803 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5803 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5803 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM7211 precursor RNA, GAM92804 precursor RNA and GAM255585 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7211 RNA, GAM92804 RNA and GAM255585 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7211 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7211 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7211 target RNA into GAM7211 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM92804 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM92804 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM92804 target RNA into GAM92804 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM255585 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM255585 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM255585 target RNA into GAM255585 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5803 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5803 gene: GAM7211 target protein, GAM92804 target protein and GAM255585 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7211, GAM92804 and GAM255585

GR5804 W95790 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5804(GR5804) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5804 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5804 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5804 gene encodes GR5804 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5804 precursor RNA folds spatially, forming GR5804 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5804 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5804 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5804 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1605 precursor RNA and GAM104999 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1605 RNA and GAM104999 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1605 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1605 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1605 target RNA into GAM1605 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM104999 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM104999 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM104999 target RNA into GAM104999 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5804 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5804 gene: GAM1605 target protein and GAM104999 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1605 and GAM104999

GR5805 BF197053 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5805(GR5805) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5805 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5805 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5805 gene encodes GR5805 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5805 precursor RNA folds spatially, forming GR5805 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5805 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5805 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5805 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3078 precursor RNA and GAM178759 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3078 RNA and GAM178759 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3078 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3078 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3078 target RNA into GAM3078 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM178759 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM178759 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM178759 target RNA into GAM178759 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5805 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5805 gene: GAM3078 target protein and GAM178759 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3078 and GAM178759

GR5806 BG105917 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5806(GR5806) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5806 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5806 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5806 gene encodes GR5806 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5806 precursor RNA folds spatially, forming GR5806 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5806 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5806 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5806 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3192 precursor RNA, GAM268308 precursor RNA and GAM286185 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3192 RNA, GAM268308 RNA and GAM286185 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3192 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3192 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3192 target RNA into GAM3192 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM268308 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM268308 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM268308 target RNA into GAM268308 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM286185 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM286185 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM286185

target RNA into GAM286185 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5806 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5806 gene: GAM3192 target protein, GAM268308 target protein and GAM286185 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3192, GAM268308 and GAM286185

GR5807 BG248422 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5807(GR5807) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5807 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5807 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5807 gene encodes GR5807 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5807 precursor RNA folds spatially, forming GR5807 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5807 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5807 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5807 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5988 precursor RNA and GAM73269 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5988 RNA and GAM73269 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5988 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5988 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5988 target RNA into GAM5988 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM73269 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM73269 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM73269 target RNA into GAM73269 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5807 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5807 gene: GAM5988 target protein and GAM73269 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5988 and GAM73269

GR5808 BG718558 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5808(GR5808) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5808 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5808 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5808 gene encodes GR5808 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5808 precursor RNA folds spatially, forming GR5808 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5808 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5808 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5808 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM31154 precursor RNA, GAM144030 precursor RNA and GAM239917 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM31154 RNA, GAM144030 RNA and GAM239917 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM31154 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM31154 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM31154 target RNA into GAM31154 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM144030 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM144030 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM144030 target RNA into GAM144030 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM239917 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM239917 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM239917 target RNA into GAM239917 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5808 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5808 gene: GAM31154 target protein, GAM144030 target protein and GAM239917 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM31154, GAM144030 and GAM239917

bioinformatically detected regulatory gene, referred to here as Genomic Record 5809(GR5809) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5809 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5809 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5809 gene encodes GR5809 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5809 precursor RNA folds spatially, forming GR5809 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5809 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5809 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5809 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4531 precursor RNA, GAM7167 precursor RNA and GAM92668 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4531 RNA, GAM7167 RNA and GAM92668 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4531 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4531 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4531 target RNA into GAM4531 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7167 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7167 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig. 8, thereby inhibiting translation of GAM7167 target RNA into GAM7167 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM92668 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM92668 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM92668 target RNA into GAM92668 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5809 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5809 gene: GAM4531 target protein, GAM7167 target protein and GAM92668 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4531, GAM7167 and GAM92668

GR5810 AA448368 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5810(GR5810) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5810 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5810 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5810 gene encodes GR5810 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5810 precursor RNA folds spatially, forming GR5810 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5810 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5810 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5810 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM141960 precursor RNA and GAM165895 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3

FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM141960 RNA and GAM165895 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM141960 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM141960 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM141960 target RNA into GAM141960 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM165895 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM165895 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM165895 target RNA into GAM165895 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5810 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5810 gene: GAM141960 target protein and GAM165895 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM141960 and GAM165895

GR5811 AA548597 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5811(GR5811) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5811 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5811 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5811 gene encodes GR5811 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5811 precursor RNA folds spatially, forming GR5811 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5811 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5811 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5811 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2472 precursor RNA and GAM325687 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2472 RNA and GAM325687 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2472 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2472 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2472 target RNA into GAM2472 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM325687 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM325687 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM325687 target RNA into GAM325687 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5811 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5811 gene: GAM2472 target protein and GAM325687 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2472 and GAM325687

5812(GR5812) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5812 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5812 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5812 gene encodes GR5812 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5812 precursor RNA folds spatially, forming GR5812 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5812 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5812 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5812 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM5023 precursor RNA, GAM8652 precursor RNA and GAM114256 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5023 RNA, GAM8652 RNA and GAM114256 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5023 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5023 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5023 target RNA into GAM5023 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8652 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8652 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8652 target RNA into

GAM8652 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM114256 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM114256 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM114256 target RNA into GAM114256 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5812 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5812 gene: GAM5023 target protein, GAM8652 target protein and GAM114256 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5023, GAM8652 and GAM114256

GR5813 AA304841 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5813(GR5813) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5813 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5813 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5813 gene encodes GR5813 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5813 precursor RNA folds spatially, forming GR5813 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5813 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5813 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5813 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM62957 precursor RNA and GAM171910 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin

shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM62957 RNA and GAM171910 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM62957 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM62957 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM62957 target RNA into GAM62957 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM171910 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM171910 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM171910 target RNA into GAM171910 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5813 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5813 gene: GAM62957 target protein and GAM171910 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM62957 and GAM171910

GR5814 BI523836 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5814(GR5814) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5814 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5814 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5814 gene encodes GR5814 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5814 precursor RNA folds spatially, forming GR5814 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5814 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5814 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5814 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM175202 precursor RNA and GAM247186 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM175202 RNA and GAM247186 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM175202 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM175202 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM175202 target RNA into GAM175202 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM247186 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM247186 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM247186 target RNA into GAM247186 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5814 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5814 gene: GAM175202 target protein and GAM247186 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM175202 and GAM247186

GR5815 BE772062 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5815(GR5815) gene, which encodes an `operon-like` cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5815 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5815 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5815 gene encodes GR5815 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5815 precursor RNA folds spatially, forming GR5815 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5815 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5815 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5815 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2186 precursor RNA, GAM83757 precursor RNA and GAM258783 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2186 RNA, GAM83757 RNA and GAM258783 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2186 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2186 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2186 target RNA into GAM2186 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM83757 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM83757 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM83757 target RNA into GAM83757 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM258783 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM258783 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM258783 target RNA into GAM258783 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5815 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5815 gene: GAM2186 target protein, GAM83757 target protein and GAM258783 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2186, GAM83757 and GAM258783

GR5816 BG531562 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5816(GR5816) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5816 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5816 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5816 gene encodes GR5816 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5816 precursor RNA folds spatially, forming GR5816 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5816 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5816 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5816 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM86488 precursor RNA, GAM294224 precursor RNA and GAM302703 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED

PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM86488 RNA, GAM294224 RNA and GAM302703 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM86488 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM86488 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM86488 target RNA into GAM86488 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM294224 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM294224 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM294224 target RNA into GAM294224 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM302703 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM302703 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM302703 target RNA into GAM302703 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5816 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5816 gene: GAM86488 target protein, GAM294224 target protein and GAM302703 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM86488, GAM294224 and GAM302703

GR5817 BG928629 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5817(GR5817) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5817 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5817 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5817 gene encodes GR5817 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5817 precursor RNA folds spatially, forming GR5817 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5817 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5817 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5817 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM5777 precursor RNA, GAM95776 precursor RNA, GAM111192 precursor RNA and GAM257261 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5777 RNA, GAM95776 RNA, GAM111192 RNA and GAM257261 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5777 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5777 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5777 target RNA into GAM5777 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM95776 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM95776 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM95776 target RNA into GAM95776 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM111192 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM111192 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM111192 target RNA into GAM111192 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM257261 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM257261 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM257261 target RNA into GAM257261 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5817 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5817 gene: GAM5777 target protein, GAM95776 target protein, GAM111192 target protein and GAM257261 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5777, GAM95776, GAM111192 and GAM257261

GR5818 BM982752 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5818(GR5818) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5818 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5818 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5818 gene encodes GR5818 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5818 precursor RNA folds spatially, forming GR5818 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5818 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5818 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5818 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2

separate GAM precursor RNAs, GAM282261 precursor RNA and GAM310227 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM282261 RNA and GAM310227 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM282261 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM282261 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM282261 target RNA into GAM282261 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM310227 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM310227 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM310227 target RNA into GAM310227 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5818 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5818 gene: GAM282261 target protein and GAM310227 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM282261 and GAM310227

GR5819 BQ063500 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5819 (GR5819) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5819 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5819 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5819 gene encodes GR5819 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR5819 precursor RNA folds spatially, forming GR5819 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5819 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5819 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5819 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM20054 precursor RNA, GAM47347 precursor RNA and GAM97875 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM20054 RNA, GAM47347 RNA and GAM97875 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM20054 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM20054 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM20054 target RNA into GAM20054 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM47347 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM47347 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM47347 target RNA into GAM47347 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM97875 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM97875 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM97875 target RNA into GAM97875 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5819 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5819 gene: GAM20054 target protein, GAM47347 target protein and GAM97875 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM20054, GAM47347 and GAM97875

GR5820 AI028742 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5820(GR5820) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5820 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5820 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5820 gene encodes GR5820 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5820 precursor RNA folds spatially, forming GR5820 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5820 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5820 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5820 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5141 precursor RNA and GAM241483 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5141 RNA and GAM241483 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5141 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5141 target RNA, herein schematically represented by

GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5141 target RNA into GAM5141 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM241483 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM241483 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM241483 target RNA into GAM241483 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5820 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5820 gene: GAM5141 target protein and GAM241483 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5141 and GAM241483

GR5821 BI194798 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5821(GR5821) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5821 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5821 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5821 gene encodes GR5821 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5821 precursor RNA folds spatially, forming GR5821 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5821 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5821 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5821 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2060 precursor RNA and GAM8372 precursor

RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2060 RNA and GAM8372 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2060 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2060 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2060 target RNA into GAM2060 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8372 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8372 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8372 target RNA into GAM8372 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5821 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5821 gene: GAM2060 target protein and GAM8372 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2060 and GAM8372

GR5822 AI627676 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5822(GR5822) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5822 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5822 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5822 gene encodes GR5822 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5822 precursor RNA folds spatially, forming GR5822 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5822 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5822 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5822 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2976 precursor RNA and GAM271655 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2976 RNA and GAM271655 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2976 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2976 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2976 target RNA into GAM2976 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM271655 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM271655 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM271655 target RNA into GAM271655 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5822 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5822 gene: GAM2976 target protein and GAM271655 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2976 and GAM271655

bioinformatically detected regulatory gene, referred to here as Genomic Record 5823(GR5823) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5823 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5823 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5823 gene encodes GR5823 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5823 precursor RNA folds spatially, forming GR5823 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5823 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5823 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5823 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM281689 precursor RNA and GAM318995 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM281689 RNA and GAM318995 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM281689 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM281689 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM281689 target RNA into GAM281689 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM318995 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM318995 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM318995

target RNA into GAM318995 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5823 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5823 gene: GAM281689 target protein and GAM318995 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM281689 and GAM318995

GR5824 BG171602 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5824(GR5824) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5824 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5824 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5824 gene encodes GR5824 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5824 precursor RNA folds spatially, forming GR5824 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5824 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5824 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5824 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM559 precursor RNA, GAM53163 precursor RNA and GAM88096 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM559 RNA, GAM53163 RNA and GAM88096 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM559 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM559 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM559 target RNA into GAM559 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM53163 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM53163 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM53163 target RNA into GAM53163 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM88096 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM88096 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM88096 target RNA into GAM88096 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5824 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5824 gene: GAM559 target protein, GAM53163 target protein and GAM88096 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM559, GAM53163 and GAM88096

GR5825 BG831315 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5825(GR5825) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5825 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5825 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5825 gene encodes GR5825 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5825 precursor RNA folds spatially, forming GR5825 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5825 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5825 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5825 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM4815 precursor RNA, GAM98839 precursor RNA, GAM216941 precursor RNA and GAM306582 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4815 RNA, GAM98839 RNA, GAM216941 RNA and GAM306582 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4815 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4815 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4815 target RNA into GAM4815 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM98839 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM98839 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM98839 target RNA into GAM98839 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM216941 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM216941 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM216941 target RNA into GAM216941 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM306582 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM306582 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM306582 target RNA into GAM306582 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5825 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5825 gene: GAM4815 target protein, GAM98839 target protein, GAM216941 target protein and GAM306582 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4815, GAM98839, GAM216941 and GAM306582

GR5826 AA757068 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5826(GR5826) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5826 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5826 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5826 gene encodes GR5826 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5826 precursor RNA folds spatially, forming GR5826 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5826 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5826 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5826 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM7733 precursor RNA, GAM73805 precursor RNA, GAM242778 precursor RNA and GAM261107 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM7733 RNA, GAM73805 RNA, GAM242778 RNA and GAM261107 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7733 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7733 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7733 target RNA into GAM7733 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM73805 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM73805 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM73805 target RNA into GAM73805 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM242778 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM242778 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM242778 target RNA into GAM242778 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM261107 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM261107 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM261107 target RNA into GAM261107 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5826 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5826 gene: GAM7733 target protein, GAM73805 target protein, GAM242778 target protein and GAM261107 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7733, GAM73805, GAM242778 and GAM261107

GR5827 AW886611 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5827(GR5827) gene, which encodes an `operon-like` cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5827 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5827 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5827 gene encodes GR5827 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5827 precursor RNA folds spatially, forming GR5827 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5827 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5827 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5827 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1020 precursor RNA and GAM243597 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1020 RNA and GAM243597 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1020 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1020 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1020 target RNA into GAM1020 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM243597 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM243597 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM243597 target RNA into GAM243597 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5827 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5827 gene: GAM1020 target protein and GAM243597 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1020 and GAM243597

GR5828 BF678435 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5828(GR5828) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5828 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5828 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5828 gene encodes GR5828 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5828 precursor RNA folds spatially, forming GR5828 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5828 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5828 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5828 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM82772 precursor RNA, GAM255644 precursor RNA and GAM285528 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM82772 RNA, GAM255644 RNA and GAM285528 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM82772 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM82772 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM82772 target RNA into GAM82772 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM255644 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM255644 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM255644 target RNA into GAM255644 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM285528 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM285528 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM285528 target RNA into GAM285528 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5828 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5828 gene: GAM82772 target protein, GAM255644 target protein and GAM285528 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM82772, GAM255644 and GAM285528

GR5829 AA291655 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5829(GR5829) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5829 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5829 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5829 gene encodes GR5829 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5829 precursor RNA folds spatially, forming GR5829 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated

that GR5829 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5829 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5829 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1386 precursor RNA and GAM121772 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1386 RNA and GAM121772 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1386 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1386 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1386 target RNA into GAM1386 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM121772 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM121772 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM121772 target RNA into GAM121772 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5829 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5829 gene: GAM1386 target protein and GAM121772 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1386 and GAM121772

GR5830 AW074192 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5830(GR5830) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR5830 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5830 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5830 gene encodes GR5830 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5830 precursor RNA folds spatially, forming GR5830 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5830 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5830 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5830 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM54518 precursor RNA and GAM224009 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM54518 RNA and GAM224009 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM54518 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM54518 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM54518 target RNA into GAM54518 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM224009 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM224009 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM224009 target RNA into GAM224009 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5830 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5830 gene: GAM54518 target protein and GAM224009 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM54518 and GAM224009

GR5831 BF432338 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5831 (GR5831) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5831 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5831 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5831 gene encodes GR5831 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5831 precursor RNA folds spatially, forming GR5831 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5831 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5831 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5831 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM236385 precursor RNA and GAM319068 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM236385 RNA and GAM319068 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM236385 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM236385 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM236385 target RNA into GAM236385 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM319068 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM319068 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM319068 target RNA into GAM319068 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5831 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5831 gene: GAM236385 target protein and GAM319068 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM236385 and GAM319068

GR5832 BE074782 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5832(GR5832) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5832 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5832 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5832 gene encodes GR5832 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5832 precursor RNA folds spatially, forming GR5832 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5832 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5832 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5832 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM80163 precursor RNA and GAM290866 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3

FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM80163 RNA and GAM290866 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM80163 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM80163 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM80163 target RNA into GAM80163 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM290866 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM290866 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM290866 target RNA into GAM290866 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5832 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5832 gene: GAM80163 target protein and GAM290866 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM80163 and GAM290866

GR5833 BG709651 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5833(GR5833) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5833 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5833 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5833 gene encodes GR5833 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5833 precursor RNA folds spatially, forming GR5833 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5833 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5833 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5833 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM33216 precursor RNA and GAM49436 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM33216 RNA and GAM49436 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM33216 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM33216 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM33216 target RNA into GAM33216 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM49436 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM49436 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM49436 target RNA into GAM49436 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5833 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5833 gene: GAM33216 target protein and GAM49436 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM33216 and GAM49436

5834(GR5834) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5834 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5834 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5834 gene encodes GR5834 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5834 precursor RNA folds spatially, forming GR5834 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5834 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5834 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5834 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM8036 precursor RNA, GAM124492 precursor RNA and GAM275795 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8036 RNA, GAM124492 RNA and GAM275795 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8036 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8036 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8036 target RNA into GAM8036 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM124492 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM124492 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM124492

target RNA into GAM124492 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM275795 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM275795 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM275795 target RNA into GAM275795 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5834 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5834 gene: GAM8036 target protein, GAM124492 target protein and GAM275795 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8036, GAM124492 and GAM275795

GR5835 BG527198 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5835(GR5835) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5835 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5835 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5835 gene encodes GR5835 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5835 precursor RNA folds spatially, forming GR5835 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5835 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5835 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5835 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM191943 precursor RNA and GAM328360 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin

shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM191943 RNA and GAM328360 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM191943 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM191943 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM191943 target RNA into GAM191943 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM328360 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM328360 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM328360 target RNA into GAM328360 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5835 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5835 gene: GAM191943 target protein and GAM328360 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM191943 and GAM328360

GR5836 BF361679 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5836(GR5836) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5836 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5836 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5836 gene encodes GR5836 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5836 precursor RNA folds spatially, forming GR5836 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5836 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5836 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5836 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4983 precursor RNA and GAM70497 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4983 RNA and GAM70497 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4983 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4983 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4983 target RNA into GAM4983 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM70497 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM70497 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM70497 target RNA into GAM70497 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5836 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5836 gene: GAM4983 target protein and GAM70497 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4983 and GAM70497

GR5837 BE695058 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5837(GR5837) gene, which encodes an `operon-like` cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5837 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5837 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5837 gene encodes GR5837 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5837 precursor RNA folds spatially, forming GR5837 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5837 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5837 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5837 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM12860 precursor RNA, GAM68228 precursor RNA and GAM211359 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM12860 RNA, GAM68228 RNA and GAM211359 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM12860 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM12860 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM12860 target RNA into GAM12860 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM68228 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM68228 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM68228 target RNA into GAM68228 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM211359 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM211359 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM211359 target RNA into GAM211359 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5837 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5837 gene: GAM12860 target protein, GAM68228 target protein and GAM211359 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM12860, GAM68228 and GAM211359

GR5838 AI820716 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5838(GR5838) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5838 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5838 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5838 gene encodes GR5838 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5838 precursor RNA folds spatially, forming GR5838 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5838 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5838 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5838 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM233693 precursor RNA and GAM245593 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM233693 RNA and GAM245593 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM233693 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM233693 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM233693 target RNA into GAM233693 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM245593 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM245593 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM245593 target RNA into GAM245593 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5838 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5838 gene: GAM233693 target protein and GAM245593 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM233693 and GAM245593

GR5839 BE062196 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5839(GR5839) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5839 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5839 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5839 gene encodes GR5839 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5839 precursor RNA folds spatially, forming GR5839 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated

that GR5839 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5839 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5839 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6689 precursor RNA and GAM222472 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6689 RNA and GAM222472 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6689 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6689 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6689 target RNA into GAM6689 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM222472 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM222472 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM222472 target RNA into GAM222472 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5839 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5839 gene: GAM6689 target protein and GAM222472 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6689 and GAM222472

GR5840 BM925930 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5840(GR5840) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR5840 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5840 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5840 gene encodes GR5840 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5840 precursor RNA folds spatially, forming GR5840 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5840 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5840 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5840 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM102231 precursor RNA, GAM129484 precursor RNA and GAM295304 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM102231 RNA, GAM129484 RNA and GAM295304 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM102231 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM102231 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM102231 target RNA into GAM102231 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM129484 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM129484 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM129484 target RNA into GAM129484 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM295304 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM295304 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM295304 target RNA into GAM295304 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5840 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5840 gene: GAM102231 target protein, GAM129484 target protein and GAM295304 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM102231, GAM129484 and GAM295304

GR5841 H69338 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5841 (GR5841) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5841 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5841 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5841 gene encodes GR5841 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5841 precursor RNA folds spatially, forming GR5841 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5841 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5841 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5841 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM32065 precursor RNA and GAM334615 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM32065 RNA and GAM334615 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM32065 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM32065 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM32065 target RNA into GAM32065 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM334615 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM334615 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM334615 target RNA into GAM334615 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5841 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5841 gene: GAM32065 target protein and GAM334615 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM32065 and GAM334615

GR5842 BM741247 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5842(GR5842) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5842 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5842 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5842 gene encodes GR5842 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5842 precursor RNA folds spatially, forming GR5842 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5842 folded precursor RNA comprises a plurality of what is known in the

art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5842 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5842 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2115 precursor RNA and GAM3776 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2115 RNA and GAM3776 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2115 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2115 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2115 target RNA into GAM2115 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM3776 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3776 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3776 target RNA into GAM3776 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5842 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5842 gene: GAM2115 target protein and GAM3776 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2115 and GAM3776

GR5843 AV646814 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5843(GR5843) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR5843 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5843 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5843 gene encodes GR5843 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5843 precursor RNA folds spatially, forming GR5843 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5843 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5843 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5843 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM43791 precursor RNA, GAM138233 precursor RNA and GAM252659 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM43791 RNA, GAM138233 RNA and GAM252659 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM43791 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM43791 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM43791 target RNA into GAM43791 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM138233 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM138233 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM138233 target RNA into GAM138233 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM252659 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM252659 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM252659 target RNA into GAM252659 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5843 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5843 gene: GAM43791 target protein, GAM138233 target protein and GAM252659 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM43791, GAM138233 and GAM252659

GR5844 BF824843 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5844(GR5844) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5844 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5844 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5844 gene encodes GR5844 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5844 precursor RNA folds spatially, forming GR5844 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5844 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5844 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5844 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5049 precursor RNA and GAM55607 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5049 RNA and GAM55607 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5049 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5049 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5049 target RNA into GAM5049 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM55607 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM55607 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM55607 target RNA into GAM55607 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5844 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5844 gene: GAM5049 target protein and GAM55607 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5049 and GAM55607

GR5845 AI638831 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5845(GR5845) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5845 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5845 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5845 gene encodes GR5845 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5845 precursor RNA folds spatially, forming GR5845 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5845 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR5845 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5845 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2772 precursor RNA, GAM147438 precursor RNA and GAM193053 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2772 RNA, GAM147438 RNA and GAM193053 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2772 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2772 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2772 target RNA into GAM2772 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM147438 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM147438 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM147438 target RNA into GAM147438 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM193053 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM193053 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM193053 target RNA into GAM193053 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5845 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5845 gene: GAM2772 target protein, GAM147438 target protein and GAM193053 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN.

The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2772, GAM147438 and GAM193053

GR5846 BF215307 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5846(GR5846) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5846 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5846 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5846 gene encodes GR5846 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5846 precursor RNA folds spatially, forming GR5846 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5846 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5846 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5846 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM8399 precursor RNA, GAM8590 precursor RNA and GAM54826 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8399 RNA, GAM8590 RNA and GAM54826 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8399 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8399 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8399 target RNA into GAM8399 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8590 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8590 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8590 target RNA into GAM8590 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM54826 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM54826 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM54826 target RNA into GAM54826 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5846 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5846 gene: GAM8399 target protein, GAM8590 target protein and GAM54826 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8399, GAM8590 and GAM54826

GR5847 AU151013 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5847(GR5847) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5847 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5847 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5847 gene encodes GR5847 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5847 precursor RNA folds spatially, forming GR5847 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5847 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5847 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5847 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM85249 precursor RNA and GAM187448 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM85249 RNA and GAM187448 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM85249 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM85249 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM85249 target RNA into GAM85249 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM187448 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM187448 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM187448 target RNA into GAM187448 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5847 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5847 gene: GAM85249 target protein and GAM187448 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM85249 and GAM187448

GR5848 BG400118 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5848(GR5848) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5848 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5848 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5848 gene encodes GR5848 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5848 precursor RNA folds spatially, forming GR5848 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5848 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5848 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5848 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM149788 precursor RNA, GAM219765 precursor RNA and GAM293683 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM149788 RNA, GAM219765 RNA and GAM293683 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM149788 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM149788 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM149788 target RNA into GAM149788 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM219765 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM219765 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM219765 target RNA into GAM219765 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM293683 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM293683 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM293683

target RNA into GAM293683 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5848 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5848 gene: GAM149788 target protein, GAM219765 target protein and GAM293683 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM149788, GAM219765 and GAM293683

GR5849 BM725049 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5849(GR5849) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5849 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5849 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5849 gene encodes GR5849 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5849 precursor RNA folds spatially, forming GR5849 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5849 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5849 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5849 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM5259 precursor RNA, GAM117038 precursor RNA, GAM155949 precursor RNA and GAM159334 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5259 RNA, GAM117038 RNA, GAM155949 RNA and GAM159334 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5259 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5259 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5259 target RNA into GAM5259 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM117038 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM117038 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM117038 target RNA into GAM117038 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM155949 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM155949 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM155949 target RNA into GAM155949 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM159334 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM159334 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM159334 target RNA into GAM159334 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5849 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5849 gene: GAM5259 target protein, GAM117038 target protein, GAM155949 target protein and GAM159334 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5259, GAM117038, GAM155949 and GAM159334

GR5850 AA326353 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5850(GR5850) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5850 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5850 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5850 gene encodes GR5850 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5850 precursor RNA folds spatially, forming GR5850 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5850 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5850 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5850 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7470 precursor RNA and GAM311637 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7470 RNA and GAM311637 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7470 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7470 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7470 target RNA into GAM7470 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM311637 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM311637 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM311637 target RNA into GAM311637 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5850 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5850 gene: GAM7470 target protein and GAM311637 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7470 and GAM311637

GR5851 BF345300 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5851(GR5851) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5851 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5851 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5851 gene encodes GR5851 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5851 precursor RNA folds spatially, forming GR5851 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5851 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5851 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5851 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM125691 precursor RNA, GAM163731 precursor RNA and GAM205306 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM125691 RNA, GAM163731 RNA and GAM205306 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM125691 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM125691 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM125691 target RNA into GAM125691 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM163731 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM163731 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM163731 target RNA into GAM163731 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM205306 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM205306 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM205306 target RNA into GAM205306 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5851 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5851 gene: GAM125691 target protein, GAM163731 target protein and GAM205306 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM125691, GAM163731 and GAM205306

GR5852 AW902571 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5852(GR5852) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5852 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5852 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5852 gene encodes GR5852 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5852 precursor RNA folds spatially, forming GR5852 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5852 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5852 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5852 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM29193 precursor RNA and GAM155076 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM29193 RNA and GAM155076 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM29193 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM29193 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM29193 target RNA into GAM29193 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM155076 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM155076 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM155076 target RNA into GAM155076 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5852 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5852 gene: GAM29193 target protein and GAM155076 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM29193 and GAM155076

GR5853 BI601921 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5853(GR5853) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5853 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5853 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5853 gene encodes GR5853 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5853 precursor RNA folds spatially, forming GR5853 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5853 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5853 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5853 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM39480 precursor RNA and GAM307379 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM39480 RNA and GAM307379 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM39480 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM39480 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM39480 target RNA into GAM39480 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM307379 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM307379 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM307379 target RNA into GAM307379 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5853 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR5853 gene: GAM39480 target protein and GAM307379 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM39480 and GAM307379

GR5854 AA741287 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5854(GR5854) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5854 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5854 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5854 gene encodes GR5854 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5854 precursor RNA folds spatially, forming GR5854 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5854 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5854 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5854 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM229119 precursor RNA and GAM245897 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM229119 RNA and GAM245897 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM229119 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM229119 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM229119 target RNA into GAM229119 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM245897 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM245897 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM245897 target RNA into GAM245897 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5854 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5854 gene: GAM229119 target protein and GAM245897 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM229119 and GAM245897

GR5855 BF475396 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5855(GR5855) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5855 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5855 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5855 gene encodes GR5855 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5855 precursor RNA folds spatially, forming GR5855 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5855 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5855 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5855 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM245344 precursor RNA and GAM255060 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM245344 RNA and GAM255060 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM245344 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM245344 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM245344 target RNA into GAM245344 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM255060 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM255060 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM255060 target RNA into GAM255060 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5855 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5855 gene: GAM245344 target protein and GAM255060 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM245344 and GAM255060

GR5856 BM760275 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5856(GR5856) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5856 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5856 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5856 gene encodes GR5856 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5856 precursor RNA folds spatially, forming GR5856 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5856 folded precursor RNA comprises a plurality of what is known in the

art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5856 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5856 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM21614 precursor RNA and GAM72476 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM21614 RNA and GAM72476 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM21614 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM21614 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM21614 target RNA into GAM21614 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM72476 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM72476 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM72476 target RNA into GAM72476 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5856 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5856 gene: GAM21614 target protein and GAM72476 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM21614 and GAM72476

GR5857 BM264439 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5857(GR5857) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR5857 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5857 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5857 gene encodes GR5857 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5857 precursor RNA folds spatially, forming GR5857 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5857 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5857 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5857 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3924 precursor RNA and GAM7596 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3924 RNA and GAM7596 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3924 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3924 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3924 target RNA into GAM3924 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7596 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7596 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7596 target RNA into GAM7596 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly

utilities, of GR5857 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5857 gene: GAM3924 target protein and GAM7596 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3924 and GAM7596

GR5858 AI017984 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5858(GR5858) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5858 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5858 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5858 gene encodes GR5858 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5858 precursor RNA folds spatially, forming GR5858 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5858 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5858 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5858 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM756 precursor RNA and GAM259301 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM756 RNA and GAM259301 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM756 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM756 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig. 8, thereby inhibiting translation of GAM756 target RNA into GAM756 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM259301 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM259301 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM259301 target RNA into GAM259301 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5858 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5858 gene: GAM756 target protein and GAM259301 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM756 and GAM259301

GR5859 AW467035 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5859(GR5859) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5859 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5859 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5859 gene encodes GR5859 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5859 precursor RNA folds spatially, forming GR5859 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5859 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5859 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5859 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM87228 precursor RNA, GAM93565 precursor RNA and GAM168566 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded

precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM87228 RNA, GAM93565 RNA and GAM168566 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM87228 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM87228 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM87228 target RNA into GAM87228 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM93565 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM93565 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM93565 target RNA into GAM93565 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM168566 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM168566 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM168566 target RNA into GAM168566 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5859 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5859 gene: GAM87228 target protein, GAM93565 target protein and GAM168566 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM87228, GAM93565 and GAM168566

GR5860 BQ056602 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5860(GR5860) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5860 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5860 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5860 gene encodes GR5860 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5860 precursor RNA folds spatially, forming GR5860 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5860 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5860 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5860 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM119245 precursor RNA and GAM263804 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM119245 RNA and GAM263804 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM119245 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM119245 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM119245 target RNA into GAM119245 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM263804 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM263804 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM263804 target RNA into GAM263804 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5860 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5860 gene: GAM119245 target protein and GAM263804 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM119245 and GAM263804

GR5861 AI281168 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5861(GR5861) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5861 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5861 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5861 gene encodes GR5861 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5861 precursor RNA folds spatially, forming GR5861 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5861 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5861 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5861 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1731 precursor RNA, GAM76029 precursor RNA and GAM243778 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1731 RNA, GAM76029 RNA and GAM243778 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1731 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1731 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig. 8, thereby inhibiting translation of GAM1731 target RNA into GAM1731 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM76029 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM76029 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM76029 target RNA into GAM76029 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM243778 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM243778 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM243778 target RNA into GAM243778 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5861 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5861 gene: GAM1731 target protein, GAM76029 target protein and GAM243778 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1731, GAM76029 and GAM243778

GR5862 AA587531 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5862(GR5862) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5862 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5862 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5862 gene encodes GR5862 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5862 precursor RNA folds spatially, forming GR5862 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5862 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5862 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5862 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM48294 precursor RNA and GAM159892 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM48294 RNA and GAM159892 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM48294 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM48294 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM48294 target RNA into GAM48294 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM159892 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM159892 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM159892 target RNA into GAM159892 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5862 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5862 gene: GAM48294 target protein and GAM159892 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM48294 and GAM159892

GR5863 BI550030 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5863(GR5863) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5863 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5863 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5863 gene encodes GR5863 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5863 precursor RNA folds spatially, forming GR5863 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5863 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5863 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5863 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1426 precursor RNA and GAM4359 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1426 RNA and GAM4359 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1426 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1426 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1426 target RNA into GAM1426 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM4359 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4359 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4359 target RNA into GAM4359 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5863 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR5863 gene: GAM1426 target protein and GAM4359 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1426 and GAM4359

GR5864 BG537279 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5864(GR5864) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5864 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5864 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5864 gene encodes GR5864 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5864 precursor RNA folds spatially, forming GR5864 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5864 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5864 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5864 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM675 precursor RNA and GAM60887 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM675 RNA and GAM60887 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM675 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM675 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM675 target RNA into GAM675 target protein, herein schematically represented by GAM1 TARGET PROTEIN

through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM60887 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM60887 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM60887 target RNA into GAM60887 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5864 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5864 gene: GAM675 target protein and GAM60887 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM675 and GAM60887

GR5865 BF672146 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5865(GR5865) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5865 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5865 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5865 gene encodes GR5865 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5865 precursor RNA folds spatially, forming GR5865 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5865 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5865 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5865 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6542 precursor RNA and GAM166315 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6542 RNA and GAM166315 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6542 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6542 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6542 target RNA into GAM6542 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM166315 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM166315 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM166315 target RNA into GAM166315 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5865 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5865 gene: GAM6542 target protein and GAM166315 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6542 and GAM166315

GR5866 AW393528 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5866(GR5866) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5866 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5866 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5866 gene encodes GR5866 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5866 precursor RNA folds spatially, forming GR5866 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5866 folded precursor RNA comprises a plurality of what is known in the

art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5866 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5866 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1155 precursor RNA and GAM7753 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1155 RNA and GAM7753 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1155 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1155 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1155 target RNA into GAM1155 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7753 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7753 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7753 target RNA into GAM7753 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5866 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5866 gene: GAM1155 target protein and GAM7753 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1155 and GAM7753

GR5867 AL704777 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5867(GR5867) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR5867 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5867 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5867 gene encodes GR5867 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5867 precursor RNA folds spatially, forming GR5867 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5867 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5867 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5867 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM724 precursor RNA and GAM73551 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM724 RNA and GAM73551 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM724 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM724 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM724 target RNA into GAM724 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM73551 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM73551 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM73551 target RNA into GAM73551 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly

utilities, of GR5867 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5867 gene: GAM724 target protein and GAM73551 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM724 and GAM73551

GR5868 BG900840 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5868(GR5868) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5868 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5868 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5868 gene encodes GR5868 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5868 precursor RNA folds spatially, forming GR5868 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5868 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5868 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5868 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM223246 precursor RNA and GAM281961 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM223246 RNA and GAM281961 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM223246 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM223246 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM223246 target RNA into GAM223246 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM281961 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM281961 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM281961 target RNA into GAM281961 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5868 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5868 gene: GAM223246 target protein and GAM281961 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM223246 and GAM281961

GR5869 BF684264 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5869(GR5869) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5869 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5869 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5869 gene encodes GR5869 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5869 precursor RNA folds spatially, forming GR5869 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5869 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5869 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5869 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM5306 precursor RNA, GAM232958 precursor RNA and GAM317452 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded

precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5306 RNA, GAM232958 RNA and GAM317452 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5306 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5306 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5306 target RNA into GAM5306 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM232958 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM232958 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM232958 target RNA into GAM232958 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM317452 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM317452 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM317452 target RNA into GAM317452 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5869 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5869 gene: GAM5306 target protein, GAM232958 target protein and GAM317452 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5306, GAM232958 and GAM317452

GR5870 BG340418 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5870(GR5870) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5870 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5870 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5870 gene encodes GR5870 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5870 precursor RNA folds spatially, forming GR5870 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5870 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5870 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5870 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM92703 precursor RNA, GAM224405 precursor RNA and GAM229897 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM92703 RNA, GAM224405 RNA and GAM229897 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM92703 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM92703 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM92703 target RNA into GAM92703 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM224405 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM224405 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM224405 target RNA into GAM224405 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM229897 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM229897 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM229897 target RNA into GAM229897 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5870 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5870 gene: GAM92703 target protein, GAM224405 target protein and GAM229897 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM92703, GAM224405 and GAM229897

GR5871 AL134398 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5871(GR5871) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5871 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5871 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5871 gene encodes GR5871 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5871 precursor RNA folds spatially, forming GR5871 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5871 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5871 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5871 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM74648 precursor RNA and GAM131670 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM74648 RNA and GAM131670 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM74648 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM74648 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM74648 target RNA into GAM74648 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM131670 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM131670 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM131670 target RNA into GAM131670 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5871 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5871 gene: GAM74648 target protein and GAM131670 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM74648 and GAM131670

GR5872 BM969394 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5872(GR5872) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5872 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5872 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5872 gene encodes GR5872 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5872 precursor RNA folds spatially, forming GR5872 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5872 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5872 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5872 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4305 precursor RNA and GAM276464 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4305 RNA and GAM276464 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4305 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4305 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4305 target RNA into GAM4305 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM276464 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM276464 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM276464 target RNA into GAM276464 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5872 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5872 gene: GAM4305 target protein and GAM276464 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4305 and GAM276464

GR5873 BG502850 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5873(GR5873) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5873 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5873 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5873 gene encodes GR5873 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5873 precursor RNA folds spatially, forming GR5873 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5873 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5873 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5873 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM792 precursor RNA and GAM238003 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM792 RNA and GAM238003 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM792 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM792 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM792 target RNA into GAM792 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM238003 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM238003 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM238003 target RNA into GAM238003 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5873 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR5873 gene: GAM792 target protein and GAM238003 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM792 and GAM238003

GR5874 BF875273 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5874(GR5874) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5874 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5874 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5874 gene encodes GR5874 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5874 precursor RNA folds spatially, forming GR5874 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5874 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5874 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5874 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3412 precursor RNA, GAM79354 precursor RNA and GAM127808 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3412 RNA, GAM79354 RNA and GAM127808 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3412 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3412 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3412 target RNA into

GAM3412 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM79354 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM79354 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM79354 target RNA into GAM79354 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM127808 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM127808 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM127808 target RNA into GAM127808 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5874 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5874 gene: GAM3412 target protein, GAM79354 target protein and GAM127808 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3412, GAM79354 and GAM127808

GR5875 BG777238 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5875(GR5875) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5875 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5875 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5875 gene encodes GR5875 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5875 precursor RNA folds spatially, forming GR5875 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5875 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5875 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5875 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3258 precursor RNA and GAM167152 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3258 RNA and GAM167152 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3258 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3258 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3258 target RNA into GAM3258 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM167152 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM167152 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM167152 target RNA into GAM167152 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5875 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5875 gene: GAM3258 target protein and GAM167152 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3258 and GAM167152

GR5876 AA808642 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5876(GR5876) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5876 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR5876 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5876 gene encodes GR5876 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5876 precursor RNA folds spatially, forming GR5876 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5876 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5876 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5876 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM119839 precursor RNA and GAM197185 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM119839 RNA and GAM197185 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM119839 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM119839 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM119839 target RNA into GAM119839 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM197185 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM197185 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM197185 target RNA into GAM197185 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5876 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5876 gene: GAM119839 target

protein and GAM197185 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM119839 and GAM197185

GR5877 AV685067 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5877(GR5877) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5877 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5877 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5877 gene encodes GR5877 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5877 precursor RNA folds spatially, forming GR5877 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5877 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5877 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5877 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM204652 precursor RNA, GAM297228 precursor RNA and GAM331924 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM204652 RNA, GAM297228 RNA and GAM331924 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM204652 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM204652 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM204652 target RNA into GAM204652 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM297228 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM297228 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM297228 target RNA into GAM297228 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM331924 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM331924 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM331924 target RNA into GAM331924 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5877 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5877 gene: GAM204652 target protein, GAM297228 target protein and GAM331924 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM204652, GAM297228 and GAM331924

GR5878 BE733475 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5878(GR5878) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5878 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5878 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5878 gene encodes GR5878 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5878 precursor RNA folds spatially, forming GR5878 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5878 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5878 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR5878 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM5389 precursor RNA, GAM217840 precursor RNA and GAM276703 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5389 RNA, GAM217840 RNA and GAM276703 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5389 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5389 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5389 target RNA into GAM5389 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM217840 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM217840 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM217840 target RNA into GAM217840 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM276703 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM276703 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM276703 target RNA into GAM276703 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5878 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5878 gene: GAM5389 target protein, GAM217840 target protein and GAM276703 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5389, GAM217840 and GAM276703

GR5879 AA258193 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5879(GR5879) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5879 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5879 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5879 gene encodes GR5879 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5879 precursor RNA folds spatially, forming GR5879 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5879 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5879 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5879 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM256964 precursor RNA and GAM322841 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM256964 RNA and GAM322841 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM256964 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM256964 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM256964 target RNA into GAM256964 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM322841 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM322841 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM322841 target RNA into GAM322841 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5879 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5879 gene: GAM256964 target protein and GAM322841 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM256964 and GAM322841

GR5880 AA828992 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5880 (GR5880) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5880 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5880 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5880 gene encodes GR5880 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5880 precursor RNA folds spatially, forming GR5880 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5880 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5880 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5880 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4327 precursor RNA and GAM28827 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4327 RNA and GAM28827 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4327 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4327 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4327 target RNA into GAM4327 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM28827 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM28827 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM28827 target RNA into GAM28827 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5880 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5880 gene: GAM4327 target protein and GAM28827 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4327 and GAM28827

GR5881 BG115582 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5881 (GR5881) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5881 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5881 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5881 gene encodes GR5881 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5881 precursor RNA folds spatially, forming GR5881 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5881 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5881 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5881 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM265 precursor RNA and GAM166358 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM265 RNA and GAM166358 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM265 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM265 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM265 target RNA into GAM265 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM166358 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM166358 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM166358 target RNA into GAM166358 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5881 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5881 gene: GAM265 target protein and GAM166358 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM265 and GAM166358

GR5882 BG545821 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5882(GR5882) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5882 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5882 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5882 gene encodes GR5882 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5882 precursor RNA folds spatially, forming GR5882 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5882 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5882 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5882 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM20347 precursor RNA and GAM40304 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM20347 RNA and GAM40304 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM20347 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM20347 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM20347 target RNA into GAM20347 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM40304 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM40304 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM40304 target RNA into GAM40304 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5882 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5882 gene: GAM20347 target protein and GAM40304 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes

is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM20347 and GAM40304

GR5883 BF340518 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5883(GR5883) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5883 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5883 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5883 gene encodes GR5883 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5883 precursor RNA folds spatially, forming GR5883 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5883 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5883 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5883 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM5642 precursor RNA, GAM7005 precursor RNA and GAM73379 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5642 RNA, GAM7005 RNA and GAM73379 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5642 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5642 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5642 target RNA into GAM5642 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7005 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7005 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7005 target RNA into GAM7005 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM73379 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM73379 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM73379 target RNA into GAM73379 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5883 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5883 gene: GAM5642 target protein, GAM7005 target protein and GAM73379 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5642, GAM7005 and GAM73379

GR5884 BG420088 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5884(GR5884) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5884 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5884 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5884 gene encodes GR5884 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5884 precursor RNA folds spatially, forming GR5884 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5884 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5884 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5884 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2188 precursor RNA, GAM57480 precursor RNA and GAM133123 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2188 RNA, GAM57480 RNA and GAM133123 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2188 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2188 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2188 target RNA into GAM2188 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM57480 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM57480 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM57480 target RNA into GAM57480 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM133123 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM133123 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM133123 target RNA into GAM133123 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5884 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5884 gene: GAM2188 target protein, GAM57480 target protein and GAM133123 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2188, GAM57480 and GAM133123

bioinformatically detected regulatory gene, referred to here as Genomic Record 5885(GR5885) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5885 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5885 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5885 gene encodes GR5885 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5885 precursor RNA folds spatially, forming GR5885 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5885 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5885 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5885 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM107435 precursor RNA and GAM233748 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM107435 RNA and GAM233748 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM107435 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM107435 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM107435 target RNA into GAM107435 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM233748 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM233748 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM233748

target RNA into GAM233748 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5885 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5885 gene: GAM107435 target protein and GAM233748 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM107435 and GAM233748

GR5886 BE397700 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5886(GR5886) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5886 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5886 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5886 gene encodes GR5886 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5886 precursor RNA folds spatially, forming GR5886 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5886 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5886 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5886 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8040 precursor RNA and GAM221763 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8040 RNA and GAM221763 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8040 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8040 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8040 target RNA into GAM8040 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM221763 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM221763 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM221763 target RNA into GAM221763 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5886 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5886 gene: GAM8040 target protein and GAM221763 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8040 and GAM221763

GR5887 N49062 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5887(GR5887) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5887 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5887 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5887 gene encodes GR5887 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5887 precursor RNA folds spatially, forming GR5887 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5887 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5887 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5887 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM43254 precursor RNA, GAM157089 precursor RNA and GAM164617 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM43254 RNA, GAM157089 RNA and GAM164617 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM43254 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM43254 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM43254 target RNA into GAM43254 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM157089 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM157089 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM157089 target RNA into GAM157089 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM164617 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM164617 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM164617 target RNA into GAM164617 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5887 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5887 gene: GAM43254 target protein, GAM157089 target protein and GAM164617 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM43254, GAM157089 and GAM164617

5888(GR5888) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5888 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5888 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5888 gene encodes GR5888 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5888 precursor RNA folds spatially, forming GR5888 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5888 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5888 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5888 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1945 precursor RNA and GAM4491 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1945 RNA and GAM4491 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1945 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1945 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1945 target RNA into GAM1945 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM4491 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4491 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4491 target RNA into GAM4491 target protein, herein schematically represented by GAM1 TARGET

PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5888 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5888 gene: GAM1945 target protein and GAM4491 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1945 and GAM4491

GR5889 BF976487 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5889(GR5889) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5889 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5889 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5889 gene encodes GR5889 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5889 precursor RNA folds spatially, forming GR5889 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5889 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5889 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5889 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM46367 precursor RNA and GAM52463 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM46367 RNA and GAM52463 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM46367 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM46367 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM46367 target RNA into GAM46367 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM52463 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM52463 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM52463 target RNA into GAM52463 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5889 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5889 gene: GAM46367 target protein and GAM52463 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM46367 and GAM52463

GR5890 BE868529 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5890(GR5890) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5890 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5890 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5890 gene encodes GR5890 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5890 precursor RNA folds spatially, forming GR5890 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5890 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5890 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5890 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3

separate GAM precursor RNAs, GAM8286 precursor RNA, GAM163960 precursor RNA and GAM213541 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8286 RNA, GAM163960 RNA and GAM213541 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8286 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8286 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8286 target RNA into GAM8286 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM163960 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM163960 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM163960 target RNA into GAM163960 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM213541 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM213541 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM213541 target RNA into GAM213541 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5890 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5890 gene: GAM8286 target protein, GAM163960 target protein and GAM213541 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8286, GAM163960 and GAM213541

GR5891 BG204721 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5891 (GR5891) gene, which encodes an `operon-like` cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5891 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5891 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5891 gene encodes GR5891 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5891 precursor RNA folds spatially, forming GR5891 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5891 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5891 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5891 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1880 precursor RNA and GAM206760 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1880 RNA and GAM206760 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1880 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1880 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1880 target RNA into GAM1880 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM206760 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM206760 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM206760 target RNA into GAM206760 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5891 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5891 gene: GAM1880 target protein and GAM206760 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1880 and GAM206760

GR5892 BE559682 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5892(GR5892) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5892 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5892 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5892 gene encodes GR5892 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5892 precursor RNA folds spatially, forming GR5892 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5892 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5892 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5892 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2957 precursor RNA and GAM257023 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2957 RNA and GAM257023 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2957 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2957 target RNA, herein schematically represented by

GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2957 target RNA into GAM2957 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM257023 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM257023 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM257023 target RNA into GAM257023 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5892 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5892 gene: GAM2957 target protein and GAM257023 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2957 and GAM257023

GR5893 AI916978 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5893(GR5893) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5893 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5893 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5893 gene encodes GR5893 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5893 precursor RNA folds spatially, forming GR5893 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5893 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5893 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5893 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5554 precursor RNA and GAM39028 precursor

RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5554 RNA and GAM39028 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5554 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5554 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5554 target RNA into GAM5554 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM39028 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM39028 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM39028 target RNA into GAM39028 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5893 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5893 gene: GAM5554 target protein and GAM39028 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5554 and GAM39028

GR5894 BF807529 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5894 (GR5894) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5894 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5894 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5894 gene encodes GR5894 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5894 precursor RNA folds spatially, forming GR5894 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5894 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5894 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5894 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM248820 precursor RNA, GAM298407 precursor RNA and GAM308806 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM248820 RNA, GAM298407 RNA and GAM308806 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM248820 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM248820 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM248820 target RNA into GAM248820 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM298407 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM298407 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM298407 target RNA into GAM298407 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM308806 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM308806 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM308806 target RNA into GAM308806 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly

utilities, of GR5894 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5894 gene: GAM248820 target protein, GAM298407 target protein and GAM308806 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM248820, GAM298407 and GAM308806

GR5895 BF332388 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5895(GR5895) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5895 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5895 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5895 gene encodes GR5895 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5895 precursor RNA folds spatially, forming GR5895 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5895 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5895 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5895 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM101919 precursor RNA and GAM288973 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM101919 RNA and GAM288973 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM101919 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM101919 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM101919 target RNA into GAM101919 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM288973 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM288973 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM288973 target RNA into GAM288973 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5895 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5895 gene: GAM101919 target protein and GAM288973 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM101919 and GAM288973

GR5896 BE158256 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5896(GR5896) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5896 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5896 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5896 gene encodes GR5896 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5896 precursor RNA folds spatially, forming GR5896 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5896 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5896 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5896 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM217544 precursor RNA and GAM299728 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3

FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM217544 RNA and GAM299728 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM217544 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM217544 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM217544 target RNA into GAM217544 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM299728 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM299728 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM299728 target RNA into GAM299728 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5896 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5896 gene: GAM217544 target protein and GAM299728 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM217544 and GAM299728

GR5897 W35195 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5897(GR5897) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5897 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5897 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5897 gene encodes GR5897 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5897 precursor RNA folds spatially, forming GR5897 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5897 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5897 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5897 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM755 precursor RNA and GAM262401 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM755 RNA and GAM262401 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM755 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM755 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM755 target RNA into GAM755 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM262401 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM262401 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM262401 target RNA into GAM262401 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5897 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5897 gene: GAM755 target protein and GAM262401 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM755 and GAM262401

5898(GR5898) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5898 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5898 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5898 gene encodes GR5898 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5898 precursor RNA folds spatially, forming GR5898 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5898 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5898 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5898 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM100636 precursor RNA, GAM110109 precursor RNA and GAM167316 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM100636 RNA, GAM110109 RNA and GAM167316 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM100636 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM100636 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM100636 target RNA into GAM100636 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM110109 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM110109 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM110109

target RNA into GAM110109 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM167316 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM167316 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM167316 target RNA into GAM167316 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5898 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5898 gene: GAM100636 target protein, GAM110109 target protein and GAM167316 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM100636, GAM110109 and GAM167316

GR5899 BF894899 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5899(GR5899) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5899 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5899 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5899 gene encodes GR5899 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5899 precursor RNA folds spatially, forming GR5899 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5899 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5899 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5899 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM143052 precursor RNA and GAM298745 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin

shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM143052 RNA and GAM298745 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM143052 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM143052 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM143052 target RNA into GAM143052 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM298745 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM298745 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM298745 target RNA into GAM298745 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5899 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5899 gene: GAM143052 target protein and GAM298745 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM143052 and GAM298745

GR5900 BG013636 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5900(GR5900) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5900 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5900 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5900 gene encodes GR5900 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5900 precursor RNA folds spatially, forming GR5900 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5900 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5900 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5900 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5013 precursor RNA and GAM250586 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5013 RNA and GAM250586 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5013 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5013 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5013 target RNA into GAM5013 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM250586 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM250586 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM250586 target RNA into GAM250586 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5900 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5900 gene: GAM5013 target protein and GAM250586 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5013 and GAM250586

GR5901 AI075711 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5901(GR5901) gene, which encodes an `operon-like` cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5901 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5901 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5901 gene encodes GR5901 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5901 precursor RNA folds spatially, forming GR5901 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5901 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5901 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5901 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM105583 precursor RNA and GAM221448 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM105583 RNA and GAM221448 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM105583 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM105583 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM105583 target RNA into GAM105583 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM221448 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM221448 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM221448 target RNA into GAM221448 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5901 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5901 gene: GAM105583 target protein and GAM221448 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM105583 and GAM221448

GR5902 BG288905 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5902(GR5902) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5902 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5902 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5902 gene encodes GR5902 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5902 precursor RNA folds spatially, forming GR5902 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5902 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5902 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5902 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4933 precursor RNA, GAM7028 precursor RNA and GAM8598 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4933 RNA, GAM7028 RNA and GAM8598 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4933 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM4933 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4933 target RNA into GAM4933 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7028 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7028 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7028 target RNA into GAM7028 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8598 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8598 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8598 target RNA into GAM8598 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5902 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5902 gene: GAM4933 target protein, GAM7028 target protein and GAM8598 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4933, GAM7028 and GAM8598

GR5903 AL598786 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5903(GR5903) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5903 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5903 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5903 gene encodes GR5903 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5903 precursor RNA folds spatially, forming GR5903 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated

that GR5903 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5903 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5903 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM533 precursor RNA and GAM99370 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM533 RNA and GAM99370 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM533 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM533 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM533 target RNA into GAM533 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM99370 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM99370 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM99370 target RNA into GAM99370 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5903 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5903 gene: GAM533 target protein and GAM99370 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM533 and GAM99370

GR5904 BG824083 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5904(GR5904) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR5904 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5904 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5904 gene encodes GR5904 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5904 precursor RNA folds spatially, forming GR5904 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5904 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5904 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5904 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM7633 precursor RNA, GAM122175 precursor RNA and GAM286047 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7633 RNA, GAM122175 RNA and GAM286047 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7633 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7633 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7633 target RNA into GAM7633 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM122175 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM122175 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM122175 target RNA into GAM122175 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM286047 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM286047 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM286047 target RNA into GAM286047 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5904 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5904 gene: GAM7633 target protein, GAM122175 target protein and GAM286047 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7633, GAM122175 and GAM286047

GR5905 BG495965 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5905(GR5905) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5905 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5905 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5905 gene encodes GR5905 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5905 precursor RNA folds spatially, forming GR5905 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5905 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5905 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5905 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM7588 precursor RNA, GAM187671 precursor RNA and GAM331990 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7588 RNA, GAM187671 RNA and GAM331990 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7588 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7588 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7588 target RNA into GAM7588 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM187671 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM187671 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM187671 target RNA into GAM187671 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM331990 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM331990 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM331990 target RNA into GAM331990 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5905 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5905 gene: GAM7588 target protein, GAM187671 target protein and GAM331990 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7588, GAM187671 and GAM331990

GR5906 AI809501 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5906(GR5906) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5906 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR5906 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5906 gene encodes GR5906 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5906 precursor RNA folds spatially, forming GR5906 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5906 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5906 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5906 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7447 precursor RNA and GAM336052 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7447 RNA and GAM336052 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7447 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7447 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7447 target RNA into GAM7447 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336052 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336052 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336052 target RNA into GAM336052 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5906 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5906 gene: GAM7447 target

protein and GAM336052 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7447 and GAM336052

GR5907 BE393107 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5907(GR5907) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5907 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5907 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5907 gene encodes GR5907 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5907 precursor RNA folds spatially, forming GR5907 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5907 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5907 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5907 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM843 precursor RNA and GAM7779 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM843 RNA and GAM7779 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM843 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM843 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM843 target RNA into GAM843 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7779 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7779 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7779 target RNA into GAM7779 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5907 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5907 gene: GAM843 target protein and GAM7779 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM843 and GAM7779

GR5908 AI690442 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5908(GR5908) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5908 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5908 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5908 gene encodes GR5908 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5908 precursor RNA folds spatially, forming GR5908 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5908 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5908 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5908 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2338 precursor RNA and GAM336117 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2338 RNA and GAM336117 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2338 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2338 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2338 target RNA into GAM2338 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336117 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336117 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336117 target RNA into GAM336117 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5908 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5908 gene: GAM2338 target protein and GAM336117 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2338 and GAM336117

GR5909 BI116781 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5909(GR5909) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5909 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5909 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5909 gene encodes GR5909 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5909 precursor RNA folds spatially, forming GR5909 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5909 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR5909 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5909 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM7720 precursor RNA, GAM68841 precursor RNA, GAM74159 precursor RNA and GAM281092 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7720 RNA, GAM68841 RNA, GAM74159 RNA and GAM281092 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7720 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7720 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7720 target RNA into GAM7720 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM68841 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM68841 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM68841 target RNA into GAM68841 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM74159 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM74159 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM74159 target RNA into GAM74159 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM281092 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM281092 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM281092 target RNA into GAM281092 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5909 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5909 gene: GAM7720 target protein, GAM68841 target protein, GAM74159 target protein and GAM281092 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7720, GAM68841, GAM74159 and GAM281092

GR5910 BE714560 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5910(GR5910) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5910 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5910 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5910 gene encodes GR5910 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5910 precursor RNA folds spatially, forming GR5910 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5910 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5910 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5910 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6938 precursor RNA and GAM194972 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6938 RNA and GAM194972 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6938 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6938 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6938 target RNA into GAM6938 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM194972 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM194972 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM194972 target RNA into GAM194972 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5910 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5910 gene: GAM6938 target protein and GAM194972 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6938 and GAM194972

GR5911 R97120 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5911(GR5911) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5911 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5911 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5911 gene encodes GR5911 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5911 precursor RNA folds spatially, forming GR5911 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5911 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5911 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5911 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6988 precursor RNA and GAM175037 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6988 RNA and GAM175037 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6988 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6988 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6988 target RNA into GAM6988 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM175037 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM175037 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM175037 target RNA into GAM175037 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5911 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5911 gene: GAM6988 target protein and GAM175037 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6988 and GAM175037

GR5912 BE973694 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5912(GR5912) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5912 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5912 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5912 gene encodes GR5912 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5912 precursor RNA folds spatially, forming GR5912 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5912 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5912 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5912 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2777 precursor RNA and GAM229927 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2777 RNA and GAM229927 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2777 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2777 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2777 target RNA into GAM2777 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM229927 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM229927 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM229927 target RNA into GAM229927 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5912 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5912 gene: GAM2777 target protein and GAM229927 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2777 and GAM229927

GR5913 AA625704 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5913(GR5913) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5913 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5913 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5913 gene encodes GR5913 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5913 precursor RNA folds spatially, forming GR5913 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5913 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5913 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5913 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4319 precursor RNA and GAM20799 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4319 RNA and GAM20799 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4319 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4319 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4319 target RNA into GAM4319 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM20799 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM20799 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM20799 target RNA into GAM20799 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5913 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5913 gene: GAM4319 target protein and GAM20799 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4319 and GAM20799

GR5914 BI772210 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5914(GR5914) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5914 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5914 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5914 gene encodes GR5914 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5914 precursor RNA folds spatially, forming GR5914 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5914 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5914 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5914 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7801 precursor RNA and GAM260448 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7801 RNA and GAM260448 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7801 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7801 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7801 target RNA into GAM7801 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM260448 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM260448 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM260448 target RNA into GAM260448 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5914 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5914 gene: GAM7801 target protein and GAM260448 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7801 and GAM260448

GR5915 BG427406 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5915(GR5915) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5915 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5915 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5915 gene encodes GR5915 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5915 precursor RNA folds spatially, forming GR5915 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5915 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5915 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5915 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM3388 precursor RNA, GAM7253 precursor RNA, GAM182523 precursor RNA and GAM248104 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3388 RNA, GAM7253 RNA, GAM182523 RNA and GAM248104 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3388 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3388 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3388 target RNA into GAM3388 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7253 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7253 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7253 target RNA into GAM7253 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM182523 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM182523 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM182523 target RNA into GAM182523 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM248104 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM248104 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM248104 target RNA into GAM248104 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5915 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5915 gene: GAM3388 target protein, GAM7253 target protein, GAM182523 target protein and GAM248104 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3388, GAM7253, GAM182523 and GAM248104

GR5916 AA378952 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5916(GR5916) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5916 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5916 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5916 gene encodes GR5916 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5916 precursor RNA folds spatially, forming GR5916 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5916 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5916 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5916 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM81884 precursor RNA and GAM301082 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM81884 RNA and GAM301082 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM81884 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM81884 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM81884 target RNA into GAM81884 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM301082 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM301082 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM301082 target RNA into GAM301082 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5916 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5916 gene: GAM81884 target protein and GAM301082 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM81884 and GAM301082

GR5917 AA993176 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5917(GR5917) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5917 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5917 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5917 gene encodes GR5917 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5917 precursor RNA folds spatially, forming GR5917 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5917 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5917 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5917 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2735 precursor RNA, GAM233308 precursor RNA and GAM314491 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded

precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2735 RNA, GAM233308 RNA and GAM314491 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2735 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2735 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2735 target RNA into GAM2735 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM233308 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM233308 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM233308 target RNA into GAM233308 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM314491 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM314491 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM314491 target RNA into GAM314491 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5917 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5917 gene: GAM2735 target protein, GAM233308 target protein and GAM314491 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2735, GAM233308 and GAM314491

GR5918 BI003912 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5918(GR5918) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5918 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5918 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5918 gene encodes GR5918 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5918 precursor RNA folds spatially, forming GR5918 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5918 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5918 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5918 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM9116 precursor RNA and GAM155555 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM9116 RNA and GAM155555 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM9116 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM9116 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM9116 target RNA into GAM9116 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM155555 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM155555 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM155555 target RNA into GAM155555 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5918 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5918 gene: GAM9116 target protein and GAM15555 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM9116 and GAM15555

GR5919 AI086967 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5919(GR5919) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5919 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5919 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5919 gene encodes GR5919 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5919 precursor RNA folds spatially, forming GR5919 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5919 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5919 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5919 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM214932 precursor RNA and GAM278765 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM214932 RNA and GAM278765 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM214932 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM214932 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM214932

target RNA into GAM214932 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM278765 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM278765 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM278765 target RNA into GAM278765 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5919 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5919 gene: GAM214932 target protein and GAM278765 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM214932 and GAM278765

GR5920 BI913234 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5920(GR5920) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5920 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5920 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5920 gene encodes GR5920 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5920 precursor RNA folds spatially, forming GR5920 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5920 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5920 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5920 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM142427 precursor RNA and GAM189394 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM142427 RNA and GAM189394 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM142427 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM142427 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM142427 target RNA into GAM142427 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM189394 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM189394 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM189394 target RNA into GAM189394 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5920 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5920 gene: GAM142427 target protein and GAM189394 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM142427 and GAM189394

GR5921 BG567142 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5921 (GR5921) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5921 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5921 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5921 gene encodes GR5921 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5921 precursor RNA folds spatially, forming GR5921 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated

that GR5921 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5921 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5921 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4054 precursor RNA, GAM77997 precursor RNA and GAM152184 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4054 RNA, GAM77997 RNA and GAM152184 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4054 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4054 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4054 target RNA into GAM4054 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM77997 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM77997 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM77997 target RNA into GAM77997 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM152184 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM152184 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM152184 target RNA into GAM152184 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5921 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5921 gene: GAM4054 target

protein, GAM77997 target protein and GAM152184 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4054, GAM77997 and GAM152184

GR5922 BF664758 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5922(GR5922) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5922 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5922 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5922 gene encodes GR5922 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5922 precursor RNA folds spatially, forming GR5922 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5922 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5922 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5922 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2467 precursor RNA and GAM144417 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2467 RNA and GAM144417 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2467 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2467 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2467 target RNA into GAM2467 target protein, herein schematically represented by GAM1 TARGET

PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM144417 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM144417 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM144417 target RNA into GAM144417 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5922 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5922 gene: GAM2467 target protein and GAM144417 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2467 and GAM144417

GR5923 BG743023 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5923(GR5923) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5923 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5923 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5923 gene encodes GR5923 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5923 precursor RNA folds spatially, forming GR5923 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5923 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5923 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5923 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3429 precursor RNA and GAM93968 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3429 RNA and GAM93968 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3429 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3429 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3429 target RNA into GAM3429 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM93968 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM93968 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM93968 target RNA into GAM93968 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5923 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5923 gene: GAM3429 target protein and GAM93968 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3429 and GAM93968

GR5924 BF222358 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5924(GR5924) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5924 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5924 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5924 gene encodes GR5924 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5924 precursor RNA folds spatially, forming GR5924 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5924 folded precursor RNA comprises a plurality of what is known in the

art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5924 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5924 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM122354 precursor RNA and GAM175010 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM122354 RNA and GAM175010 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM122354 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM122354 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM122354 target RNA into GAM122354 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM175010 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM175010 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM175010 target RNA into GAM175010 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5924 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5924 gene: GAM122354 target protein and GAM175010 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM122354 and GAM175010

GR5925 AI240717 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5925(GR5925) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR5925 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5925 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5925 gene encodes GR5925 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5925 precursor RNA folds spatially, forming GR5925 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5925 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5925 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5925 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8355 precursor RNA and GAM192523 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8355 RNA and GAM192523 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8355 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8355 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8355 target RNA into GAM8355 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM192523 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM192523 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM192523 target RNA into GAM192523 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly

utilities, of GR5925 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5925 gene: GAM8355 target protein and GAM192523 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8355 and GAM192523

GR5926 BF795431 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5926(GR5926) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5926 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5926 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5926 gene encodes GR5926 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5926 precursor RNA folds spatially, forming GR5926 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5926 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5926 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5926 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2477 precursor RNA and GAM89991 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2477 RNA and GAM89991 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2477 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2477 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig. 8, thereby inhibiting translation of GAM2477 target RNA into GAM2477 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM89991 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM89991 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM89991 target RNA into GAM89991 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5926 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5926 gene: GAM2477 target protein and GAM89991 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2477 and GAM89991

GR5927 N31336 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5927(GR5927) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5927 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5927 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5927 gene encodes GR5927 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5927 precursor RNA folds spatially, forming GR5927 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5927 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5927 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5927 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7662 precursor RNA and GAM183809 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin

shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7662 RNA and GAM183809 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7662 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7662 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7662 target RNA into GAM7662 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM183809 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM183809 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM183809 target RNA into GAM183809 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5927 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5927 gene: GAM7662 target protein and GAM183809 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7662 and GAM183809

GR5928 AA725898 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5928(GR5928) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5928 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5928 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5928 gene encodes GR5928 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5928 precursor RNA folds spatially, forming GR5928 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5928 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5928 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5928 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4989 precursor RNA and GAM103378 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4989 RNA and GAM103378 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4989 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4989 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4989 target RNA into GAM4989 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM103378 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM103378 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM103378 target RNA into GAM103378 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5928 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5928 gene: GAM4989 target protein and GAM103378 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4989 and GAM103378

GR5929 BG121032 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5929(GR5929) gene, which encodes an `operon-like` cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5929 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5929 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5929 gene encodes GR5929 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5929 precursor RNA folds spatially, forming GR5929 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5929 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5929 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5929 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM85043 precursor RNA and GAM140384 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM85043 RNA and GAM140384 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM85043 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM85043 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM85043 target RNA into GAM85043 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM140384 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM140384 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM140384 target RNA into GAM140384 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5929 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5929 gene: GAM85043 target protein and GAM140384 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM85043 and GAM140384

GR5930 BG475201 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5930(GR5930) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5930 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5930 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5930 gene encodes GR5930 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5930 precursor RNA folds spatially, forming GR5930 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5930 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5930 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5930 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM7973 precursor RNA, GAM8272 precursor RNA, GAM56117 precursor RNA and GAM224579 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7973 RNA, GAM8272 RNA, GAM56117 RNA and GAM224579 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7973 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM7973 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7973 target RNA into GAM7973 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8272 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8272 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8272 target RNA into GAM8272 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM56117 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM56117 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM56117 target RNA into GAM56117 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM224579 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM224579 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM224579 target RNA into GAM224579 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5930 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5930 gene: GAM7973 target protein, GAM8272 target protein, GAM56117 target protein and GAM224579 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7973, GAM8272, GAM56117 and GAM224579

GR5931 BE270646 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5931(GR5931) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5931 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5931

gene was detected is described hereinabove with reference to Figs. 8-18.

GR5931 gene encodes GR5931 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5931 precursor RNA folds spatially, forming GR5931 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5931 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5931 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5931 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1140 precursor RNA and GAM75353 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1140 RNA and GAM75353 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1140 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1140 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1140 target RNA into GAM1140 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM75353 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM75353 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM75353 target RNA into GAM75353 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5931 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5931 gene: GAM1140 target protein and GAM75353 target protein, herein schematically represented by GAM1

TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1140 and GAM75353

GR5932 AA421702 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5932(GR5932) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5932 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5932 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5932 gene encodes GR5932 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5932 precursor RNA folds spatially, forming GR5932 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5932 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5932 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5932 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM87639 precursor RNA and GAM190189 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM87639 RNA and GAM190189 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM87639 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM87639 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM87639 target RNA into GAM87639 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM190189 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM190189 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM190189 target RNA into GAM190189 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5932 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5932 gene: GAM87639 target protein and GAM190189 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM87639 and GAM190189

GR5933 BG257812 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5933(GR5933) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5933 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5933 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5933 gene encodes GR5933 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5933 precursor RNA folds spatially, forming GR5933 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5933 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5933 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5933 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7629 precursor RNA and GAM195002 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM7629 RNA and GAM195002 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7629 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7629 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7629 target RNA into GAM7629 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM195002 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM195002 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM195002 target RNA into GAM195002 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5933 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5933 gene: GAM7629 target protein and GAM195002 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7629 and GAM195002

GR5934 BG749136 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5934(GR5934) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5934 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5934 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5934 gene encodes GR5934 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5934 precursor RNA folds spatially, forming GR5934 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5934 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5934 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5934 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM9052 precursor RNA and GAM239370 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM9052 RNA and GAM239370 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM9052 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM9052 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM9052 target RNA into GAM9052 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM239370 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM239370 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM239370 target RNA into GAM239370 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5934 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5934 gene: GAM9052 target protein and GAM239370 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM9052 and GAM239370

GR5935 AW246245 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5935(GR5935) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5935 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5935 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5935 gene encodes GR5935 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5935 precursor RNA folds spatially, forming GR5935 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5935 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5935 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5935 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM89317 precursor RNA and GAM224948 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM89317 RNA and GAM224948 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM89317 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM89317 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM89317 target RNA into GAM89317 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM224948 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM224948 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM224948 target RNA into GAM224948 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5935 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR5935 gene: GAM89317 target protein and GAM224948 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM89317 and GAM224948

GR5936 AW953396 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5936(GR5936) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5936 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5936 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5936 gene encodes GR5936 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5936 precursor RNA folds spatially, forming GR5936 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5936 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5936 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5936 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM93055 precursor RNA, GAM240101 precursor RNA and GAM257278 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM93055 RNA, GAM240101 RNA and GAM257278 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM93055 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM93055 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM93055

target RNA into GAM93055 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM240101 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM240101 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM240101 target RNA into GAM240101 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM257278 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM257278 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM257278 target RNA into GAM257278 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5936 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5936 gene: GAM93055 target protein, GAM240101 target protein and GAM257278 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM93055, GAM240101 and GAM257278

GR5937 BI763579 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5937(GR5937) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5937 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5937 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5937 gene encodes GR5937 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5937 precursor RNA folds spatially, forming GR5937 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5937 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5937 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5937 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6772 precursor RNA and GAM46785 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6772 RNA and GAM46785 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6772 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6772 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6772 target RNA into GAM6772 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM46785 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM46785 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM46785 target RNA into GAM46785 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5937 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5937 gene: GAM6772 target protein and GAM46785 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6772 and GAM46785

GR5938 T62489 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5938(GR5938) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5938 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR5938 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5938 gene encodes GR5938 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5938 precursor RNA folds spatially, forming GR5938 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5938 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5938 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5938 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM16568 precursor RNA, GAM27015 precursor RNA and GAM129856 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM16568 RNA, GAM27015 RNA and GAM129856 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM16568 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM16568 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM16568 target RNA into GAM16568 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM27015 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM27015 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM27015 target RNA into GAM27015 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM129856 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM129856 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM129856 target RNA into GAM129856 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5938 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5938 gene: GAM16568 target protein, GAM27015 target protein and GAM129856 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM16568, GAM27015 and GAM129856

GR5939 BG618166 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5939(GR5939) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5939 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5939 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5939 gene encodes GR5939 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5939 precursor RNA folds spatially, forming GR5939 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5939 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5939 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5939 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM80070 precursor RNA, GAM161955 precursor RNA and GAM275591 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM80070 RNA, GAM161955 RNA and GAM275591 RNA, herein

schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM80070 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM80070 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM80070 target RNA into GAM80070 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM161955 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM161955 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM161955 target RNA into GAM161955 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM275591 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM275591 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM275591 target RNA into GAM275591 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5939 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5939 gene: GAM80070 target protein, GAM161955 target protein and GAM275591 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM80070, GAM161955 and GAM275591

GR5940 AV730074 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5940(GR5940) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5940 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5940 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5940 gene encodes GR5940 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5940 precursor RNA folds spatially, forming GR5940 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5940 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5940 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5940 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM19079 precursor RNA, GAM39296 precursor RNA and GAM297279 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM19079 RNA, GAM39296 RNA and GAM297279 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM19079 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM19079 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM19079 target RNA into GAM19079 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM39296 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM39296 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM39296 target RNA into GAM39296 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM297279 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM297279 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM297279 target RNA into GAM297279 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5940 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5940 gene: GAM19079 target protein, GAM39296 target protein and GAM297279 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM19079, GAM39296 and GAM297279

GR5941 BI457750 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5941 (GR5941) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5941 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5941 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5941 gene encodes GR5941 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5941 precursor RNA folds spatially, forming GR5941 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5941 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5941 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5941 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1367 precursor RNA and GAM6630 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1367 RNA and GAM6630 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1367 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM1367 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1367 target RNA into GAM1367 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6630 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6630 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6630 target RNA into GAM6630 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5941 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5941 gene: GAM1367 target protein and GAM6630 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1367 and GAM6630

GR5942 BF902948 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5942(GR5942) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5942 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5942 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5942 gene encodes GR5942 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5942 precursor RNA folds spatially, forming GR5942 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5942 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5942 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5942 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2

separate GAM precursor RNAs, GAM28114 precursor RNA and GAM262933 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM28114 RNA and GAM262933 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM28114 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM28114 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM28114 target RNA into GAM28114 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM262933 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM262933 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM262933 target RNA into GAM262933 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5942 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5942 gene: GAM28114 target protein and GAM262933 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM28114 and GAM262933

GR5943 AW999683 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5943 (GR5943) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5943 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5943 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5943 gene encodes GR5943 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR5943 precursor RNA folds spatially, forming GR5943 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5943 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5943 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5943 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2055 precursor RNA, GAM187328 precursor RNA and GAM242542 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2055 RNA, GAM187328 RNA and GAM242542 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2055 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2055 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2055 target RNA into GAM2055 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM187328 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM187328 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM187328 target RNA into GAM187328 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM242542 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM242542 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM242542 target RNA into GAM242542 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5943 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5943 gene: GAM2055 target protein, GAM187328 target protein and GAM242542 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2055, GAM187328 and GAM242542

GR5944 AW590564 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5944(GR5944) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5944 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5944 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5944 gene encodes GR5944 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5944 precursor RNA folds spatially, forming GR5944 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5944 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5944 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5944 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6791 precursor RNA and GAM277976 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6791 RNA and GAM277976 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6791 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6791 target RNA, herein schematically represented by

GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6791 target RNA into GAM6791 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM277976 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM277976 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM277976 target RNA into GAM277976 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5944 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5944 gene: GAM6791 target protein and GAM277976 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6791 and GAM277976

GR5945 AA617887 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5945(GR5945) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5945 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5945 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5945 gene encodes GR5945 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5945 precursor RNA folds spatially, forming GR5945 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5945 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5945 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5945 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6571 precursor RNA and GAM221440 precursor

RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6571 RNA and GAM221440 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6571 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6571 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6571 target RNA into GAM6571 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM221440 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM221440 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM221440 target RNA into GAM221440 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5945 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5945 gene: GAM6571 target protein and GAM221440 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6571 and GAM221440

GR5946 BQ010533 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5946 (GR5946) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5946 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5946 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5946 gene encodes GR5946 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5946 precursor RNA folds spatially, forming GR5946 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5946 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5946 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5946 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM121985 precursor RNA, GAM178187 precursor RNA and GAM260918 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM121985 RNA, GAM178187 RNA and GAM260918 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM121985 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM121985 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM121985 target RNA into GAM121985 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM178187 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM178187 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM178187 target RNA into GAM178187 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM260918 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM260918 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM260918 target RNA into GAM260918 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly

utilities, of GR5946 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5946 gene: GAM121985 target protein, GAM178187 target protein and GAM260918 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM121985, GAM178187 and GAM260918

GR5947 BG284512 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5947(GR5947) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5947 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5947 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5947 gene encodes GR5947 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5947 precursor RNA folds spatially, forming GR5947 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5947 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5947 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5947 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1093 precursor RNA and GAM6974 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1093 RNA and GAM6974 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1093 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1093 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds

to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1093 target RNA into GAM1093 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6974 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6974 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6974 target RNA into GAM6974 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5947 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5947 gene: GAM1093 target protein and GAM6974 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1093 and GAM6974

GR5948 AU125559 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5948(GR5948) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5948 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5948 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5948 gene encodes GR5948 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5948 precursor RNA folds spatially, forming GR5948 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5948 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5948 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5948 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM738 precursor RNA and GAM135707 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3

FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM738 RNA and GAM135707 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM738 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM738 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM738 target RNA into GAM738 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM135707 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM135707 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM135707 target RNA into GAM135707 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5948 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5948 gene: GAM738 target protein and GAM135707 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM738 and GAM135707

GR5949 AA394278 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5949(GR5949) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5949 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5949 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5949 gene encodes GR5949 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5949 precursor RNA folds spatially, forming GR5949 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5949 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5949 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5949 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM692 precursor RNA, GAM224552 precursor RNA and GAM316096 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM692 RNA, GAM224552 RNA and GAM316096 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM692 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM692 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM692 target RNA into GAM692 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM224552 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM224552 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM224552 target RNA into GAM224552 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM316096 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM316096 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM316096 target RNA into GAM316096 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5949 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5949 gene: GAM692 target protein, GAM224552 target protein and GAM316096 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM692, GAM224552 and GAM316096

GR5950 H23140 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5950(GR5950) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5950 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5950 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5950 gene encodes GR5950 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5950 precursor RNA folds spatially, forming GR5950 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5950 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5950 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5950 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2366 precursor RNA, GAM5542 precursor RNA and GAM146299 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2366 RNA, GAM5542 RNA and GAM146299 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2366 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2366 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds

to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2366 target RNA into GAM2366 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5542 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5542 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5542 target RNA into GAM5542 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM146299 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM146299 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM146299 target RNA into GAM146299 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5950 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5950 gene: GAM2366 target protein, GAM5542 target protein and GAM146299 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2366, GAM5542 and GAM146299

GR5951 R19435 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5951 (GR5951) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5951 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5951 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5951 gene encodes GR5951 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5951 precursor RNA folds spatially, forming GR5951 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5951 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR5951 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5951 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM7170 precursor RNA, GAM7920 precursor RNA and GAM17061 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7170 RNA, GAM7920 RNA and GAM17061 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7170 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7170 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7170 target RNA into GAM7170 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7920 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7920 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7920 target RNA into GAM7920 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM17061 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM17061 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM17061 target RNA into GAM17061 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5951 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5951 gene: GAM7170 target protein, GAM7920 target protein and GAM17061 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN.

The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7170, GAM7920 and GAM17061

GR5952 BM016999 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5952(GR5952) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5952 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5952 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5952 gene encodes GR5952 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5952 precursor RNA folds spatially, forming GR5952 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5952 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5952 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5952 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7501 precursor RNA and GAM95283 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7501 RNA and GAM95283 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7501 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7501 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7501 target RNA into GAM7501 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM95283 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM95283 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM95283 target RNA into GAM95283 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5952 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5952 gene: GAM7501 target protein and GAM95283 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7501 and GAM95283

GR5953 AV741182 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5953(GR5953) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5953 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5953 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5953 gene encodes GR5953 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5953 precursor RNA folds spatially, forming GR5953 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5953 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5953 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5953 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7880 precursor RNA and GAM230228 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM7880 RNA and GAM230228 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7880 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7880 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7880 target RNA into GAM7880 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM230228 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM230228 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM230228 target RNA into GAM230228 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5953 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5953 gene: GAM7880 target protein and GAM230228 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7880 and GAM230228

GR5954 BM702658 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5954(GR5954) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5954 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5954 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5954 gene encodes GR5954 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5954 precursor RNA folds spatially, forming GR5954 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5954 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5954 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5954 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM141 precursor RNA, GAM17944 precursor RNA and GAM287953 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM141 RNA, GAM17944 RNA and GAM287953 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM141 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM141 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM141 target RNA into GAM141 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM17944 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM17944 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM17944 target RNA into GAM17944 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM287953 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM287953 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM287953 target RNA into GAM287953 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5954 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5954 gene: GAM141 target protein, GAM17944 target protein and GAM287953 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6,

hereby incorporated by reference, with references to GAM141, GAM17944 and GAM287953

GR5955 BF132492 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5955(GR5955) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5955 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5955 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5955 gene encodes GR5955 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5955 precursor RNA folds spatially, forming GR5955 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5955 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5955 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5955 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6438 precursor RNA and GAM221357 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6438 RNA and GAM221357 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6438 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6438 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6438 target RNA into GAM6438 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM221357 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM221357 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM221357 target RNA into GAM221357 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5955 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5955 gene: GAM6438 target protein and GAM221357 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6438 and GAM221357

GR5956 BI024016 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5956(GR5956) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5956 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5956 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5956 gene encodes GR5956 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5956 precursor RNA folds spatially, forming GR5956 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5956 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5956 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5956 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1882 precursor RNA and GAM3079 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1882 RNA and GAM3079 RNA, herein schematically

represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1882 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1882 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1882 target RNA into GAM1882 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM3079 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3079 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3079 target RNA into GAM3079 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5956 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5956 gene: GAM1882 target protein and GAM3079 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1882 and GAM3079

GR5957 BG106325 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5957(GR5957) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5957 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5957 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5957 gene encodes GR5957 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5957 precursor RNA folds spatially, forming GR5957 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5957 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5957 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5957 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 5 separate GAM precursor RNAs, GAM5797 precursor RNA, GAM23448 precursor RNA, GAM239761 precursor RNA, GAM294533 precursor RNA and GAM311312 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5797 RNA, GAM23448 RNA, GAM239761 RNA, GAM294533 RNA and GAM311312 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5797 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5797 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5797 target RNA into GAM5797 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM23448 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM23448 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM23448 target RNA into GAM23448 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM239761 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM239761 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM239761 target RNA into GAM239761 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM294533 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM294533 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM294533 target RNA into GAM294533 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM311312 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM311312 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM311312 target RNA into GAM311312 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5957 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5957 gene: GAM5797 target protein, GAM23448 target protein, GAM239761 target protein, GAM294533 target protein and GAM311312 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5797, GAM23448, GAM239761, GAM294533 and GAM311312

GR5958 BM012610 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5958(GR5958) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5958 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5958 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5958 gene encodes GR5958 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5958 precursor RNA folds spatially, forming GR5958 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5958 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5958 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5958 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1561 precursor RNA and GAM2693 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1561 RNA and GAM2693 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1561 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1561 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1561 target RNA into GAM1561 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM2693 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2693 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2693 target RNA into GAM2693 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5958 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5958 gene: GAM1561 target protein and GAM2693 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1561 and GAM2693

GR5959 AI219481 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5959(GR5959) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5959 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5959 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5959 gene encodes GR5959 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5959 precursor RNA folds spatially, forming GR5959 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5959 folded precursor RNA comprises a plurality of what is known in the

art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5959 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5959 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7336 precursor RNA and GAM302736 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7336 RNA and GAM302736 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7336 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7336 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7336 target RNA into GAM7336 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM302736 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM302736 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM302736 target RNA into GAM302736 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5959 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5959 gene: GAM7336 target protein and GAM302736 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7336 and GAM302736

GR5960 BM838893 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5960 (GR5960) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR5960 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5960 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5960 gene encodes GR5960 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5960 precursor RNA folds spatially, forming GR5960 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5960 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5960 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5960 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4354 precursor RNA and GAM101622 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4354 RNA and GAM101622 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4354 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4354 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4354 target RNA into GAM4354 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM101622 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM101622 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM101622 target RNA into GAM101622 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly

utilities, of GR5960 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5960 gene: GAM4354 target protein and GAM101622 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4354 and GAM101622

GR5961 BF570671 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5961 (GR5961) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5961 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5961 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5961 gene encodes GR5961 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5961 precursor RNA folds spatially, forming GR5961 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5961 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5961 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5961 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM6690 precursor RNA, GAM36246 precursor RNA and GAM303704 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6690 RNA, GAM36246 RNA and GAM303704 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6690 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6690 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds

to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6690 target RNA into GAM6690 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM36246 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM36246 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM36246 target RNA into GAM36246 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM303704 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM303704 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM303704 target RNA into GAM303704 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5961 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5961 gene: GAM6690 target protein, GAM36246 target protein and GAM303704 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6690, GAM36246 and GAM303704

GR5962 BG953277 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5962(GR5962) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5962 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5962 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5962 gene encodes GR5962 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5962 precursor RNA folds spatially, forming GR5962 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5962 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR5962 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5962 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5507 precursor RNA and GAM87341 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5507 RNA and GAM87341 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5507 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5507 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5507 target RNA into GAM5507 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM87341 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM87341 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM87341 target RNA into GAM87341 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5962 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5962 gene: GAM5507 target protein and GAM87341 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5507 and GAM87341

GR5963 BI464954 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5963(GR5963) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5963 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5963 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5963 gene encodes GR5963 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5963 precursor RNA folds spatially, forming GR5963 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5963 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5963 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5963 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4658 precursor RNA, GAM8009 precursor RNA and GAM124547 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4658 RNA, GAM8009 RNA and GAM124547 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4658 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4658 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4658 target RNA into GAM4658 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8009 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8009 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8009 target RNA into GAM8009 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM124547 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM124547 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM124547 target RNA into GAM124547 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5963 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5963 gene: GAM4658 target protein, GAM8009 target protein and GAM124547 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4658, GAM8009 and GAM124547

GR5964 BG759825 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5964(GR5964) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5964 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5964 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5964 gene encodes GR5964 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5964 precursor RNA folds spatially, forming GR5964 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5964 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5964 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5964 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7739 precursor RNA and GAM59933 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM7739 RNA and GAM59933 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7739 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7739 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7739 target RNA into GAM7739 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM59933 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM59933 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM59933 target RNA into GAM59933 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5964 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5964 gene: GAM7739 target protein and GAM59933 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7739 and GAM59933

GR5965 BM714514 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5965(GR5965) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5965 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5965 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5965 gene encodes GR5965 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5965 precursor RNA folds spatially, forming GR5965 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5965 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5965 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5965 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM10294 precursor RNA and GAM124158 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM10294 RNA and GAM124158 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM10294 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM10294 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM10294 target RNA into GAM10294 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM124158 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM124158 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM124158 target RNA into GAM124158 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5965 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5965 gene: GAM10294 target protein and GAM124158 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM10294 and GAM124158

GR5966 BE792805 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5966(GR5966) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5966 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5966 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5966 gene encodes GR5966 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5966 precursor RNA folds spatially, forming GR5966 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5966 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5966 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5966 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM100924 precursor RNA and GAM279735 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM100924 RNA and GAM279735 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM100924 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM100924 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM100924 target RNA into GAM100924 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM279735 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM279735 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM279735 target RNA into GAM279735 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5966 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR5966 gene: GAM100924 target protein and GAM279735 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM100924 and GAM279735

GR5967 BE297479 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5967(GR5967) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5967 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5967 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5967 gene encodes GR5967 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5967 precursor RNA folds spatially, forming GR5967 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5967 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5967 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5967 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4148 precursor RNA, GAM6672 precursor RNA and GAM240699 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4148 RNA, GAM6672 RNA and GAM240699 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4148 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4148 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4148 target RNA into

GAM4148 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6672 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6672 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6672 target RNA into GAM6672 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM240699 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM240699 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM240699 target RNA into GAM240699 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5967 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5967 gene: GAM4148 target protein, GAM6672 target protein and GAM240699 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4148, GAM6672 and GAM240699

GR5968 BE612879 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5968(GR5968) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5968 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5968 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5968 gene encodes GR5968 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5968 precursor RNA folds spatially, forming GR5968 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5968 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5968 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5968 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2760 precursor RNA, GAM207255 precursor RNA and GAM276346 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2760 RNA, GAM207255 RNA and GAM276346 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2760 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2760 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2760 target RNA into GAM2760 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM207255 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM207255 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM207255 target RNA into GAM207255 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM276346 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM276346 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM276346 target RNA into GAM276346 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5968 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5968 gene: GAM2760 target protein, GAM207255 target protein and GAM276346 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2760, GAM207255 and

GR5969 BF125590 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5969 (GR5969) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5969 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5969 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5969 gene encodes GR5969 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5969 precursor RNA folds spatially, forming GR5969 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5969 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5969 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5969 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM809 precursor RNA, GAM4835 precursor RNA and GAM275544 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM809 RNA, GAM4835 RNA and GAM275544 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM809 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM809 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM809 target RNA into GAM809 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM4835 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM4835 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4835 target RNA into GAM4835 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM275544 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM275544 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM275544 target RNA into GAM275544 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5969 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5969 gene: GAM809 target protein, GAM4835 target protein and GAM275544 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM809, GAM4835 and GAM275544

GR5970 AV722500 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5970(GR5970) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5970 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5970 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5970 gene encodes GR5970 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5970 precursor RNA folds spatially, forming GR5970 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5970 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5970 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5970 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM232102 precursor RNA and GAM332111 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM232102 RNA and GAM332111 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM232102 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM232102 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM232102 target RNA into GAM232102 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM332111 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM332111 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM332111 target RNA into GAM332111 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5970 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5970 gene: GAM232102 target protein and GAM332111 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM232102 and GAM332111

GR5971 BM683230 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5971 (GR5971) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5971 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5971 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5971 gene encodes GR5971 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5971 precursor RNA folds spatially, forming GR5971 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5971 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5971 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5971 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM12574 precursor RNA and GAM178201 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM12574 RNA and GAM178201 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM12574 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM12574 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM12574 target RNA into GAM12574 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM178201 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM178201 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM178201 target RNA into GAM178201 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5971 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5971 gene: GAM12574 target protein and GAM178201 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM12574 and GAM178201

GR5972 AW571528 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5972(GR5972) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5972 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5972 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5972 gene encodes GR5972 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5972 precursor RNA folds spatially, forming GR5972 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5972 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5972 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5972 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM77811 precursor RNA and GAM332823 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM77811 RNA and GAM332823 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM77811 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM77811 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM77811 target RNA into GAM77811 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM332823 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM332823 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM332823 target RNA into GAM332823 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5972 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5972 gene: GAM77811 target protein and GAM332823 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM77811 and GAM332823

GR5973 BG680850 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5973(GR5973) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5973 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5973 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5973 gene encodes GR5973 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5973 precursor RNA folds spatially, forming GR5973 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5973 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5973 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5973 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM219344 precursor RNA and GAM257329 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM219344 RNA and GAM257329 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM219344 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM219344 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM219344 target RNA into GAM219344 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM257329 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM257329 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM257329 target RNA into GAM257329 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5973 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5973 gene: GAM219344 target protein and GAM257329 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM219344 and GAM257329

GR5974 AV758154 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5974(GR5974) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5974 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5974 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5974 gene encodes GR5974 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5974 precursor RNA folds spatially, forming GR5974 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5974 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5974 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5974 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1631 precursor RNA and GAM172684 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1631 RNA and GAM172684 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1631 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1631 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1631 target RNA into GAM1631 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM172684 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM172684 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM172684 target RNA into GAM172684 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5974 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5974 gene: GAM1631 target protein and GAM172684 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1631 and GAM172684

GR5975 BE263710 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5975(GR5975) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5975 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5975 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5975 gene encodes GR5975 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5975 precursor RNA folds spatially, forming GR5975 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5975 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5975 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5975 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM5996 precursor RNA, GAM252130 precursor RNA and GAM308797 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5996 RNA, GAM252130 RNA and GAM308797 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5996 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5996 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5996 target RNA into GAM5996 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM252130 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM252130 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM252130 target RNA into GAM252130 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM308797 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM308797 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM308797

target RNA into GAM308797 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5975 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5975 gene: GAM5996 target protein, GAM252130 target protein and GAM308797 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5996, GAM252130 and GAM308797

GR5976 BM806526 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5976(GR5976) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5976 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5976 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5976 gene encodes GR5976 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5976 precursor RNA folds spatially, forming GR5976 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5976 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5976 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5976 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM845 precursor RNA, GAM3460 precursor RNA, GAM7244 precursor RNA and GAM265125 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM845 RNA, GAM3460 RNA, GAM7244 RNA and GAM265125 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM845 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM845 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM845 target RNA into GAM845 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM3460 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3460 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3460 target RNA into GAM3460 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7244 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7244 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7244 target RNA into GAM7244 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM265125 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM265125 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM265125 target RNA into GAM265125 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5976 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5976 gene: GAM845 target protein, GAM3460 target protein, GAM7244 target protein and GAM265125 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM845, GAM3460, GAM7244 and GAM265125

GR5977 BI821113 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5977(GR5977) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5977 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5977 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5977 gene encodes GR5977 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5977 precursor RNA folds spatially, forming GR5977 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5977 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5977 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5977 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2831 precursor RNA, GAM6984 precursor RNA and GAM89356 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2831 RNA, GAM6984 RNA and GAM89356 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2831 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2831 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2831 target RNA into GAM2831 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6984 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6984 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6984 target RNA into GAM6984 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM89356 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM89356 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM89356 target RNA into GAM89356 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5977 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5977 gene: GAM2831 target protein, GAM6984 target protein and GAM89356 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2831, GAM6984 and GAM89356

GR5978 AW295179 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5978(GR5978) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5978 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5978 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5978 gene encodes GR5978 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5978 precursor RNA folds spatially, forming GR5978 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5978 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5978 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5978 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4661 precursor RNA, GAM4917 precursor RNA and GAM269858 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4661 RNA, GAM4917 RNA and GAM269858 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4661 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4661 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4661 target RNA into GAM4661 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM4917 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4917 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4917 target RNA into GAM4917 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM269858 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM269858 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM269858 target RNA into GAM269858 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5978 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5978 gene: GAM4661 target protein, GAM4917 target protein and GAM269858 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4661, GAM4917 and GAM269858

GR5979 AW630730 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5979(GR5979) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5979 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5979 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5979 gene encodes GR5979 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5979 precursor RNA folds spatially, forming GR5979 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5979 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5979 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5979 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM256628 precursor RNA and GAM278826 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM256628 RNA and GAM278826 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM256628 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM256628 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM256628 target RNA into GAM256628 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM278826 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM278826 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM278826 target RNA into GAM278826 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5979 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5979 gene: GAM256628 target protein and GAM278826 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes

is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM256628 and GAM278826

GR5980 BI261274 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5980(GR5980) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5980 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5980 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5980 gene encodes GR5980 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5980 precursor RNA folds spatially, forming GR5980 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5980 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5980 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5980 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM268867 precursor RNA, GAM272738 precursor RNA and GAM305281 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM268867 RNA, GAM272738 RNA and GAM305281 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM268867 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM268867 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM268867 target RNA into GAM268867 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM272738 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM272738 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM272738 target RNA into GAM272738 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM305281 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM305281 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM305281 target RNA into GAM305281 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5980 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5980 gene: GAM268867 target protein, GAM272738 target protein and GAM305281 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM268867, GAM272738 and GAM305281

GR5981 BM998851 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5981 (GR5981) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5981 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5981 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5981 gene encodes GR5981 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5981 precursor RNA folds spatially, forming GR5981 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5981 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5981 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5981 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM158158 precursor RNA, GAM225773 precursor RNA and GAM269142 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM158158 RNA, GAM225773 RNA and GAM269142 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM158158 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM158158 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM158158 target RNA into GAM158158 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM225773 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM225773 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM225773 target RNA into GAM225773 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM269142 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM269142 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM269142 target RNA into GAM269142 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5981 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5981 gene: GAM158158 target protein, GAM225773 target protein and GAM269142 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM158158, GAM225773 and GAM269142

bioinformatically detected regulatory gene, referred to here as Genomic Record 5982(GR5982) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5982 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5982 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5982 gene encodes GR5982 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5982 precursor RNA folds spatially, forming GR5982 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5982 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5982 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5982 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM102919 precursor RNA and GAM277323 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM102919 RNA and GAM277323 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM102919 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM102919 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM102919 target RNA into GAM102919 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM277323 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM277323 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM277323

target RNA into GAM277323 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5982 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5982 gene: GAM102919 target protein and GAM277323 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM102919 and GAM277323

GR5983 BE883349 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5983(GR5983) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5983 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5983 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5983 gene encodes GR5983 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5983 precursor RNA folds spatially, forming GR5983 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5983 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5983 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5983 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4842 precursor RNA, GAM46335 precursor RNA and GAM309564 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4842 RNA, GAM46335 RNA and GAM309564 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4842 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4842 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4842 target RNA into GAM4842 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM46335 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM46335 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM46335 target RNA into GAM46335 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM309564 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM309564 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM309564 target RNA into GAM309564 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5983 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5983 gene: GAM4842 target protein, GAM46335 target protein and GAM309564 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4842, GAM46335 and GAM309564

GR5984 AI956085 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5984(GR5984) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5984 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5984 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5984 gene encodes GR5984 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5984 precursor RNA folds spatially, forming GR5984 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5984 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5984 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5984 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM149034 precursor RNA and GAM303296 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM149034 RNA and GAM303296 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM149034 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM149034 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM149034 target RNA into GAM149034 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM303296 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM303296 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM303296 target RNA into GAM303296 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5984 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5984 gene: GAM149034 target protein and GAM303296 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM149034 and GAM303296

5985(GR5985) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5985 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5985 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5985 gene encodes GR5985 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5985 precursor RNA folds spatially, forming GR5985 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5985 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5985 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5985 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4722 precursor RNA, GAM79545 precursor RNA and GAM182882 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4722 RNA, GAM79545 RNA and GAM182882 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4722 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4722 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4722 target RNA into GAM4722 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM79545 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM79545 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM79545

target RNA into GAM79545 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM182882 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM182882 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM182882 target RNA into GAM182882 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5985 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5985 gene: GAM4722 target protein, GAM79545 target protein and GAM182882 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4722, GAM79545 and GAM182882

GR5986 BM801417 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5986(GR5986) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5986 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5986 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5986 gene encodes GR5986 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5986 precursor RNA folds spatially, forming GR5986 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5986 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5986 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5986 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM233649 precursor RNA, GAM246990 precursor RNA and GAM329297 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded

precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM233649 RNA, GAM246990 RNA and GAM329297 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM233649 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM233649 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM233649 target RNA into GAM233649 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM246990 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM246990 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM246990 target RNA into GAM246990 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM329297 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM329297 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM329297 target RNA into GAM329297 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5986 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5986 gene: GAM233649 target protein, GAM246990 target protein and GAM329297 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM233649, GAM246990 and GAM329297

GR5987 BE766922 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5987(GR5987) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5987 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5987 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5987 gene encodes GR5987 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5987 precursor RNA folds spatially, forming GR5987 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5987 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5987 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5987 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM24512 precursor RNA, GAM60565 precursor RNA and GAM100249 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM24512 RNA, GAM60565 RNA and GAM100249 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM24512 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM24512 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM24512 target RNA into GAM24512 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM60565 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM60565 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM60565 target RNA into GAM60565 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM100249 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM100249 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM100249 target RNA into GAM100249 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5987 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5987 gene: GAM24512 target protein, GAM60565 target protein and GAM100249 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM24512, GAM60565 and GAM100249

GR5988 AV697781 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5988(GR5988) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5988 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5988 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5988 gene encodes GR5988 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5988 precursor RNA folds spatially, forming GR5988 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5988 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5988 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5988 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1783 precursor RNA and GAM27365 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM1783 RNA and GAM27365 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1783 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1783 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1783 target RNA into GAM1783 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM27365 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM27365 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM27365 target RNA into GAM27365 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5988 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5988 gene: GAM1783 target protein and GAM27365 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1783 and GAM27365

GR5989 BE065514 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5989 (GR5989) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5989 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5989 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5989 gene encodes GR5989 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5989 precursor RNA folds spatially, forming GR5989 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5989 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5989 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5989 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM196840 precursor RNA and GAM261640 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM196840 RNA and GAM261640 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM196840 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM196840 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM196840 target RNA into GAM196840 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM261640 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM261640 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM261640 target RNA into GAM261640 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5989 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5989 gene: GAM196840 target protein and GAM261640 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM196840 and GAM261640

GR5990 BE536187 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5990 (GR5990) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5990 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5990 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5990 gene encodes GR5990 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5990 precursor RNA folds spatially, forming GR5990 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5990 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5990 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5990 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM113 precursor RNA and GAM42467 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM113 RNA and GAM42467 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM113 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM113 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM113 target RNA into GAM113 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM42467 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM42467 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM42467 target RNA into GAM42467 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5990 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR5990 gene: GAM113 target protein and GAM42467 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM113 and GAM42467

GR5991 BI254381 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5991 (GR5991) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5991 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5991 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5991 gene encodes GR5991 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5991 precursor RNA folds spatially, forming GR5991 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5991 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5991 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5991 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM71748 precursor RNA, GAM294987 precursor RNA and GAM319334 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM71748 RNA, GAM294987 RNA and GAM319334 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM71748 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM71748 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM71748

target RNA into GAM71748 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM294987 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM294987 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM294987 target RNA into GAM294987 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM319334 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM319334 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM319334 target RNA into GAM319334 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5991 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5991 gene: GAM71748 target protein, GAM294987 target protein and GAM319334 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM71748, GAM294987 and GAM319334

GR5992 BE314459 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5992(GR5992) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5992 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5992 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5992 gene encodes GR5992 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5992 precursor RNA folds spatially, forming GR5992 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5992 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5992 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5992 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM34 precursor RNA, GAM4743 precursor RNA and GAM20469 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM34 RNA, GAM4743 RNA and GAM20469 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM34 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM34 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM34 target RNA into GAM34 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM4743 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4743 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4743 target RNA into GAM4743 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM20469 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM20469 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM20469 target RNA into GAM20469 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5992 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5992 gene: GAM34 target protein, GAM4743 target protein and GAM20469 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM34, GAM4743 and

GR5993 BE617353 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5993(GR5993) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5993 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5993 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5993 gene encodes GR5993 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5993 precursor RNA folds spatially, forming GR5993 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5993 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5993 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5993 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM45422 precursor RNA and GAM119221 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM45422 RNA and GAM119221 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM45422 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM45422 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM45422 target RNA into GAM45422 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM119221 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM119221 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM119221 target RNA into GAM119221 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5993 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5993 gene: GAM45422 target protein and GAM119221 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM45422 and GAM119221

GR5994 BM454210 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5994(GR5994) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5994 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5994 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5994 gene encodes GR5994 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5994 precursor RNA folds spatially, forming GR5994 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5994 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5994 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5994 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM3936 precursor RNA, GAM7480 precursor RNA, GAM56234 precursor RNA and GAM319961 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3936 RNA, GAM7480 RNA, GAM56234 RNA and GAM319961

RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3936 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3936 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3936 target RNA into GAM3936 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7480 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7480 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7480 target RNA into GAM7480 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM56234 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM56234 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM56234 target RNA into GAM56234 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM319961 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM319961 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM319961 target RNA into GAM319961 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5994 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5994 gene: GAM3936 target protein, GAM7480 target protein, GAM56234 target protein and GAM319961 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3936, GAM7480, GAM56234 and GAM319961

GR5995 BG773888 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5995(GR5995) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR5995 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5995 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5995 gene encodes GR5995 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5995 precursor RNA folds spatially, forming GR5995 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5995 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5995 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5995 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM118900 precursor RNA and GAM147522 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM118900 RNA and GAM147522 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM118900 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM118900 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM118900 target RNA into GAM118900 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM147522 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM147522 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM147522 target RNA into GAM147522 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5995 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5995 gene: GAM118900 target protein and GAM147522 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM118900 and GAM147522

GR5996 BI517507 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5996(GR5996) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5996 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5996 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5996 gene encodes GR5996 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5996 precursor RNA folds spatially, forming GR5996 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5996 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5996 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5996 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM109937 precursor RNA, GAM171043 precursor RNA, GAM218054 precursor RNA and GAM224659 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM109937 RNA, GAM171043 RNA, GAM218054 RNA and GAM224659 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM109937 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM109937 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM109937 target RNA into GAM109937 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM171043 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM171043 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM171043 target RNA into GAM171043 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM218054 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM218054 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM218054 target RNA into GAM218054 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM224659 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM224659 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM224659 target RNA into GAM224659 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5996 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5996 gene: GAM109937 target protein, GAM171043 target protein, GAM218054 target protein and GAM224659 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM109937, GAM171043, GAM218054 and GAM224659

GR5997 H02675 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5997(GR5997) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5997 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5997 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5997 gene encodes GR5997 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5997 precursor RNA folds spatially, forming GR5997 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5997 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5997 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5997 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM72905 precursor RNA, GAM186582 precursor RNA and GAM250001 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM72905 RNA, GAM186582 RNA and GAM250001 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM72905 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM72905 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM72905 target RNA into GAM72905 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM186582 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM186582 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM186582 target RNA into GAM186582 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM250001 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM250001 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM250001

target RNA into GAM250001 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5997 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5997 gene: GAM72905 target protein, GAM186582 target protein and GAM250001 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM72905, GAM186582 and GAM250001

GR5998 BM992274 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5998(GR5998) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5998 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5998 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5998 gene encodes GR5998 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5998 precursor RNA folds spatially, forming GR5998 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5998 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5998 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5998 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM774 precursor RNA, GAM52626 precursor RNA and GAM67261 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM774 RNA, GAM52626 RNA and GAM67261 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM774 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM774 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM774 target RNA into GAM774 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM52626 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM52626 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM52626 target RNA into GAM52626 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM67261 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM67261 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM67261 target RNA into GAM67261 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR5998 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5998 gene: GAM774 target protein, GAM52626 target protein and GAM67261 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM774, GAM52626 and GAM67261

GR5999 BI603738 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 5999 (GR5999) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR5999 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR5999 gene was detected is described hereinabove with reference to Figs. 8-18.

GR5999 gene encodes GR5999 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR5999 precursor RNA folds spatially, forming GR5999 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR5999 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR5999 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR5999 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1808 precursor RNA, GAM7590 precursor RNA and GAM145229 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1808 RNA, GAM7590 RNA and GAM145229 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1808 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1808 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1808 target RNA into GAM1808 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7590 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7590 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7590 target RNA into GAM7590 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM145229 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM145229 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM145229 target RNA into GAM145229 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly

utilities, of GR5999 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR5999 gene: GAM1808 target protein, GAM7590 target protein and GAM145229 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1808, GAM7590 and GAM145229

GR6000 BQ023361 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6000(GR6000) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6000 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6000 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6000 gene encodes GR6000 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6000 precursor RNA folds spatially, forming GR6000 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6000 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6000 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6000 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM184804 precursor RNA and GAM256696 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM184804 RNA and GAM256696 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM184804 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM184804 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM184804 target RNA into GAM184804 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM256696 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM256696 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM256696 target RNA into GAM256696 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6000 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6000 gene: GAM184804 target protein and GAM256696 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM184804 and GAM256696

GR6001 AL041789 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6001 (GR6001) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6001 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6001 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6001 gene encodes GR6001 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6001 precursor RNA folds spatially, forming GR6001 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6001 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6001 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6001 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM157855 precursor RNA, GAM237364 precursor RNA and GAM283394 precursor RNA, herein schematically represented by GAM1 FOLDED

PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM157855 RNA, GAM237364 RNA and GAM283394 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM157855 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM157855 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM157855 target RNA into GAM157855 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM237364 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM237364 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM237364 target RNA into GAM237364 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM283394 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM283394 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM283394 target RNA into GAM283394 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6001 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6001 gene: GAM157855 target protein, GAM237364 target protein and GAM283394 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM157855, GAM237364 and GAM283394

GR6002 AA658495 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6002(GR6002) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR6002 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6002 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6002 gene encodes GR6002 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6002 precursor RNA folds spatially, forming GR6002 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6002 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6002 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6002 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4381 precursor RNA and GAM96593 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4381 RNA and GAM96593 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4381 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4381 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4381 target RNA into GAM4381 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM96593 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM96593 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM96593 target RNA into GAM96593 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly

utilities, of GR6002 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6002 gene: GAM4381 target protein and GAM96593 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4381 and GAM96593

GR6003 AW750619 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6003(GR6003) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6003 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6003 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6003 gene encodes GR6003 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6003 precursor RNA folds spatially, forming GR6003 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6003 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6003 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6003 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM5669 precursor RNA, GAM156706 precursor RNA and GAM197358 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5669 RNA, GAM156706 RNA and GAM197358 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5669 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5669 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds

to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5669 target RNA into GAM5669 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM156706 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM156706 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM156706 target RNA into GAM156706 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM197358 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM197358 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM197358 target RNA into GAM197358 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6003 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6003 gene: GAM5669 target protein, GAM156706 target protein and GAM197358 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5669, GAM156706 and GAM197358

GR6004 AA449949 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6004(GR6004) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6004 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6004 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6004 gene encodes GR6004 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6004 precursor RNA folds spatially, forming GR6004 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6004 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR6004 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6004 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7484 precursor RNA and GAM54560 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7484 RNA and GAM54560 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7484 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7484 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7484 target RNA into GAM7484 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM54560 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM54560 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM54560 target RNA into GAM54560 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6004 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6004 gene: GAM7484 target protein and GAM54560 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7484 and GAM54560

GR6005 BI224160 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6005(GR6005) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6005 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6005 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6005 gene encodes GR6005 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6005 precursor RNA folds spatially, forming GR6005 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6005 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6005 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6005 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM273385 precursor RNA and GAM308622 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM273385 RNA and GAM308622 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM273385 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM273385 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM273385 target RNA into GAM273385 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM308622 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM308622 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM308622 target RNA into GAM308622 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6005 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6005 gene: GAM273385 target protein and GAM308622 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM273385 and GAM308622

GR6006 BI057225 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6006(GR6006) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6006 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6006 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6006 gene encodes GR6006 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6006 precursor RNA folds spatially, forming GR6006 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6006 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6006 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6006 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM88003 precursor RNA and GAM322211 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM88003 RNA and GAM322211 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM88003 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM88003 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM88003

target RNA into GAM88003 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM322211 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM322211 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM322211 target RNA into GAM322211 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6006 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6006 gene: GAM88003 target protein and GAM322211 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM88003 and GAM322211

GR6007 AA903402 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6007(GR6007) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6007 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6007 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6007 gene encodes GR6007 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6007 precursor RNA folds spatially, forming GR6007 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6007 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6007 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6007 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM194802 precursor RNA and GAM335570 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM194802 RNA and GAM335570 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM194802 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM194802 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM194802 target RNA into GAM194802 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM335570 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM335570 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM335570 target RNA into GAM335570 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6007 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6007 gene: GAM194802 target protein and GAM335570 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM194802 and GAM335570

GR6008 AV707975 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6008(GR6008) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6008 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6008 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6008 gene encodes GR6008 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6008 precursor RNA folds spatially, forming GR6008 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated

that GR6008 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6008 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6008 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM291099 precursor RNA and GAM332156 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM291099 RNA and GAM332156 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM291099 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM291099 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM291099 target RNA into GAM291099 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM332156 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM332156 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM332156 target RNA into GAM332156 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6008 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6008 gene: GAM291099 target protein and GAM332156 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM291099 and GAM332156

GR6009 N64660 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6009(GR6009) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR6009 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6009 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6009 gene encodes GR6009 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6009 precursor RNA folds spatially, forming GR6009 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6009 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6009 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6009 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1598 precursor RNA and GAM336077 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1598 RNA and GAM336077 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1598 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1598 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1598 target RNA into GAM1598 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336077 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336077 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336077 target RNA into GAM336077 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6009 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6009 gene: GAM1598 target protein and GAM336077 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1598 and GAM336077

GR6010 AI554595 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6010 (GR6010) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6010 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6010 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6010 gene encodes GR6010 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6010 precursor RNA folds spatially, forming GR6010 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6010 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6010 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6010 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM108021 precursor RNA, GAM178228 precursor RNA and GAM302180 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM108021 RNA, GAM178228 RNA and GAM302180 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM108021 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM108021 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM108021 target RNA into GAM108021 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM178228 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM178228 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM178228 target RNA into GAM178228 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM302180 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM302180 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM302180 target RNA into GAM302180 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6010 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6010 gene: GAM108021 target protein, GAM178228 target protein and GAM302180 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM108021, GAM178228 and GAM302180

GR6011 AI791644 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6011(GR6011) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6011 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6011 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6011 gene encodes GR6011 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6011 precursor RNA folds spatially, forming GR6011 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6011 folded precursor RNA comprises a plurality of what is known in the

art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6011 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6011 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM407 precursor RNA and GAM316952 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM407 RNA and GAM316952 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM407 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM407 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM407 target RNA into GAM407 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM316952 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM316952 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM316952 target RNA into GAM316952 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6011 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6011 gene: GAM407 target protein and GAM316952 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM407 and GAM316952

GR6012 BI916060 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6012(GR6012) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR6012 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6012 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6012 gene encodes GR6012 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6012 precursor RNA folds spatially, forming GR6012 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6012 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6012 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6012 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM128404 precursor RNA and GAM231166 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM128404 RNA and GAM231166 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM128404 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM128404 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM128404 target RNA into GAM128404 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM231166 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM231166 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM231166 target RNA into GAM231166 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly

utilities, of GR6012 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6012 gene: GAM128404 target protein and GAM231166 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM128404 and GAM231166

GR6013 BM903662 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6013 (GR6013) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6013 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6013 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6013 gene encodes GR6013 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6013 precursor RNA folds spatially, forming GR6013 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6013 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6013 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6013 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1936 precursor RNA, GAM6536 precursor RNA and GAM282341 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1936 RNA, GAM6536 RNA and GAM282341 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1936 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1936 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds

to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1936 target RNA into GAM1936 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6536 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6536 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6536 target RNA into GAM6536 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM282341 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM282341 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM282341 target RNA into GAM282341 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6013 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6013 gene: GAM1936 target protein, GAM6536 target protein and GAM282341 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1936, GAM6536 and GAM282341

GR6014 BI522820 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6014 (GR6014) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6014 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6014 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6014 gene encodes GR6014 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6014 precursor RNA folds spatially, forming GR6014 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6014 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR6014 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6014 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7909 precursor RNA and GAM239288 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7909 RNA and GAM239288 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7909 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7909 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7909 target RNA into GAM7909 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM239288 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM239288 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM239288 target RNA into GAM239288 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6014 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6014 gene: GAM7909 target protein and GAM239288 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7909 and GAM239288

GR6015 AW945732 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6015(GR6015) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6015 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6015 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6015 gene encodes GR6015 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6015 precursor RNA folds spatially, forming GR6015 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6015 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6015 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6015 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM113228 precursor RNA, GAM201994 precursor RNA and GAM325798 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM113228 RNA, GAM201994 RNA and GAM325798 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM113228 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM113228 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM113228 target RNA into GAM113228 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM201994 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM201994 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM201994 target RNA into GAM201994 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM325798 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM325798 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM325798 target RNA into GAM325798 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6015 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6015 gene: GAM113228 target protein, GAM201994 target protein and GAM325798 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM113228, GAM201994 and GAM325798

GR6016 BE621649 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6016 (GR6016) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6016 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6016 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6016 gene encodes GR6016 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6016 precursor RNA folds spatially, forming GR6016 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6016 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6016 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6016 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM2664 precursor RNA, GAM26742 precursor RNA, GAM263925 precursor RNA and GAM292056 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2664 RNA, GAM26742 RNA, GAM263925 RNA and GAM292056 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2664 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2664 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2664 target RNA into GAM2664 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM26742 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM26742 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM26742 target RNA into GAM26742 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM263925 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM263925 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM263925 target RNA into GAM263925 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM292056 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM292056 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM292056 target RNA into GAM292056 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6016 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6016 gene: GAM2664 target protein, GAM26742 target protein, GAM263925 target protein and GAM292056 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2664, GAM26742, GAM263925 and GAM292056

6017(GR6017) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6017 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6017 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6017 gene encodes GR6017 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6017 precursor RNA folds spatially, forming GR6017 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6017 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6017 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6017 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM9896 precursor RNA, GAM168034 precursor RNA and GAM302508 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM9896 RNA, GAM168034 RNA and GAM302508 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM9896 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM9896 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM9896 target RNA into GAM9896 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM168034 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM168034 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM168034

target RNA into GAM168034 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM302508 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM302508 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM302508 target RNA into GAM302508 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6017 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6017 gene: GAM9896 target protein, GAM168034 target protein and GAM302508 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM9896, GAM168034 and GAM302508

GR6018 BF919251 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6018(GR6018) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6018 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6018 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6018 gene encodes GR6018 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6018 precursor RNA folds spatially, forming GR6018 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6018 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6018 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6018 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4495 precursor RNA, GAM7171 precursor RNA and GAM7835 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded

precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4495 RNA, GAM7171 RNA and GAM7835 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4495 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4495 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4495 target RNA into GAM4495 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7171 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7171 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7171 target RNA into GAM7171 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7835 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7835 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7835 target RNA into GAM7835 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6018 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6018 gene: GAM4495 target protein, GAM7171 target protein and GAM7835 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4495, GAM7171 and GAM7835

GR6019 AI363959 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6019(GR6019) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6019 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6019 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6019 gene encodes GR6019 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6019 precursor RNA folds spatially, forming GR6019 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6019 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6019 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6019 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM81044 precursor RNA, GAM100654 precursor RNA and GAM214334 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM81044 RNA, GAM100654 RNA and GAM214334 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM81044 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM81044 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM81044 target RNA into GAM81044 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM100654 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM100654 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM100654 target RNA into GAM100654 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM214334 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM214334 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM214334 target RNA into GAM214334 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6019 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6019 gene: GAM81044 target protein, GAM100654 target protein and GAM214334 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM81044, GAM100654 and GAM214334.

GR6020 AU098742 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6020(GR6020) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6020 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6020 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6020 gene encodes GR6020 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6020 precursor RNA folds spatially, forming GR6020 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6020 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6020 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6020 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM60631 precursor RNA, GAM64190 precursor RNA and GAM304639 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM60631 RNA, GAM64190 RNA and GAM304639 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM60631 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM60631 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM60631 target RNA into GAM60631 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM64190 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM64190 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM64190 target RNA into GAM64190 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM304639 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM304639 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM304639 target RNA into GAM304639 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6020 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6020 gene: GAM60631 target protein, GAM64190 target protein and GAM304639 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM60631, GAM64190 and GAM304639

GR6021 BF106763 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6021(GR6021) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6021 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6021 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6021 gene encodes GR6021 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6021 precursor RNA folds spatially, forming GR6021 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6021 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6021 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6021 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1845 precursor RNA, GAM100592 precursor RNA and GAM113243 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1845 RNA, GAM100592 RNA and GAM113243 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1845 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1845 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1845 target RNA into GAM1845 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM100592 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM100592 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM100592 target RNA into GAM100592 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM113243 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM113243 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM113243

target RNA into GAM113243 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6021 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6021 gene: GAM1845 target protein, GAM100592 target protein and GAM113243 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1845, GAM100592 and GAM113243

GR6022 AI971397 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6022(GR6022) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6022 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6022 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6022 gene encodes GR6022 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6022 precursor RNA folds spatially, forming GR6022 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6022 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6022 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6022 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7760 precursor RNA and GAM72297 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7760 RNA and GAM72297 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7760 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7760 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7760 target RNA into GAM7760 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM72297 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM72297 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM72297 target RNA into GAM72297 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6022 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6022 gene: GAM7760 target protein and GAM72297 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7760 and GAM72297

GR6023 BM792653 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6023(GR6023) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6023 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6023 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6023 gene encodes GR6023 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6023 precursor RNA folds spatially, forming GR6023 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6023 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6023 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6023 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3332 precursor RNA, GAM18457 precursor RNA and GAM260675 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3332 RNA, GAM18457 RNA and GAM260675 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3332 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3332 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3332 target RNA into GAM3332 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM18457 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM18457 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM18457 target RNA into GAM18457 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM260675 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM260675 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM260675 target RNA into GAM260675 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6023 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6023 gene: GAM3332 target protein, GAM18457 target protein and GAM260675 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3332, GAM18457 and GAM260675

bioinformatically detected regulatory gene, referred to here as Genomic Record 6024 (GR6024) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6024 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6024 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6024 gene encodes GR6024 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6024 precursor RNA folds spatially, forming GR6024 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6024 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6024 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6024 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7204 precursor RNA and GAM89256 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7204 RNA and GAM89256 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7204 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7204 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7204 target RNA into GAM7204 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM89256 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM89256 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM89256

target RNA into GAM89256 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6024 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6024 gene: GAM7204 target protein and GAM89256 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7204 and GAM89256

GR6025 BF985930 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6025(GR6025) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6025 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6025 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6025 gene encodes GR6025 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6025 precursor RNA folds spatially, forming GR6025 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6025 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6025 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6025 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM5473 precursor RNA, GAM174138 precursor RNA and GAM257680 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5473 RNA, GAM174138 RNA and GAM257680 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5473 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5473 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5473 target RNA into GAM5473 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM174138 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM174138 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM174138 target RNA into GAM174138 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM257680 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM257680 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM257680 target RNA into GAM257680 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6025 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6025 gene: GAM5473 target protein, GAM174138 target protein and GAM257680 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5473, GAM174138 and GAM257680

GR6026 BF830883 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6026(GR6026) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6026 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6026 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6026 gene encodes GR6026 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6026 precursor RNA folds spatially, forming GR6026 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6026 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6026 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6026 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1939 precursor RNA and GAM180895 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1939 RNA and GAM180895 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1939 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1939 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1939 target RNA into GAM1939 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM180895 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM180895 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM180895 target RNA into GAM180895 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6026 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6026 gene: GAM1939 target protein and GAM180895 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1939 and GAM180895

6027(GR6027) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6027 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6027 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6027 gene encodes GR6027 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6027 precursor RNA folds spatially, forming GR6027 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6027 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6027 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6027 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM6859 precursor RNA, GAM121666 precursor RNA, GAM275055 precursor RNA and GAM335942 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6859 RNA, GAM121666 RNA, GAM275055 RNA and GAM335942 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6859 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6859 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6859 target RNA into GAM6859 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM121666 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM121666 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM121666

target RNA into GAM121666 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM275055 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM275055 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM275055 target RNA into GAM275055 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM335942 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM335942 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM335942 target RNA into GAM335942 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6027 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6027 gene: GAM6859 target protein, GAM121666 target protein, GAM275055 target protein and GAM335942 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6859, GAM121666, GAM275055 and GAM335942

GR6028 AW510460 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6028(GR6028) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6028 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6028 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6028 gene encodes GR6028 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6028 precursor RNA folds spatially, forming GR6028 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6028 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6028 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6028 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM83573 precursor RNA and GAM235729 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM83573 RNA and GAM235729 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM83573 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM83573 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM83573 target RNA into GAM83573 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM235729 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM235729 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM235729 target RNA into GAM235729 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6028 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6028 gene: GAM83573 target protein and GAM235729 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM83573 and GAM235729

GR6029 BE539630 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6029 (GR6029) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6029 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR6029 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6029 gene encodes GR6029 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6029 precursor RNA folds spatially, forming GR6029 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6029 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6029 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6029 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM6922 precursor RNA, GAM133904 precursor RNA and GAM265071 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6922 RNA, GAM133904 RNA and GAM265071 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6922 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6922 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6922 target RNA into GAM6922 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM133904 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM133904 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM133904 target RNA into GAM133904 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM265071 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM265071 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM265071 target RNA into GAM265071 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6029 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6029 gene: GAM6922 target protein, GAM133904 target protein and GAM265071 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6922, GAM133904 and GAM265071

GR6030 AI890763 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6030(GR6030) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6030 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6030 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6030 gene encodes GR6030 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6030 precursor RNA folds spatially, forming GR6030 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6030 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6030 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6030 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2684 precursor RNA, GAM3675 precursor RNA and GAM92776 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2684 RNA, GAM3675 RNA and GAM92776 RNA, herein

schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2684 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2684 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2684 target RNA into GAM2684 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM3675 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3675 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3675 target RNA into GAM3675 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM92776 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM92776 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM92776 target RNA into GAM92776 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6030 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6030 gene: GAM2684 target protein, GAM3675 target protein and GAM92776 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2684, GAM3675 and GAM92776

GR6031 BG913775 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6031(GR6031) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6031 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6031 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6031 gene encodes GR6031 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6031 precursor RNA folds spatially, forming GR6031 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6031 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6031 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6031 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM59 precursor RNA, GAM6470 precursor RNA and GAM293079 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM59 RNA, GAM6470 RNA and GAM293079 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM59 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM59 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM59 target RNA into GAM59 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6470 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6470 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6470 target RNA into GAM6470 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM293079 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM293079 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM293079 target RNA into GAM293079 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6031 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6031 gene: GAM59 target protein, GAM6470 target protein and GAM293079 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM59, GAM6470 and GAM293079

GR6032 BG723483 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6032(GR6032) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6032 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6032 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6032 gene encodes GR6032 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6032 precursor RNA folds spatially, forming GR6032 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6032 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6032 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6032 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2320 precursor RNA, GAM237622 precursor RNA and GAM306787 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2320 RNA, GAM237622 RNA and GAM306787 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2320 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2320 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2320 target RNA into GAM2320 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM237622 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM237622 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM237622 target RNA into GAM237622 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM306787 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM306787 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM306787 target RNA into GAM306787 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6032 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6032 gene: GAM2320 target protein, GAM237622 target protein and GAM306787 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2320, GAM237622 and GAM306787

GR6033 BM006853 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6033(GR6033) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6033 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6033 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6033 gene encodes GR6033 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6033 precursor RNA folds spatially, forming GR6033 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6033 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6033 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6033 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2876 precursor RNA and GAM233737 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2876 RNA and GAM233737 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2876 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2876 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2876 target RNA into GAM2876 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM233737 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM233737 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM233737 target RNA into GAM233737 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6033 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6033 gene: GAM2876 target protein and GAM233737 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2876 and GAM233737

GR6034 AV762751 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6034(GR6034) gene, which encodes an `operon-like` cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6034 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6034 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6034 gene encodes GR6034 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6034 precursor RNA folds spatially, forming GR6034 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6034 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6034 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6034 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2073 precursor RNA and GAM11679 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2073 RNA and GAM11679 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2073 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2073 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2073 target RNA into GAM2073 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM11679 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM11679 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM11679 target RNA into GAM11679 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6034 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6034 gene: GAM2073 target protein and GAM11679 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2073 and GAM11679

GR6035 AA436229 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6035(GR6035) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6035 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6035 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6035 gene encodes GR6035 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6035 precursor RNA folds spatially, forming GR6035 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6035 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6035 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6035 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6755 precursor RNA and GAM280646 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6755 RNA and GAM280646 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6755 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6755 target RNA, herein schematically represented by

GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6755 target RNA into GAM6755 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM280646 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM280646 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM280646 target RNA into GAM280646 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6035 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6035 gene: GAM6755 target protein and GAM280646 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6755 and GAM280646

GR6036 AI026868 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6036(GR6036) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6036 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6036 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6036 gene encodes GR6036 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6036 precursor RNA folds spatially, forming GR6036 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6036 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6036 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6036 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM188369 precursor RNA, GAM236673 precursor RNA

and GAM237508 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM188369 RNA, GAM236673 RNA and GAM237508 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM188369 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM188369 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM188369 target RNA into GAM188369 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM236673 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM236673 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM236673 target RNA into GAM236673 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM237508 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM237508 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM237508 target RNA into GAM237508 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6036 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6036 gene: GAM188369 target protein, GAM236673 target protein and GAM237508 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM188369, GAM236673 and GAM237508

GR6037 BI041644 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6037(GR6037) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR6037 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6037 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6037 gene encodes GR6037 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6037 precursor RNA folds spatially, forming GR6037 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6037 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6037 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6037 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8593 precursor RNA and GAM57598 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8593 RNA and GAM57598 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8593 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8593 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8593 target RNA into GAM8593 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM57598 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM57598 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM57598 target RNA into GAM57598 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6037 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6037 gene: GAM8593 target protein and GAM57598 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8593 and GAM57598

GR6038 AU141071 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6038(GR6038) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6038 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6038 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6038 gene encodes GR6038 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6038 precursor RNA folds spatially, forming GR6038 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6038 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6038 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6038 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1060 precursor RNA and GAM38086 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1060 RNA and GAM38086 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1060 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1060 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds

to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1060 target RNA into GAM1060 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM38086 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM38086 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM38086 target RNA into GAM38086 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6038 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6038 gene: GAM1060 target protein and GAM38086 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1060 and GAM38086

GR6039 BF306674 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6039(GR6039) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6039 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6039 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6039 gene encodes GR6039 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6039 precursor RNA folds spatially, forming GR6039 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6039 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6039 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6039 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM8476 precursor RNA, GAM65830 precursor RNA and GAM145978 precursor RNA, herein schematically represented by GAM1 FOLDED

PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8476 RNA, GAM65830 RNA and GAM145978 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8476 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8476 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8476 target RNA into GAM8476 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM65830 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM65830 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM65830 target RNA into GAM65830 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM145978 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM145978 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM145978 target RNA into GAM145978 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6039 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6039 gene: GAM8476 target protein, GAM65830 target protein and GAM145978 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8476, GAM65830 and GAM145978

GR6040 BM273256 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6040(GR6040) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR6040 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6040 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6040 gene encodes GR6040 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6040 precursor RNA folds spatially, forming GR6040 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6040 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6040 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6040 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM178964 precursor RNA and GAM283942 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM178964 RNA and GAM283942 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM178964 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM178964 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM178964 target RNA into GAM178964 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM283942 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM283942 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM283942 target RNA into GAM283942 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly

utilities, of GR6040 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6040 gene: GAM178964 target protein and GAM283942 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM178964 and GAM283942

GR6041 T49772 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6041 (GR6041) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6041 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6041 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6041 gene encodes GR6041 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6041 precursor RNA folds spatially, forming GR6041 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6041 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6041 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6041 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM30262 precursor RNA, GAM40652 precursor RNA and GAM137982 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM30262 RNA, GAM40652 RNA and GAM137982 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM30262 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM30262 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM30262 target RNA into GAM30262 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM40652 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM40652 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM40652 target RNA into GAM40652 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM137982 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM137982 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM137982 target RNA into GAM137982 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6041 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6041 gene: GAM30262 target protein, GAM40652 target protein and GAM137982 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM30262, GAM40652 and GAM137982

GR6042 BG768371 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6042(GR6042) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6042 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6042 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6042 gene encodes GR6042 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6042 precursor RNA folds spatially, forming GR6042 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6042 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR6042 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6042 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3659 precursor RNA, GAM101348 precursor RNA and GAM286046 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3659 RNA, GAM101348 RNA and GAM286046 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3659 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3659 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3659 target RNA into GAM3659 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM101348 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM101348 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM101348 target RNA into GAM101348 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM286046 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM286046 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM286046 target RNA into GAM286046 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6042 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6042 gene: GAM3659 target protein, GAM101348 target protein and GAM286046 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN.

The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3659, GAM101348 and GAM286046

GR6043 BF980073 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6043(GR6043) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6043 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6043 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6043 gene encodes GR6043 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6043 precursor RNA folds spatially, forming GR6043 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6043 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6043 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6043 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM31681 precursor RNA, GAM122713 precursor RNA and GAM206854 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM31681 RNA, GAM122713 RNA and GAM206854 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM31681 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM31681 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM31681 target RNA into GAM31681 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM122713 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM122713 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM122713 target RNA into GAM122713 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM206854 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM206854 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM206854 target RNA into GAM206854 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6043 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6043 gene: GAM31681 target protein, GAM122713 target protein and GAM206854 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM31681, GAM122713 and GAM206854

GR6044 BI548979 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6044(GR6044) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6044 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6044 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6044 gene encodes GR6044 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6044 precursor RNA folds spatially, forming GR6044 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6044 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6044 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6044 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM45770 precursor RNA and GAM90122 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM45770 RNA and GAM90122 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM45770 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM45770 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM45770 target RNA into GAM45770 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM90122 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM90122 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM90122 target RNA into GAM90122 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6044 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6044 gene: GAM45770 target protein and GAM90122 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM45770 and GAM90122

GR6045 AW834894 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6045(GR6045) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6045 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6045 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6045 gene encodes GR6045 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6045 precursor RNA folds spatially, forming GR6045 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6045 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6045 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6045 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM204154 precursor RNA and GAM296321 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM204154 RNA and GAM296321 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM204154 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM204154 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM204154 target RNA into GAM204154 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM296321 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM296321 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM296321 target RNA into GAM296321 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6045 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6045 gene: GAM204154 target protein and GAM296321 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes

is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM204154 and GAM296321

GR6046 AI332446 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6046 (GR6046) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6046 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6046 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6046 gene encodes GR6046 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6046 precursor RNA folds spatially, forming GR6046 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6046 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6046 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6046 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6080 precursor RNA and GAM8184 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6080 RNA and GAM8184 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6080 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6080 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6080 target RNA into GAM6080 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8184 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM8184 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8184 target RNA into GAM8184 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6046 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6046 gene: GAM6080 target protein and GAM8184 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6080 and GAM8184

GR6047 BM924317 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6047(GR6047) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6047 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6047 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6047 gene encodes GR6047 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6047 precursor RNA folds spatially, forming GR6047 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6047 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6047 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6047 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM26294 precursor RNA and GAM203503 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM26294 RNA and GAM203503 RNA, herein schematically

represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM26294 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM26294 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM26294 target RNA into GAM26294 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM203503 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM203503 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM203503 target RNA into GAM203503 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6047 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6047 gene: GAM26294 target protein and GAM203503 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM26294 and GAM203503

GR6048 AW377307 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6048(GR6048) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6048 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6048 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6048 gene encodes GR6048 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6048 precursor RNA folds spatially, forming GR6048 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6048 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6048 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6048 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM287821 precursor RNA and GAM326280 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM287821 RNA and GAM326280 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM287821 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM287821 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM287821 target RNA into GAM287821 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM326280 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM326280 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM326280 target RNA into GAM326280 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6048 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6048 gene: GAM287821 target protein and GAM326280 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM287821 and GAM326280

GR6049 BE972809 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6049(GR6049) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6049 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR6049 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6049 gene encodes GR6049 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6049 precursor RNA folds spatially, forming GR6049 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6049 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6049 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6049 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM74909 precursor RNA and GAM199395 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM74909 RNA and GAM199395 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM74909 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM74909 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM74909 target RNA into GAM74909 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM199395 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM199395 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM199395 target RNA into GAM199395 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6049 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6049 gene: GAM74909 target

protein and GAM199395 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM74909 and GAM199395

GR6050 W69715 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6050(GR6050) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6050 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6050 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6050 gene encodes GR6050 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6050 precursor RNA folds spatially, forming GR6050 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6050 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6050 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6050 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5028 precursor RNA and GAM74472 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5028 RNA and GAM74472 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5028 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5028 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5028 target RNA into GAM5028 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM74472 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM74472 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM74472 target RNA into GAM74472 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6050 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6050 gene: GAM5028 target protein and GAM74472 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5028 and GAM74472

GR6051 AI671538 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6051 (GR6051) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6051 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6051 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6051 gene encodes GR6051 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6051 precursor RNA folds spatially, forming GR6051 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6051 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6051 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6051 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM20869 precursor RNA and GAM140689 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM20869 RNA and GAM140689 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM20869 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM20869 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM20869 target RNA into GAM20869 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM140689 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM140689 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM140689 target RNA into GAM140689 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6051 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6051 gene: GAM20869 target protein and GAM140689 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM20869 and GAM140689

GR6052 BF203250 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6052(GR6052) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6052 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6052 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6052 gene encodes GR6052 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6052 precursor RNA folds spatially, forming GR6052 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6052 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR6052 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6052 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM389 precursor RNA and GAM108753 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM389 RNA and GAM108753 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM389 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM389 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM389 target RNA into GAM389 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM108753 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM108753 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM108753 target RNA into GAM108753 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6052 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6052 gene: GAM389 target protein and GAM108753 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM389 and GAM108753

GR6053 BE676499 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6053(GR6053) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6053 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6053 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6053 gene encodes GR6053 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6053 precursor RNA folds spatially, forming GR6053 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6053 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6053 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6053 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM3527 precursor RNA, GAM3662 precursor RNA, GAM38138 precursor RNA and GAM208504 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3527 RNA, GAM3662 RNA, GAM38138 RNA and GAM208504 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3527 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3527 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3527 target RNA into GAM3527 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM3662 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3662 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3662 target RNA into GAM3662 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM38138 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM38138 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM38138 target RNA into GAM38138 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM208504 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM208504 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM208504 target RNA into GAM208504 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6053 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6053 gene: GAM3527 target protein, GAM3662 target protein, GAM38138 target protein and GAM208504 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3527, GAM3662, GAM38138 and GAM208504

GR6054 BM762538 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6054(GR6054) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6054 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6054 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6054 gene encodes GR6054 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6054 precursor RNA folds spatially, forming GR6054 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6054 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6054 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6054 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4043 precursor RNA and GAM194124 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4043 RNA and GAM194124 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4043 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4043 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4043 target RNA into GAM4043 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM194124 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM194124 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM194124 target RNA into GAM194124 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6054 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6054 gene: GAM4043 target protein and GAM194124 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4043 and GAM194124

GR6055 BF804929 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6055(GR6055) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6055 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6055 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6055 gene encodes GR6055 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6055 precursor RNA folds spatially, forming GR6055 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6055 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6055 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6055 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4193 precursor RNA and GAM265260 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4193 RNA and GAM265260 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4193 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4193 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4193 target RNA into GAM4193 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM265260 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM265260 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM265260 target RNA into GAM265260 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6055 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6055 gene: GAM4193 target protein and GAM265260 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4193 and GAM265260

GR6056 BF997927 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6056 (GR6056) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6056 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6056 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6056 gene encodes GR6056 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6056 precursor RNA folds spatially, forming GR6056 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6056 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6056 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6056 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM114071 precursor RNA and GAM305796 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM114071 RNA and GAM305796 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM114071 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM114071 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM114071 target RNA into GAM114071 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM305796 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM305796 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM305796 target RNA into GAM305796 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6056 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6056 gene: GAM114071 target protein and GAM305796 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM114071 and GAM305796

GR6057 AI864204 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6057(GR6057) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6057 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6057 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6057 gene encodes GR6057 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6057 precursor RNA folds spatially, forming GR6057 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6057 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6057 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6057 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6999 precursor RNA and GAM31821 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6999 RNA and GAM31821 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6999 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6999 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6999 target RNA into GAM6999 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM31821 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM31821 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM31821 target RNA into GAM31821 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6057 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6057 gene: GAM6999 target protein and GAM31821 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6999 and GAM31821

GR6058 BI117636 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6058(GR6058) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6058 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6058 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6058 gene encodes GR6058 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6058 precursor RNA folds spatially, forming GR6058 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6058 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6058 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6058 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM49371 precursor RNA and GAM180436 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM49371 RNA and GAM180436 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM49371 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM49371 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM49371 target RNA into GAM49371 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM180436 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM180436 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM180436 target RNA into GAM180436 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6058 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6058 gene: GAM49371 target protein and GAM180436 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM49371 and GAM180436

GR6059 AL703830 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6059(GR6059) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6059 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6059 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6059 gene encodes GR6059 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6059 precursor RNA folds spatially, forming GR6059 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6059 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6059 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6059 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM6380 precursor RNA, GAM254415 precursor RNA and GAM300472 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6380 RNA, GAM254415 RNA and GAM300472 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6380 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6380 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6380 target RNA into GAM6380 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM254415 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM254415 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM254415 target RNA into GAM254415 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM300472 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM300472 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM300472

target RNA into GAM300472 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6059 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6059 gene: GAM6380 target protein, GAM254415 target protein and GAM300472 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6380, GAM254415 and GAM300472

GR6060 AA243818 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6060(GR6060) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6060 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6060 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6060 gene encodes GR6060 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6060 precursor RNA folds spatially, forming GR6060 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6060 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6060 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6060 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM8029 precursor RNA, GAM40315 precursor RNA and GAM210118 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8029 RNA, GAM40315 RNA and GAM210118 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8029 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8029 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8029 target RNA into GAM8029 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM40315 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM40315 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM40315 target RNA into GAM40315 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM210118 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM210118 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM210118 target RNA into GAM210118 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6060 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6060 gene: GAM8029 target protein, GAM40315 target protein and GAM210118 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8029, GAM40315 and GAM210118

GR6061 BG535615 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6061 (GR6061) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6061 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6061 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6061 gene encodes GR6061 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6061 precursor RNA folds spatially, forming GR6061 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6061 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6061 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6061 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM26532 precursor RNA and GAM112481 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM26532 RNA and GAM112481 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM26532 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM26532 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM26532 target RNA into GAM26532 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM112481 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM112481 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM112481 target RNA into GAM112481 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6061 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6061 gene: GAM26532 target protein and GAM112481 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM26532 and GAM112481

bioinformatically detected regulatory gene, referred to here as Genomic Record 6062(GR6062) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6062 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6062 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6062 gene encodes GR6062 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6062 precursor RNA folds spatially, forming GR6062 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6062 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6062 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6062 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM118415 precursor RNA and GAM133105 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM118415 RNA and GAM133105 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM118415 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM118415 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM118415 target RNA into GAM118415 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM133105 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM133105 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM133105

target RNA into GAM133105 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6062 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6062 gene: GAM118415 target protein and GAM133105 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM118415 and GAM133105

GR6063 AA526817 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6063(GR6063) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6063 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6063 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6063 gene encodes GR6063 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6063 precursor RNA folds spatially, forming GR6063 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6063 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6063 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6063 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5671 precursor RNA and GAM243911 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5671 RNA and GAM243911 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5671 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5671 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5671 target RNA into GAM5671 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM243911 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM243911 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM243911 target RNA into GAM243911 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6063 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6063 gene: GAM5671 target protein and GAM243911 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5671 and GAM243911

GR6064 BG397009 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6064(GR6064) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6064 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6064 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6064 gene encodes GR6064 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6064 precursor RNA folds spatially, forming GR6064 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6064 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6064 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6064 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM7174 precursor RNA, GAM64497 precursor RNA and GAM113076 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7174 RNA, GAM64497 RNA and GAM113076 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7174 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7174 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7174 target RNA into GAM7174 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM64497 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM64497 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM64497 target RNA into GAM64497 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM113076 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM113076 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM113076 target RNA into GAM113076 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6064 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6064 gene: GAM7174 target protein, GAM64497 target protein and GAM113076 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7174, GAM64497 and GAM113076

6065(GR6065) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6065 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6065 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6065 gene encodes GR6065 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6065 precursor RNA folds spatially, forming GR6065 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6065 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6065 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6065 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM89135 precursor RNA and GAM234805 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM89135 RNA and GAM234805 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM89135 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM89135 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM89135 target RNA into GAM89135 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM234805 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM234805 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM234805 target RNA into GAM234805 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6065 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6065 gene: GAM89135 target protein and GAM234805 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM89135 and GAM234805

GR6066 AA259198 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6066(GR6066) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6066 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6066 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6066 gene encodes GR6066 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6066 precursor RNA folds spatially, forming GR6066 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6066 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6066 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6066 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM167201 precursor RNA and GAM237359 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM167201 RNA and GAM237359 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM167201 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM167201 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM167201 target RNA into GAM167201 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM237359 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM237359 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM237359 target RNA into GAM237359 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6066 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6066 gene: GAM167201 target protein and GAM237359 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM167201 and GAM237359

GR6067 BG200771 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6067(GR6067) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6067 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6067 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6067 gene encodes GR6067 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6067 precursor RNA folds spatially, forming GR6067 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6067 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6067 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6067 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3

separate GAM precursor RNAs, GAM2288 precursor RNA, GAM6959 precursor RNA and GAM37909 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2288 RNA, GAM6959 RNA and GAM37909 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2288 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2288 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2288 target RNA into GAM2288 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6959 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6959 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6959 target RNA into GAM6959 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM37909 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM37909 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM37909 target RNA into GAM37909 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6067 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6067 gene: GAM2288 target protein, GAM6959 target protein and GAM37909 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2288, GAM6959 and GAM37909

GR6068 AW367253 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6068(GR6068) gene, which encodes an `operon-like` cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6068 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6068 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6068 gene encodes GR6068 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6068 precursor RNA folds spatially, forming GR6068 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6068 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6068 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6068 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5092 precursor RNA and GAM135626 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5092 RNA and GAM135626 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5092 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5092 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5092 target RNA into GAM5092 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM135626 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM135626 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM135626 target RNA into GAM135626 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6068 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6068 gene: GAM5092 target protein and GAM135626 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5092 and GAM135626

GR6069 AA722034 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6069(GR6069) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6069 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6069 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6069 gene encodes GR6069 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6069 precursor RNA folds spatially, forming GR6069 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6069 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6069 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6069 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM138921 precursor RNA, GAM296142 precursor RNA and GAM306329 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM138921 RNA, GAM296142 RNA and GAM306329 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM138921 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM138921 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM138921 target RNA into GAM138921 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM296142 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM296142 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM296142 target RNA into GAM296142 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM306329 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM306329 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM306329 target RNA into GAM306329 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6069 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6069 gene: GAM138921 target protein, GAM296142 target protein and GAM306329 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM138921, GAM296142 and GAM306329

GR6070 BF347832 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6070(GR6070) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6070 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6070 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6070 gene encodes GR6070 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6070 precursor RNA folds spatially, forming GR6070 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated

that GR6070 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6070 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6070 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM7175 precursor RNA, GAM8623 precursor RNA and GAM277232 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7175 RNA, GAM8623 RNA and GAM277232 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7175 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7175 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7175 target RNA into GAM7175 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8623 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8623 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8623 target RNA into GAM8623 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM277232 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM277232 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM277232 target RNA into GAM277232 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6070 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6070 gene: GAM7175 target

protein, GAM8623 target protein and GAM277232 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7175, GAM8623 and GAM277232

GR6071 BF375575 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6071 (GR6071) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6071 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6071 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6071 gene encodes GR6071 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6071 precursor RNA folds spatially, forming GR6071 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6071 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6071 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6071 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5854 precursor RNA and GAM197819 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5854 RNA and GAM197819 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5854 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5854 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5854 target RNA into GAM5854 target protein, herein schematically represented by GAM1 TARGET

PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM197819 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM197819 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM197819 target RNA into GAM197819 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6071 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6071 gene: GAM5854 target protein and GAM197819 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5854 and GAM197819

GR6072 BE394159 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6072(GR6072) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6072 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6072 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6072 gene encodes GR6072 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6072 precursor RNA folds spatially, forming GR6072 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6072 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6072 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6072 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM218192 precursor RNA and GAM270474 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM218192 RNA and GAM270474 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM218192 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM218192 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM218192 target RNA into GAM218192 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM270474 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM270474 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM270474 target RNA into GAM270474 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6072 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6072 gene: GAM218192 target protein and GAM270474 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM218192 and GAM270474

GR6073 AW051887 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6073(GR6073) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6073 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6073 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6073 gene encodes GR6073 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6073 precursor RNA folds spatially, forming GR6073 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6073 folded precursor RNA comprises a plurality of what is known in the

art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6073 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6073 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM35871 precursor RNA and GAM104358 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM35871 RNA and GAM104358 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM35871 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM35871 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM35871 target RNA into GAM35871 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM104358 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM104358 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM104358 target RNA into GAM104358 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6073 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6073 gene: GAM35871 target protein and GAM104358 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM35871 and GAM104358

GR6074 BG184978 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6074(GR6074) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR6074 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6074 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6074 gene encodes GR6074 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6074 precursor RNA folds spatially, forming GR6074 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6074 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6074 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6074 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM2249 precursor RNA, GAM238358 precursor RNA, GAM240648 precursor RNA and GAM277659 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2249 RNA, GAM238358 RNA, GAM240648 RNA and GAM277659 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2249 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2249 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2249 target RNA into GAM2249 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM238358 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM238358 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM238358 target RNA into GAM238358 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM240648 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM240648 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM240648 target RNA into GAM240648 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM277659 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM277659 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM277659 target RNA into GAM277659 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6074 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6074 gene: GAM2249 target protein, GAM238358 target protein, GAM240648 target protein and GAM277659 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2249, GAM238358, GAM240648 and GAM277659

GR6075 BG717485 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6075(GR6075) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6075 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6075 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6075 gene encodes GR6075 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6075 precursor RNA folds spatially, forming GR6075 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6075 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6075 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6075 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4225 precursor RNA, GAM100351 precursor RNA and GAM158969 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4225 RNA, GAM100351 RNA and GAM158969 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4225 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4225 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4225 target RNA into GAM4225 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM100351 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM100351 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM100351 target RNA into GAM100351 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM158969 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM158969 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM158969 target RNA into GAM158969 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6075 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6075 gene: GAM4225 target protein, GAM100351 target protein and GAM158969 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4225, GAM100351 and GAM158969

bioinformatically detected regulatory gene, referred to here as Genomic Record 6076(GR6076) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6076 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6076 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6076 gene encodes GR6076 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6076 precursor RNA folds spatially, forming GR6076 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6076 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6076 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6076 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5145 precursor RNA and GAM203526 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5145 RNA and GAM203526 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5145 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5145 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5145 target RNA into GAM5145 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM203526 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM203526 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM203526

target RNA into GAM203526 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6076 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6076 gene: GAM5145 target protein and GAM203526 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5145 and GAM203526

GR6077 BF670284 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6077(GR6077) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6077 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6077 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6077 gene encodes GR6077 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6077 precursor RNA folds spatially, forming GR6077 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6077 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6077 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6077 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1788 precursor RNA and GAM5997 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1788 RNA and GAM5997 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1788 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1788 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1788 target RNA into GAM1788 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5997 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5997 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5997 target RNA into GAM5997 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6077 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6077 gene: GAM1788 target protein and GAM5997 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1788 and GAM5997

GR6078 BG206566 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6078(GR6078) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6078 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6078 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6078 gene encodes GR6078 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6078 precursor RNA folds spatially, forming GR6078 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6078 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6078 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6078 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3131 precursor RNA, GAM239855 precursor RNA and GAM278737 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3131 RNA, GAM239855 RNA and GAM278737 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3131 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3131 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3131 target RNA into GAM3131 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM239855 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM239855 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM239855 target RNA into GAM239855 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM278737 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM278737 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM278737 target RNA into GAM278737 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6078 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6078 gene: GAM3131 target protein, GAM239855 target protein and GAM278737 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3131, GAM239855 and GAM278737

6079(GR6079) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6079 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6079 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6079 gene encodes GR6079 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6079 precursor RNA folds spatially, forming GR6079 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6079 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6079 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6079 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM99396 precursor RNA and GAM237769 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM99396 RNA and GAM237769 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM99396 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM99396 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM99396 target RNA into GAM99396 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM237769 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM237769 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM237769 target RNA into GAM237769 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6079 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6079 gene: GAM99396 target protein and GAM237769 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM99396 and GAM237769

GR6080 BE387596 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6080(GR6080) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6080 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6080 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6080 gene encodes GR6080 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6080 precursor RNA folds spatially, forming GR6080 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6080 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6080 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6080 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM8060 precursor RNA, GAM62703 precursor RNA, GAM113285 precursor RNA and GAM229890 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8060 RNA, GAM62703 RNA, GAM113285 RNA and GAM229890 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8060 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8060 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8060 target RNA into GAM8060 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM62703 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM62703 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM62703 target RNA into GAM62703 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM113285 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM113285 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM113285 target RNA into GAM113285 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM229890 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM229890 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM229890 target RNA into GAM229890 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6080 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6080 gene: GAM8060 target protein, GAM62703 target protein, GAM113285 target protein and GAM229890 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8060, GAM62703, GAM113285 and GAM229890

GR6081 AW021507 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6081 (GR6081) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6081 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR6081 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6081 gene encodes GR6081 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6081 precursor RNA folds spatially, forming GR6081 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6081 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6081 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6081 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM179740 precursor RNA and GAM236187 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM179740 RNA and GAM236187 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM179740 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM179740 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM179740 target RNA into GAM179740 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM236187 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM236187 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM236187 target RNA into GAM236187 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6081 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6081 gene: GAM179740 target

protein and GAM236187 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM179740 and GAM236187

GR6082 BG708029 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6082(GR6082) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6082 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6082 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6082 gene encodes GR6082 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6082 precursor RNA folds spatially, forming GR6082 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6082 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6082 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6082 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM192708 precursor RNA and GAM247663 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM192708 RNA and GAM247663 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM192708 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM192708 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM192708 target RNA into GAM192708 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM247663 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM247663 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM247663 target RNA into GAM247663 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6082 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6082 gene: GAM192708 target protein and GAM247663 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM192708 and GAM247663

GR6083 BE501862 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6083(GR6083) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6083 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6083 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6083 gene encodes GR6083 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6083 precursor RNA folds spatially, forming GR6083 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6083 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6083 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6083 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM6912 precursor RNA, GAM7687 precursor RNA and GAM261566 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6912 RNA, GAM7687 RNA and GAM261566 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6912 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6912 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6912 target RNA into GAM6912 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7687 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7687 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7687 target RNA into GAM7687 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM261566 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM261566 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM261566 target RNA into GAM261566 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6083 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6083 gene: GAM6912 target protein, GAM7687 target protein and GAM261566 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6912, GAM7687 and GAM261566

GR6084 BM472551 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6084(GR6084) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6084 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6084

gene was detected is described hereinabove with reference to Figs. 8-18.

GR6084 gene encodes GR6084 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6084 precursor RNA folds spatially, forming GR6084 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6084 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6084 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6084 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7634 precursor RNA and GAM172085 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7634 RNA and GAM172085 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7634 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7634 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7634 target RNA into GAM7634 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM172085 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM172085 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM172085 target RNA into GAM172085 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6084 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6084 gene: GAM7634 target protein and GAM172085 target protein, herein schematically represented by GAM1

TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7634 and GAM172085

GR6085 BE081075 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6085(GR6085) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6085 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6085 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6085 gene encodes GR6085 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6085 precursor RNA folds spatially, forming GR6085 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6085 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6085 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6085 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2353 precursor RNA and GAM299769 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2353 RNA and GAM299769 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2353 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2353 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2353 target RNA into GAM2353 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM299769 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM299769 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM299769 target RNA into GAM299769 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6085 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6085 gene: GAM2353 target protein and GAM299769 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2353 and GAM299769

GR6086 BG779565 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6086(GR6086) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6086 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6086 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6086 gene encodes GR6086 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6086 precursor RNA folds spatially, forming GR6086 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6086 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6086 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6086 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM5722 precursor RNA, GAM148443 precursor RNA and GAM188775 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5722 RNA, GAM148443 RNA and GAM188775 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5722 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5722 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5722 target RNA into GAM5722 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM148443 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM148443 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM148443 target RNA into GAM148443 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM188775 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM188775 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM188775 target RNA into GAM188775 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6086 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6086 gene: GAM5722 target protein, GAM148443 target protein and GAM188775 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5722, GAM148443 and GAM188775

GR6087 BG500802 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6087(GR6087) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6087 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6087 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6087 gene encodes GR6087 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6087 precursor RNA folds spatially, forming GR6087 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6087 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6087 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6087 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2738 precursor RNA, GAM3996 precursor RNA and GAM113396 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2738 RNA, GAM3996 RNA and GAM113396 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2738 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2738 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2738 target RNA into GAM2738 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM3996 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3996 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3996 target RNA into GAM3996 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM113396 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM113396 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM113396

target RNA into GAM113396 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6087 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6087 gene: GAM2738 target protein, GAM3996 target protein and GAM113396 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2738, GAM3996 and GAM113396

GR6088 BI545353 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6088(GR6088) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6088 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6088 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6088 gene encodes GR6088 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6088 precursor RNA folds spatially, forming GR6088 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6088 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6088 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6088 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM165 precursor RNA, GAM4094 precursor RNA and GAM305918 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM165 RNA, GAM4094 RNA and GAM305918 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM165 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM165 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM165 target RNA into GAM165 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM4094 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4094 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4094 target RNA into GAM4094 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM305918 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM305918 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM305918 target RNA into GAM305918 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6088 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6088 gene: GAM165 target protein, GAM4094 target protein and GAM305918 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM165, GAM4094 and GAM305918

GR6089 BG177735 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6089 (GR6089) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6089 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6089 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6089 gene encodes GR6089 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6089 precursor RNA folds spatially, forming GR6089 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6089 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6089 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6089 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6364 precursor RNA and GAM255799 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6364 RNA and GAM255799 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6364 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6364 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6364 target RNA into GAM6364 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM255799 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM255799 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM255799 target RNA into GAM255799 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6089 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6089 gene: GAM6364 target protein and GAM255799 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6364 and GAM255799

bioinformatically detected regulatory gene, referred to here as Genomic Record 6090 (GR6090) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6090 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6090 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6090 gene encodes GR6090 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6090 precursor RNA folds spatially, forming GR6090 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6090 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6090 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6090 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM194449 precursor RNA and GAM254168 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM194449 RNA and GAM254168 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM194449 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM194449 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM194449 target RNA into GAM194449 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM254168 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM254168 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM254168

target RNA into GAM254168 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6090 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6090 gene: GAM194449 target protein and GAM254168 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM194449 and GAM254168

GR6091 BM975528 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6091 (GR6091) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6091 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6091 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6091 gene encodes GR6091 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6091 precursor RNA folds spatially, forming GR6091 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6091 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6091 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6091 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM6935 precursor RNA, GAM112286 precursor RNA and GAM179922 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6935 RNA, GAM112286 RNA and GAM179922 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6935 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6935 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6935 target RNA into GAM6935 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM112286 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM112286 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM112286 target RNA into GAM112286 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM179922 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM179922 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM179922 target RNA into GAM179922 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6091 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6091 gene: GAM6935 target protein, GAM112286 target protein and GAM179922 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6935, GAM112286 and GAM179922

GR6092 BF062843 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6092(GR6092) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6092 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6092 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6092 gene encodes GR6092 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6092 precursor RNA folds spatially, forming GR6092 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6092 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6092 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6092 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2812 precursor RNA and GAM50395 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2812 RNA and GAM50395 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2812 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2812 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2812 target RNA into GAM2812 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM50395 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM50395 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM50395 target RNA into GAM50395 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6092 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6092 gene: GAM2812 target protein and GAM50395 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2812 and GAM50395

6093(GR6093) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6093 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6093 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6093 gene encodes GR6093 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6093 precursor RNA folds spatially, forming GR6093 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6093 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6093 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6093 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM28270 precursor RNA, GAM215039 precursor RNA and GAM245177 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM28270 RNA, GAM215039 RNA and GAM245177 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM28270 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM28270 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM28270 target RNA into GAM28270 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM215039 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM215039 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM215039

target RNA into GAM215039 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM245177 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM245177 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM245177 target RNA into GAM245177 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6093 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6093 gene: GAM28270 target protein, GAM215039 target protein and GAM245177 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM28270, GAM215039 and GAM245177

GR6094 BI912561 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6094(GR6094) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6094 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6094 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6094 gene encodes GR6094 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6094 precursor RNA folds spatially, forming GR6094 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6094 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6094 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6094 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM7560 precursor RNA, GAM126409 precursor RNA and GAM149112 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded

precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7560 RNA, GAM126409 RNA and GAM149112 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7560 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7560 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7560 target RNA into GAM7560 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM126409 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM126409 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM126409 target RNA into GAM126409 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM149112 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM149112 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM149112 target RNA into GAM149112 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6094 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6094 gene: GAM7560 target protein, GAM126409 target protein and GAM149112 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7560, GAM126409 and GAM149112

GR6095 BM914482 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6095(GR6095) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6095 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6095 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6095 gene encodes GR6095 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6095 precursor RNA folds spatially, forming GR6095 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6095 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6095 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6095 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM116326 precursor RNA and GAM259545 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM116326 RNA and GAM259545 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM116326 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM116326 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM116326 target RNA into GAM116326 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM259545 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM259545 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM259545 target RNA into GAM259545 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6095 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6095 gene: GAM116326 target protein and GAM259545 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM116326 and GAM259545

GR6096 AI285633 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6096(GR6096) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6096 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6096 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6096 gene encodes GR6096 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6096 precursor RNA folds spatially, forming GR6096 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6096 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6096 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6096 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4296 precursor RNA and GAM151755 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4296 RNA and GAM151755 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4296 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4296 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4296 target RNA into

GAM4296 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM151755 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM151755 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM151755 target RNA into GAM151755 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6096 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6096 gene: GAM4296 target protein and GAM151755 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4296 and GAM151755

GR6097 AI652319 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6097(GR6097) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6097 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6097 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6097 gene encodes GR6097 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6097 precursor RNA folds spatially, forming GR6097 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6097 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6097 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6097 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM124355 precursor RNA and GAM213219 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM124355 RNA and GAM213219 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM124355 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM124355 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM124355 target RNA into GAM124355 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM213219 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM213219 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM213219 target RNA into GAM213219 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6097 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6097 gene: GAM124355 target protein and GAM213219 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM124355 and GAM213219

GR6098 BM781835 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6098(GR6098) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6098 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6098 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6098 gene encodes GR6098 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6098 precursor RNA folds spatially, forming GR6098 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated

that GR6098 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6098 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6098 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM47115 precursor RNA and GAM274584 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM47115 RNA and GAM274584 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM47115 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM47115 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM47115 target RNA into GAM47115 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM274584 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM274584 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM274584 target RNA into GAM274584 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6098 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6098 gene: GAM47115 target protein and GAM274584 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM47115 and GAM274584

GR6099 W90338 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6099(GR6099) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR6099 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6099 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6099 gene encodes GR6099 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6099 precursor RNA folds spatially, forming GR6099 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6099 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6099 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6099 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM6028 precursor RNA, GAM97259 precursor RNA and GAM169107 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6028 RNA, GAM97259 RNA and GAM169107 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6028 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6028 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6028 target RNA into GAM6028 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM97259 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM97259 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM97259 target RNA into GAM97259 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM169107 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM169107 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM169107 target RNA into GAM169107 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6099 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6099 gene: GAM6028 target protein, GAM97259 target protein and GAM169107 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6028, GAM97259 and GAM169107

GR6100 AW104990 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6100(GR6100) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6100 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6100 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6100 gene encodes GR6100 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6100 precursor RNA folds spatially, forming GR6100 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6100 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6100 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6100 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM49767 precursor RNA and GAM57821 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM49767 RNA and GAM57821 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM49767 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM49767 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM49767 target RNA into GAM49767 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM57821 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM57821 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM57821 target RNA into GAM57821 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6100 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6100 gene: GAM49767 target protein and GAM57821 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM49767 and GAM57821

GR6101 BM744299 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6101(GR6101) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6101 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6101 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6101 gene encodes GR6101 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6101 precursor RNA folds spatially, forming GR6101 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6101 folded precursor RNA comprises a plurality of what is known in the

art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6101 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6101 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM248363 precursor RNA and GAM324762 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM248363 RNA and GAM324762 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM248363 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM248363 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM248363 target RNA into GAM248363 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM324762 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM324762 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM324762 target RNA into GAM324762 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6101 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6101 gene: GAM248363 target protein and GAM324762 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM248363 and GAM324762

GR6102 AA332461 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6102(GR6102) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR6102 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6102 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6102 gene encodes GR6102 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6102 precursor RNA folds spatially, forming GR6102 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6102 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6102 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6102 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM117319 precursor RNA and GAM329703 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM117319 RNA and GAM329703 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM117319 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM117319 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM117319 target RNA into GAM117319 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM329703 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM329703 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM329703 target RNA into GAM329703 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly

utilities, of GR6102 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6102 gene: GAM117319 target protein and GAM329703 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM117319 and GAM329703

GR6103 BG391370 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6103(GR6103) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6103 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6103 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6103 gene encodes GR6103 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6103 precursor RNA folds spatially, forming GR6103 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6103 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6103 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6103 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM91005 precursor RNA, GAM95691 precursor RNA and GAM95692 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM91005 RNA, GAM95691 RNA and GAM95692 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM91005 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM91005 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM91005 target RNA into GAM91005 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM95691 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM95691 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM95691 target RNA into GAM95691 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM95692 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM95692 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM95692 target RNA into GAM95692 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6103 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6103 gene: GAM91005 target protein, GAM95691 target protein and GAM95692 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM91005, GAM95691 and GAM95692

GR6104 H75815 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6104(GR6104) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6104 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6104 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6104 gene encodes GR6104 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6104 precursor RNA folds spatially, forming GR6104 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6104 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR6104 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6104 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2328 precursor RNA and GAM165102 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2328 RNA and GAM165102 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2328 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2328 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2328 target RNA into GAM2328 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM165102 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM165102 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM165102 target RNA into GAM165102 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6104 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6104 gene: GAM2328 target protein and GAM165102 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2328 and GAM165102

GR6105 BG542254 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6105(GR6105) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6105 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6105 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6105 gene encodes GR6105 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6105 precursor RNA folds spatially, forming GR6105 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6105 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6105 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6105 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM164236 precursor RNA and GAM206703 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM164236 RNA and GAM206703 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM164236 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM164236 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM164236 target RNA into GAM164236 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM206703 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM206703 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM206703 target RNA into GAM206703 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6105 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6105 gene: GAM164236 target protein and GAM206703 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM164236 and GAM206703

GR6106 BG015402 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6106(GR6106) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6106 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6106 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6106 gene encodes GR6106 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6106 precursor RNA folds spatially, forming GR6106 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6106 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6106 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6106 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM20846 precursor RNA and GAM69597 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM20846 RNA and GAM69597 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM20846 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM20846 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM20846

target RNA into GAM20846 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM69597 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM69597 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM69597 target RNA into GAM69597 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6106 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6106 gene: GAM20846 target protein and GAM69597 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM20846 and GAM69597

GR6107 BG167558 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6107(GR6107) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6107 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6107 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6107 gene encodes GR6107 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6107 precursor RNA folds spatially, forming GR6107 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6107 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6107 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6107 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2048 precursor RNA, GAM6058 precursor RNA and GAM54271 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED

PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2048 RNA, GAM6058 RNA and GAM54271 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2048 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2048 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2048 target RNA into GAM2048 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6058 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6058 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6058 target RNA into GAM6058 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM54271 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM54271 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM54271 target RNA into GAM54271 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6107 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6107 gene: GAM2048 target protein, GAM6058 target protein and GAM54271 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2048, GAM6058 and GAM54271

GR6108 AI609115 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6108(GR6108) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6108 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6108 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6108 gene encodes GR6108 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6108 precursor RNA folds spatially, forming GR6108 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6108 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6108 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6108 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM7637 precursor RNA, GAM290415 precursor RNA and GAM303428 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7637 RNA, GAM290415 RNA and GAM303428 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7637 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7637 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7637 target RNA into GAM7637 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM290415 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM290415 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM290415 target RNA into GAM290415 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM303428 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM303428 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM303428 target RNA into GAM303428 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6108 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6108 gene: GAM7637 target protein, GAM290415 target protein and GAM303428 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7637, GAM290415 and GAM303428

GR6109 AA193508 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6109 (GR6109) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6109 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6109 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6109 gene encodes GR6109 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6109 precursor RNA folds spatially, forming GR6109 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6109 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6109 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6109 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM142224 precursor RNA and GAM335412 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM142224 RNA and GAM335412 RNA, herein schematically

represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM142224 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM142224 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM142224 target RNA into GAM142224 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM335412 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM335412 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM335412 target RNA into GAM335412 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6109 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6109 gene: GAM142224 target protein and GAM335412 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM142224 and GAM335412

GR6110 R98710 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6110(GR6110) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6110 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6110 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6110 gene encodes GR6110 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6110 precursor RNA folds spatially, forming GR6110 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6110 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6110 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6110 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM113331 precursor RNA and GAM120049 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM113331 RNA and GAM120049 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM113331 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM113331 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM113331 target RNA into GAM113331 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM120049 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM120049 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM120049 target RNA into GAM120049 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6110 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6110 gene: GAM113331 target protein and GAM120049 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM113331 and GAM120049

GR6111 AI242354 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6111 (GR6111) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6111 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR6111 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6111 gene encodes GR6111 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6111 precursor RNA folds spatially, forming GR6111 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6111 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6111 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6111 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM238621 precursor RNA and GAM280264 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM238621 RNA and GAM280264 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM238621 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM238621 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM238621 target RNA into GAM238621 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM280264 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM280264 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM280264 target RNA into GAM280264 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6111 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6111 gene: GAM238621 target

protein and GAM280264 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM238621 and GAM280264

GR6112 BF507360 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6112(GR6112) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6112 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6112 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6112 gene encodes GR6112 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6112 precursor RNA folds spatially, forming GR6112 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6112 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6112 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6112 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM66990 precursor RNA and GAM251760 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM66990 RNA and GAM251760 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM66990 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM66990 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM66990 target RNA into GAM66990 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM251760 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM251760 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM251760 target RNA into GAM251760 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6112 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6112 gene: GAM66990 target protein and GAM251760 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM66990 and GAM251760

GR6113 N34090 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6113(GR6113) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6113 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6113 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6113 gene encodes GR6113 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6113 precursor RNA folds spatially, forming GR6113 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6113 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6113 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6113 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM52812 precursor RNA and GAM177601 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM52812 RNA and GAM177601 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM52812 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM52812 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM52812 target RNA into GAM52812 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM177601 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM177601 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM177601 target RNA into GAM177601 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6113 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6113 gene: GAM52812 target protein and GAM177601 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM52812 and GAM177601

GR6114 AI090515 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6114(GR6114) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6114 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6114 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6114 gene encodes GR6114 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6114 precursor RNA folds spatially, forming GR6114 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6114 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR6114 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6114 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM26638 precursor RNA, GAM87459 precursor RNA and GAM176382 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM26638 RNA, GAM87459 RNA and GAM176382 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM26638 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM26638 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM26638 target RNA into GAM26638 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM87459 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM87459 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM87459 target RNA into GAM87459 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM176382 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM176382 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM176382 target RNA into GAM176382 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6114 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6114 gene: GAM26638 target protein, GAM87459 target protein and GAM176382 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN.

The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM26638, GAM87459 and GAM176382

GR6115 AA682955 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6115(GR6115) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6115 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6115 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6115 gene encodes GR6115 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6115 precursor RNA folds spatially, forming GR6115 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6115 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6115 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6115 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM219036 precursor RNA and GAM255654 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM219036 RNA and GAM255654 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM219036 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM219036 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM219036 target RNA into GAM219036 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM255654 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM255654 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM255654 target RNA into GAM255654 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6115 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6115 gene: GAM219036 target protein and GAM255654 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM219036 and GAM255654

GR6116 AL597246 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6116(GR6116) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6116 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6116 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6116 gene encodes GR6116 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6116 precursor RNA folds spatially, forming GR6116 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6116 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6116 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6116 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1911 precursor RNA and GAM77134 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM1911 RNA and GAM77134 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1911 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1911 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1911 target RNA into GAM1911 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM77134 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM77134 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM77134 target RNA into GAM77134 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6116 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6116 gene: GAM1911 target protein and GAM77134 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1911 and GAM77134

GR6117 BF216653 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6117(GR6117) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6117 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6117 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6117 gene encodes GR6117 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6117 precursor RNA folds spatially, forming GR6117 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6117 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6117 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6117 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM995 precursor RNA and GAM325667 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM995 RNA and GAM325667 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM995 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM995 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM995 target RNA into GAM995 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM325667 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM325667 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM325667 target RNA into GAM325667 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6117 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6117 gene: GAM995 target protein and GAM325667 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM995 and GAM325667

GR6118 BF665400 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6118(GR6118) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6118 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6118 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6118 gene encodes GR6118 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6118 precursor RNA folds spatially, forming GR6118 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6118 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6118 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6118 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM99025 precursor RNA and GAM113656 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM99025 RNA and GAM113656 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM99025 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM99025 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM99025 target RNA into GAM99025 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM113656 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM113656 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM113656 target RNA into GAM113656 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6118 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR6118 gene: GAM99025 target protein and GAM113656 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM99025 and GAM113656

GR6119 R35904 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6119(GR6119) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6119 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6119 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6119 gene encodes GR6119 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6119 precursor RNA folds spatially, forming GR6119 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6119 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6119 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6119 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4732 precursor RNA and GAM164674 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4732 RNA and GAM164674 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4732 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4732 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4732 target RNA into GAM4732 target protein, herein schematically represented by GAM1 TARGET

PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM164674 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM164674 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM164674 target RNA into GAM164674 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6119 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6119 gene: GAM4732 target protein and GAM164674 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4732 and GAM164674

GR6120 BG360930 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6120(GR6120) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6120 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6120 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6120 gene encodes GR6120 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6120 precursor RNA folds spatially, forming GR6120 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6120 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6120 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6120 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM98936 precursor RNA and GAM109876 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM98936 RNA and GAM109876 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM98936 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM98936 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM98936 target RNA into GAM98936 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM109876 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM109876 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM109876 target RNA into GAM109876 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6120 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6120 gene: GAM98936 target protein and GAM109876 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM98936 and GAM109876

GR6121 BF759478 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6121(GR6121) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6121 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6121 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6121 gene encodes GR6121 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6121 precursor RNA folds spatially, forming GR6121 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6121 folded precursor RNA comprises a plurality of what is known in the

art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6121 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6121 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4511 precursor RNA and GAM51226 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4511 RNA and GAM51226 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4511 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4511 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4511 target RNA into GAM4511 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM51226 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM51226 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM51226 target RNA into GAM51226 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6121 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6121 gene: GAM4511 target protein and GAM51226 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4511 and GAM51226

GR6122 AW874464 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6122(GR6122) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR6122 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6122 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6122 gene encodes GR6122 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6122 precursor RNA folds spatially, forming GR6122 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6122 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6122 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6122 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5520 precursor RNA and GAM178369 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5520 RNA and GAM178369 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5520 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5520 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5520 target RNA into GAM5520 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM178369 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM178369 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM178369 target RNA into GAM178369 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly

utilities, of GR6122 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6122 gene: GAM5520 target protein and GAM178369 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5520 and GAM178369

GR6123 BF592249 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6123(GR6123) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6123 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6123 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6123 gene encodes GR6123 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6123 precursor RNA folds spatially, forming GR6123 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6123 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6123 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6123 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2138 precursor RNA and GAM75411 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2138 RNA and GAM75411 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2138 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2138 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig. 8, thereby inhibiting translation of GAM2138 target RNA into GAM2138 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM75411 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM75411 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM75411 target RNA into GAM75411 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6123 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6123 gene: GAM2138 target protein and GAM75411 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2138 and GAM75411

GR6124 BG027993 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6124(GR6124) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6124 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6124 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6124 gene encodes GR6124 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6124 precursor RNA folds spatially, forming GR6124 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6124 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6124 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6124 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8557 precursor RNA and GAM324803 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin

shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8557 RNA and GAM324803 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8557 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8557 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8557 target RNA into GAM8557 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM324803 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM324803 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM324803 target RNA into GAM324803 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6124 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6124 gene: GAM8557 target protein and GAM324803 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8557 and GAM324803

GR6125 BG220510 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6125(GR6125) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6125 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6125 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6125 gene encodes GR6125 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6125 precursor RNA folds spatially, forming GR6125 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6125 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6125 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6125 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM132368 precursor RNA and GAM207418 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM132368 RNA and GAM207418 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM132368 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM132368 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM132368 target RNA into GAM132368 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM207418 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM207418 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM207418 target RNA into GAM207418 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6125 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6125 gene: GAM132368 target protein and GAM207418 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM132368 and GAM207418

GR6126 BG336566 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6126(GR6126) gene, which encodes an `operon-like` cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6126 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6126 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6126 gene encodes GR6126 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6126 precursor RNA folds spatially, forming GR6126 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6126 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6126 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6126 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM156143 precursor RNA and GAM259108 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM156143 RNA and GAM259108 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM156143 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM156143 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM156143 target RNA into GAM156143 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM259108 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM259108 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM259108 target RNA into GAM259108 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6126 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6126 gene: GAM156143 target protein and GAM259108 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM156143 and GAM259108

GR6127 AA934757 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6127(GR6127) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6127 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6127 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6127 gene encodes GR6127 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6127 precursor RNA folds spatially, forming GR6127 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6127 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6127 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6127 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2615 precursor RNA and GAM10267 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2615 RNA and GAM10267 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2615 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2615 target RNA, herein schematically represented by

GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2615 target RNA into GAM2615 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM10267 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM10267 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM10267 target RNA into GAM10267 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6127 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6127 gene: GAM2615 target protein and GAM10267 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2615 and GAM10267

GR6128 BF315326 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6128(GR6128) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6128 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6128 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6128 gene encodes GR6128 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6128 precursor RNA folds spatially, forming GR6128 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6128 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6128 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6128 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM13381 precursor RNA, GAM65099 precursor RNA

and GAM314565 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM13381 RNA, GAM65099 RNA and GAM314565 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM13381 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM13381 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM13381 target RNA into GAM13381 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM65099 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM65099 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM65099 target RNA into GAM65099 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM314565 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM314565 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM314565 target RNA into GAM314565 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6128 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6128 gene: GAM13381 target protein, GAM65099 target protein and GAM314565 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM13381, GAM65099 and GAM314565

GR6129 BF223405 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6129(GR6129) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR6129 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6129 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6129 gene encodes GR6129 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6129 precursor RNA folds spatially, forming GR6129 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6129 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6129 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6129 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3799 precursor RNA and GAM255793 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3799 RNA and GAM255793 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3799 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3799 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3799 target RNA into GAM3799 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM255793 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM255793 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM255793 target RNA into GAM255793 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6129 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6129 gene: GAM3799 target protein and GAM255793 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3799 and GAM255793

GR6130 BG571846 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6130(GR6130) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6130 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6130 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6130 gene encodes GR6130 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6130 precursor RNA folds spatially, forming GR6130 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6130 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6130 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6130 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2914 precursor RNA and GAM125192 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2914 RNA and GAM125192 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2914 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2914 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds

to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2914 target RNA into GAM2914 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM125192 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM125192 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM125192 target RNA into GAM125192 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6130 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6130 gene: GAM2914 target protein and GAM125192 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2914 and GAM125192

GR6131 AW974814 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6131 (GR6131) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6131 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6131 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6131 gene encodes GR6131 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6131 precursor RNA folds spatially, forming GR6131 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6131 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6131 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6131 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM24729 precursor RNA, GAM76388 precursor RNA and GAM302942 precursor RNA, herein schematically represented by GAM1 FOLDED

PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM24729 RNA, GAM76388 RNA and GAM302942 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM24729 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM24729 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM24729 target RNA into GAM24729 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM76388 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM76388 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM76388 target RNA into GAM76388 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM302942 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM302942 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM302942 target RNA into GAM302942 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6131 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6131 gene: GAM24729 target protein, GAM76388 target protein and GAM302942 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM24729, GAM76388 and GAM302942

GR6132 BE732295 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6132(GR6132) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR6132 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6132 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6132 gene encodes GR6132 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6132 precursor RNA folds spatially, forming GR6132 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6132 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6132 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6132 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM49768 precursor RNA and GAM186426 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM49768 RNA and GAM186426 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM49768 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM49768 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM49768 target RNA into GAM49768 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM186426 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM186426 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM186426 target RNA into GAM186426 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly

utilities, of GR6132 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6132 gene: GAM49768 target protein and GAM186426 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM49768 and GAM186426

GR6133 AW410105 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6133(GR6133) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6133 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6133 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6133 gene encodes GR6133 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6133 precursor RNA folds spatially, forming GR6133 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6133 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6133 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6133 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM585 precursor RNA and GAM4190 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM585 RNA and GAM4190 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM585 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM585 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig. 8, thereby inhibiting translation of GAM585 target RNA into GAM585 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM4190 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4190 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4190 target RNA into GAM4190 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6133 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6133 gene: GAM585 target protein and GAM4190 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM585 and GAM4190

GR6134 BF185687 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6134(GR6134) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6134 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6134 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6134 gene encodes GR6134 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6134 precursor RNA folds spatially, forming GR6134 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6134 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6134 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6134 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM74511 precursor RNA, GAM105095 precursor RNA and GAM176489 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded

precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM74511 RNA, GAM105095 RNA and GAM176489 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM74511 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM74511 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM74511 target RNA into GAM74511 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM105095 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM105095 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM105095 target RNA into GAM105095 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM176489 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM176489 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM176489 target RNA into GAM176489 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6134 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6134 gene: GAM74511 target protein, GAM105095 target protein and GAM176489 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM74511, GAM105095 and GAM176489

GR6135 BG425783 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6135(GR6135) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6135 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6135 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6135 gene encodes GR6135 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6135 precursor RNA folds spatially, forming GR6135 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6135 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6135 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6135 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM6958 precursor RNA, GAM8481 precursor RNA and GAM17684 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6958 RNA, GAM8481 RNA and GAM17684 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6958 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6958 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6958 target RNA into GAM6958 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8481 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8481 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8481 target RNA into GAM8481 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM17684 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM17684 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM17684 target RNA into GAM17684 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6135 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6135 gene: GAM6958 target protein, GAM8481 target protein and GAM17684 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6958, GAM8481 and GAM17684

GR6136 AL602921 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6136(GR6136) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6136 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6136 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6136 gene encodes GR6136 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6136 precursor RNA folds spatially, forming GR6136 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6136 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6136 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6136 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM64444 precursor RNA and GAM134043 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM64444 RNA and GAM134043 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM64444 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM64444 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM64444 target RNA into GAM64444 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM134043 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM134043 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM134043 target RNA into GAM134043 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6136 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6136 gene: GAM64444 target protein and GAM134043 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM64444 and GAM134043

GR6137 AA079357 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6137(GR6137) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6137 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6137 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6137 gene encodes GR6137 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6137 precursor RNA folds spatially, forming GR6137 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6137 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6137 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6137 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6179 precursor RNA and GAM216755 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6179 RNA and GAM216755 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6179 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6179 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6179 target RNA into GAM6179 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM216755 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM216755 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM216755 target RNA into GAM216755 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6137 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6137 gene: GAM6179 target protein and GAM216755 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6179 and GAM216755

GR6138 BE857403 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6138(GR6138) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6138 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6138 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6138 gene encodes GR6138 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6138 precursor RNA folds spatially, forming GR6138 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6138 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6138 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6138 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM212709 precursor RNA and GAM254851 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM212709 RNA and GAM254851 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM212709 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM212709 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM212709 target RNA into GAM212709 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM254851 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM254851 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM254851 target RNA into GAM254851 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6138 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR6138 gene: GAM212709 target protein and GAM254851 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM212709 and GAM254851

GR6139 AI123114 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6139(GR6139) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6139 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6139 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6139 gene encodes GR6139 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6139 precursor RNA folds spatially, forming GR6139 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6139 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6139 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6139 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6346 precursor RNA and GAM84132 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6346 RNA and GAM84132 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6346 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6346 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6346 target RNA into GAM6346 target protein, herein schematically represented by GAM1 TARGET

PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM84132 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM84132 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM84132 target RNA into GAM84132 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6139 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6139 gene: GAM6346 target protein and GAM84132 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6346 and GAM84132

GR6140 AI634709 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6140 (GR6140) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6140 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6140 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6140 gene encodes GR6140 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6140 precursor RNA folds spatially, forming GR6140 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6140 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6140 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6140 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8459 precursor RNA and GAM330376 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8459 RNA and GAM330376 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8459 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8459 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8459 target RNA into GAM8459 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM330376 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM330376 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM330376 target RNA into GAM330376 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6140 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6140 gene: GAM8459 target protein and GAM330376 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8459 and GAM330376

GR6141 BM042737 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6141(GR6141) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6141 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6141 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6141 gene encodes GR6141 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6141 precursor RNA folds spatially, forming GR6141 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6141 folded precursor RNA comprises a plurality of what is known in the

art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6141 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6141 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4363 precursor RNA, GAM154763 precursor RNA and GAM239591 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4363 RNA, GAM154763 RNA and GAM239591 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4363 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4363 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4363 target RNA into GAM4363 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM154763 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM154763 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM154763 target RNA into GAM154763 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM239591 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM239591 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM239591 target RNA into GAM239591 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6141 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6141 gene: GAM4363 target protein, GAM154763 target protein and GAM239591 target protein, herein

schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4363, GAM154763 and GAM239591

GR6142 BF688018 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6142(GR6142) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6142 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6142 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6142 gene encodes GR6142 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6142 precursor RNA folds spatially, forming GR6142 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6142 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6142 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6142 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4201 precursor RNA, GAM166867 precursor RNA and GAM303521 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4201 RNA, GAM166867 RNA and GAM303521 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4201 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4201 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4201 target RNA into GAM4201 target protein, herein schematically represented by GAM1 TARGET

PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM166867 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM166867 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM166867 target RNA into GAM166867 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM303521 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM303521 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM303521 target RNA into GAM303521 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6142 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6142 gene: GAM4201 target protein, GAM166867 target protein and GAM303521 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4201, GAM166867 and GAM303521

GR6143 AA488375 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6143(GR6143) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6143 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6143 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6143 gene encodes GR6143 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6143 precursor RNA folds spatially, forming GR6143 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6143 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6143 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR6143 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM97002 precursor RNA, GAM237041 precursor RNA and GAM261744 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM97002 RNA, GAM237041 RNA and GAM261744 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM97002 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM97002 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM97002 target RNA into GAM97002 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM237041 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM237041 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM237041 target RNA into GAM237041 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM261744 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM261744 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM261744 target RNA into GAM261744 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6143 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6143 gene: GAM97002 target protein, GAM237041 target protein and GAM261744 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM97002, GAM237041 and GAM261744

GR6144 BE711540 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6144(GR6144) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6144 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6144 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6144 gene encodes GR6144 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6144 precursor RNA folds spatially, forming GR6144 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6144 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6144 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6144 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6721 precursor RNA and GAM231096 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6721 RNA and GAM231096 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6721 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6721 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6721 target RNA into GAM6721 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM231096 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM231096 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM231096 target RNA into GAM231096 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6144 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6144 gene: GAM6721 target protein and GAM231096 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6721 and GAM231096

GR6145 BG984537 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6145(GR6145) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6145 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6145 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6145 gene encodes GR6145 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6145 precursor RNA folds spatially, forming GR6145 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6145 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6145 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6145 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7305 precursor RNA and GAM77334 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7305 RNA and GAM77334 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7305 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7305 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7305 target RNA into GAM7305 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM77334 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM77334 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM77334 target RNA into GAM77334 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6145 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6145 gene: GAM7305 target protein and GAM77334 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7305 and GAM77334

GR6146 BF966088 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6146(GR6146) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6146 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6146 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6146 gene encodes GR6146 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6146 precursor RNA folds spatially, forming GR6146 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6146 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6146 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6146 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM56278 precursor RNA and GAM64461 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM56278 RNA and GAM64461 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM56278 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM56278 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM56278 target RNA into GAM56278 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM64461 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM64461 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM64461 target RNA into GAM64461 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6146 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6146 gene: GAM56278 target protein and GAM64461 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM56278 and GAM64461

GR6147 BG431660 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6147(GR6147) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6147 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6147 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6147 gene encodes GR6147 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6147 precursor RNA folds spatially, forming GR6147 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6147 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6147 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6147 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7834 precursor RNA and GAM242376 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7834 RNA and GAM242376 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7834 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7834 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7834 target RNA into GAM7834 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM242376 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM242376 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM242376 target RNA into GAM242376 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6147 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6147 gene: GAM7834 target protein and GAM242376 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes

is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7834 and GAM242376

GR6148 BG703737 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6148(GR6148) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6148 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6148 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6148 gene encodes GR6148 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6148 precursor RNA folds spatially, forming GR6148 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6148 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6148 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6148 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3561 precursor RNA, GAM185710 precursor RNA and GAM314460 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3561 RNA, GAM185710 RNA and GAM314460 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3561 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3561 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3561 target RNA into GAM3561 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM185710 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM185710 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM185710 target RNA into GAM185710 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM314460 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM314460 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM314460 target RNA into GAM314460 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6148 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6148 gene: GAM3561 target protein, GAM185710 target protein and GAM314460 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3561, GAM185710 and GAM314460

GR6149 BF772809 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6149(GR6149) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6149 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6149 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6149 gene encodes GR6149 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6149 precursor RNA folds spatially, forming GR6149 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6149 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6149 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6149 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8012 precursor RNA and GAM327881 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8012 RNA and GAM327881 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8012 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8012 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8012 target RNA into GAM8012 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM327881 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM327881 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM327881 target RNA into GAM327881 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6149 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6149 gene: GAM8012 target protein and GAM327881 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8012 and GAM327881

GR6150 BM691778 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6150(GR6150) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6150 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6150 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6150 gene encodes GR6150 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6150 precursor RNA folds spatially, forming GR6150 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6150 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6150 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6150 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM89965 precursor RNA and GAM305781 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM89965 RNA and GAM305781 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM89965 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM89965 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM89965 target RNA into GAM89965 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM305781 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM305781 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM305781 target RNA into GAM305781 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6150 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6150 gene: GAM89965 target protein and GAM305781 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference,

with references to GAM89965 and GAM305781

GR6151 AW388679 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6151 (GR6151) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6151 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6151 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6151 gene encodes GR6151 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6151 precursor RNA folds spatially, forming GR6151 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6151 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6151 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6151 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM106539 precursor RNA, GAM146736 precursor RNA and GAM233181 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM106539 RNA, GAM146736 RNA and GAM233181 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM106539 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM106539 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM106539 target RNA into GAM106539 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM146736 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM146736 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM146736 target RNA into GAM146736 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM233181 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM233181 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM233181 target RNA into GAM233181 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6151 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6151 gene: GAM106539 target protein, GAM146736 target protein and GAM233181 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM106539, GAM146736 and GAM233181

GR6152 BM547741 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6152(GR6152) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6152 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6152 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6152 gene encodes GR6152 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6152 precursor RNA folds spatially, forming GR6152 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6152 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6152 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6152 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM107264 precursor RNA and GAM258402 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM107264 RNA and GAM258402 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM107264 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM107264 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM107264 target RNA into GAM107264 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM258402 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM258402 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM258402 target RNA into GAM258402 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6152 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6152 gene: GAM107264 target protein and GAM258402 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM107264 and GAM258402

GR6153 AA603682 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6153(GR6153) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6153 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6153 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6153 gene encodes GR6153 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6153 precursor RNA folds spatially, forming GR6153 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6153 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6153 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6153 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2122 precursor RNA and GAM114124 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2122 RNA and GAM114124 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2122 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2122 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2122 target RNA into GAM2122 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM114124 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM114124 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM114124 target RNA into GAM114124 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6153 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6153 gene: GAM2122 target protein and GAM114124 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2122 and GAM114124

GR6154 BI906835 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6154(GR6154) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6154 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6154 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6154 gene encodes GR6154 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6154 precursor RNA folds spatially, forming GR6154 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6154 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6154 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6154 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2903 precursor RNA and GAM4885 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2903 RNA and GAM4885 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2903 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2903 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2903 target RNA into GAM2903 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM4885 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4885 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds

to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4885 target RNA into GAM4885 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6154 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6154 gene: GAM2903 target protein and GAM4885 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2903 and GAM4885

GR6155 BG495168 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6155(GR6155) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6155 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6155 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6155 gene encodes GR6155 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6155 precursor RNA folds spatially, forming GR6155 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6155 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6155 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6155 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6530 precursor RNA and GAM118821 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6530 RNA and GAM118821 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6530 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6530 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6530 target RNA into GAM6530 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM118821 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM118821 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM118821 target RNA into GAM118821 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6155 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6155 gene: GAM6530 target protein and GAM118821 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6530 and GAM118821

GR6156 AW853156 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6156(GR6156) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6156 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6156 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6156 gene encodes GR6156 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6156 precursor RNA folds spatially, forming GR6156 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6156 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6156 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6156 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM65584 precursor RNA, GAM304147 precursor RNA and GAM328115 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM65584 RNA, GAM304147 RNA and GAM328115 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM65584 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM65584 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM65584 target RNA into GAM65584 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM304147 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM304147 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM304147 target RNA into GAM304147 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM328115 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM328115 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM328115 target RNA into GAM328115 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6156 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6156 gene: GAM65584 target protein, GAM304147 target protein and GAM328115 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM65584, GAM304147 and GAM328115

GR6157 BF525825 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6157(GR6157) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6157 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6157 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6157 gene encodes GR6157 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6157 precursor RNA folds spatially, forming GR6157 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6157 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6157 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6157 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM108270 precursor RNA, GAM271189 precursor RNA and GAM305104 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM108270 RNA, GAM271189 RNA and GAM305104 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM108270 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM108270 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM108270 target RNA into GAM108270 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM271189 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM271189 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM271189 target RNA into GAM271189 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM305104 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM305104 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM305104 target RNA into GAM305104 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6157 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6157 gene: GAM108270 target protein, GAM271189 target protein and GAM305104 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM108270, GAM271189 and GAM305104

GR6158 BG251488 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6158(GR6158) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6158 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6158 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6158 gene encodes GR6158 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6158 precursor RNA folds spatially, forming GR6158 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6158 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6158 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6158 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM745 precursor RNA and GAM177317 precursor

RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM745 RNA and GAM177317 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM745 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM745 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM745 target RNA into GAM745 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM177317 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM177317 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM177317 target RNA into GAM177317 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6158 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6158 gene: GAM745 target protein and GAM177317 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM745 and GAM177317

GR6159 BG744630 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6159 (GR6159) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6159 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6159 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6159 gene encodes GR6159 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6159 precursor RNA folds spatially, forming GR6159 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6159 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6159 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6159 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1311 precursor RNA, GAM119137 precursor RNA and GAM172821 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1311 RNA, GAM119137 RNA and GAM172821 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1311 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1311 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1311 target RNA into GAM1311 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM119137 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM119137 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM119137 target RNA into GAM119137 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM172821 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM172821 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM172821 target RNA into GAM172821 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly

utilities, of GR6159 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6159 gene: GAM1311 target protein, GAM119137 target protein and GAM172821 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1311, GAM119137 and GAM172821

GR6160 T54278 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6160(GR6160) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6160 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6160 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6160 gene encodes GR6160 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6160 precursor RNA folds spatially, forming GR6160 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6160 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6160 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6160 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8217 precursor RNA and GAM71951 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8217 RNA and GAM71951 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8217 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8217 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds

to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8217 target RNA into GAM8217 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM71951 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM71951 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM71951 target RNA into GAM71951 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6160 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6160 gene: GAM8217 target protein and GAM71951 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8217 and GAM71951

GR6161 BG478649 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6161 (GR6161) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6161 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6161 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6161 gene encodes GR6161 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6161 precursor RNA folds spatially, forming GR6161 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6161 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6161 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6161 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM7321 precursor RNA, GAM74053 precursor RNA and GAM75383 precursor RNA, herein schematically represented by GAM1 FOLDED

PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7321 RNA, GAM74053 RNA and GAM75383 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7321 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7321 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7321 target RNA into GAM7321 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM74053 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM74053 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM74053 target RNA into GAM74053 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM75383 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM75383 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM75383 target RNA into GAM75383 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6161 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6161 gene: GAM7321 target protein, GAM74053 target protein and GAM75383 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7321, GAM74053 and GAM75383

GR6162 AI752015 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6162(GR6162) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR6162 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6162 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6162 gene encodes GR6162 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6162 precursor RNA folds spatially, forming GR6162 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6162 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6162 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6162 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM83209 precursor RNA and GAM132377 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM83209 RNA and GAM132377 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM83209 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM83209 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM83209 target RNA into GAM83209 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM132377 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM132377 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM132377 target RNA into GAM132377 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly

utilities, of GR6162 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6162 gene: GAM83209 target protein and GAM132377 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM83209 and GAM132377

GR6163 BM050485 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6163(GR6163) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6163 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6163 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6163 gene encodes GR6163 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6163 precursor RNA folds spatially, forming GR6163 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6163 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6163 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6163 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4160 precursor RNA and GAM58774 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4160 RNA and GAM58774 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4160 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4160 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig. 8, thereby inhibiting translation of GAM4160 target RNA into GAM4160 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM58774 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM58774 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM58774 target RNA into GAM58774 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6163 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6163 gene: GAM4160 target protein and GAM58774 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4160 and GAM58774

GR6164 BM837162 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6164(GR6164) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6164 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6164 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6164 gene encodes GR6164 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6164 precursor RNA folds spatially, forming GR6164 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6164 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6164 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6164 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2544 precursor RNA, GAM273864 precursor RNA and GAM304327 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded

precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2544 RNA, GAM273864 RNA and GAM304327 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2544 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2544 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2544 target RNA into GAM2544 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM273864 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM273864 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM273864 target RNA into GAM273864 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM304327 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM304327 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM304327 target RNA into GAM304327 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6164 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6164 gene: GAM2544 target protein, GAM273864 target protein and GAM304327 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2544, GAM273864 and GAM304327

GR6165 H30426 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6165(GR6165) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6165 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6165 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6165 gene encodes GR6165 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6165 precursor RNA folds spatially, forming GR6165 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6165 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6165 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6165 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM7161 precursor RNA, GAM7830 precursor RNA and GAM169238 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7161 RNA, GAM7830 RNA and GAM169238 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7161 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7161 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7161 target RNA into GAM7161 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7830 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7830 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7830 target RNA into GAM7830 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM169238 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM169238 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM169238 target RNA into GAM169238 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6165 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6165 gene: GAM7161 target protein, GAM7830 target protein and GAM169238 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7161, GAM7830 and GAM169238

GR6166 AI159753 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6166(GR6166) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6166 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6166 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6166 gene encodes GR6166 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6166 precursor RNA folds spatially, forming GR6166 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6166 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6166 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6166 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM82980 precursor RNA, GAM212783 precursor RNA and GAM324350 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM82980 RNA, GAM212783 RNA and GAM324350 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM82980 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM82980 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM82980 target RNA into GAM82980 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM212783 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM212783 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM212783 target RNA into GAM212783 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM324350 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM324350 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM324350 target RNA into GAM324350 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6166 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6166 gene: GAM82980 target protein, GAM212783 target protein and GAM324350 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM82980, GAM212783 and GAM324350

GR6167 BF182944 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6167(GR6167) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6167 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6167 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6167 gene encodes GR6167 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6167 precursor RNA folds spatially, forming GR6167 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6167 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6167 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6167 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1008 precursor RNA, GAM7245 precursor RNA and GAM110296 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1008 RNA, GAM7245 RNA and GAM110296 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1008 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1008 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1008 target RNA into GAM1008 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7245 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7245 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7245 target RNA into GAM7245 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM110296 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM110296 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM110296

target RNA into GAM110296 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6167 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6167 gene: GAM1008 target protein, GAM7245 target protein and GAM110296 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1008, GAM7245 and GAM110296

GR6168 BM695248 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6168(GR6168) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6168 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6168 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6168 gene encodes GR6168 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6168 precursor RNA folds spatially, forming GR6168 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6168 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6168 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6168 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM18801 precursor RNA and GAM93640 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM18801 RNA and GAM93640 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM18801 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM18801 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM18801 target RNA into GAM18801 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM93640 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM93640 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM93640 target RNA into GAM93640 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6168 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6168 gene: GAM18801 target protein and GAM93640 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM18801 and GAM93640

GR6169 AI969843 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6169(GR6169) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6169 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6169 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6169 gene encodes GR6169 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6169 precursor RNA folds spatially, forming GR6169 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6169 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6169 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6169 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM196748 precursor RNA and GAM323260 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM196748 RNA and GAM323260 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM196748 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM196748 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM196748 target RNA into GAM196748 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM323260 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM323260 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM323260 target RNA into GAM323260 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6169 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6169 gene: GAM196748 target protein and GAM323260 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM196748 and GAM323260

GR6170 AA854617 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6170(GR6170) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6170 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6170 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6170 gene encodes GR6170 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6170 precursor RNA folds spatially, forming GR6170 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6170 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6170 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6170 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2563 precursor RNA and GAM29296 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2563 RNA and GAM29296 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2563 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2563 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2563 target RNA into GAM2563 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM29296 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM29296 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM29296 target RNA into GAM29296 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6170 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6170 gene: GAM2563 target protein and GAM29296 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference,

with references to GAM2563 and GAM29296

GR6171 BG990766 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6171 (GR6171) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6171 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6171 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6171 gene encodes GR6171 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6171 precursor RNA folds spatially, forming GR6171 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6171 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6171 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6171 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM61 precursor RNA and GAM312334 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM61 RNA and GAM312334 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM61 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM61 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM61 target RNA into GAM61 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM312334 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM312334 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM312334 target RNA into GAM312334 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6171 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6171 gene: GAM61 target protein and GAM312334 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM61 and GAM312334

GR6172 AW177184 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6172(GR6172) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6172 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6172 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6172 gene encodes GR6172 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6172 precursor RNA folds spatially, forming GR6172 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6172 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6172 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6172 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM166357 precursor RNA and GAM292151 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM166357 RNA and GAM292151 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding

to GAM RNA of Fig. 8.

GAM166357 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM166357 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM166357 target RNA into GAM166357 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM292151 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM292151 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM292151 target RNA into GAM292151 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6172 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6172 gene: GAM166357 target protein and GAM292151 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM166357 and GAM292151

GR6173 BF700316 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6173(GR6173) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6173 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6173 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6173 gene encodes GR6173 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6173 precursor RNA folds spatially, forming GR6173 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6173 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6173 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR6173 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2951 precursor RNA, GAM124480 precursor RNA and GAM196991 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2951 RNA, GAM124480 RNA and GAM196991 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2951 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2951 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2951 target RNA into GAM2951 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM124480 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM124480 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM124480 target RNA into GAM124480 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM196991 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM196991 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM196991 target RNA into GAM196991 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6173 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6173 gene: GAM2951 target protein, GAM124480 target protein and GAM196991 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2951, GAM124480 and GAM196991

GR6174 AW984116 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6174(GR6174) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6174 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6174 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6174 gene encodes GR6174 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6174 precursor RNA folds spatially, forming GR6174 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6174 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6174 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6174 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1105 precursor RNA and GAM1792 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1105 RNA and GAM1792 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1105 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1105 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1105 target RNA into GAM1105 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM1792 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1792 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds

to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1792 target RNA into GAM1792 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6174 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6174 gene: GAM1105 target protein and GAM1792 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1105 and GAM1792

GR6175 BG956520 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6175(GR6175) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6175 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6175 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6175 gene encodes GR6175 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6175 precursor RNA folds spatially, forming GR6175 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6175 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6175 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6175 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM352 precursor RNA and GAM10404 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM352 RNA and GAM10404 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM352 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM352 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM352 target RNA into GAM352 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM10404 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM10404 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM10404 target RNA into GAM10404 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6175 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6175 gene: GAM352 target protein and GAM10404 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM352 and GAM10404

GR6176 BI464334 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6176(GR6176) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6176 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6176 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6176 gene encodes GR6176 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6176 precursor RNA folds spatially, forming GR6176 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6176 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6176 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6176 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM177 precursor RNA, GAM83722 precursor RNA and GAM224382 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM177 RNA, GAM83722 RNA and GAM224382 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM177 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM177 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM177 target RNA into GAM177 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM83722 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM83722 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM83722 target RNA into GAM83722 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM224382 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM224382 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM224382 target RNA into GAM224382 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6176 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6176 gene: GAM177 target protein, GAM83722 target protein and GAM224382 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM177, GAM83722 and GAM224382

GR6177 BG260140 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6177(GR6177) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6177 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6177 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6177 gene encodes GR6177 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6177 precursor RNA folds spatially, forming GR6177 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6177 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6177 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6177 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM39081 precursor RNA and GAM272662 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM39081 RNA and GAM272662 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM39081 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM39081 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM39081 target RNA into GAM39081 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM272662 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM272662 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM272662 target RNA into GAM272662 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6177 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6177 gene: GAM39081 target protein and GAM272662 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM39081 and GAM272662

GR6178 AA424770 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6178(GR6178) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6178 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6178 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6178 gene encodes GR6178 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6178 precursor RNA folds spatially, forming GR6178 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6178 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6178 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6178 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM9835 precursor RNA, GAM92982 precursor RNA and GAM93435 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM9835 RNA, GAM92982 RNA and GAM93435 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM9835 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM9835 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM9835 target RNA into GAM9835 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM92982 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM92982 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM92982 target RNA into GAM92982 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM93435 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM93435 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM93435 target RNA into GAM93435 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6178 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6178 gene: GAM9835 target protein, GAM92982 target protein and GAM93435 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM9835, GAM92982 and GAM93435

GR6179 AA628057 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6179(GR6179) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6179 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6179 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6179 gene encodes GR6179 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6179 precursor RNA folds spatially, forming GR6179 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6179 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6179 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6179 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM580 precursor RNA, GAM7165 precursor RNA and GAM301981 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM580 RNA, GAM7165 RNA and GAM301981 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM580 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM580 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM580 target RNA into GAM580 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7165 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7165 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7165 target RNA into GAM7165 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM301981 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM301981 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM301981 target RNA into GAM301981 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly

utilities, of GR6179 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6179 gene: GAM580 target protein, GAM7165 target protein and GAM301981 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM580, GAM7165 and GAM301981

GR6180 BQ016665 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6180 (GR6180) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6180 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6180 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6180 gene encodes GR6180 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6180 precursor RNA folds spatially, forming GR6180 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6180 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6180 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6180 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM77178 precursor RNA, GAM237701 precursor RNA and GAM324878 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM77178 RNA, GAM237701 RNA and GAM324878 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM77178 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM77178 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM77178 target RNA into GAM77178 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM237701 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM237701 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM237701 target RNA into GAM237701 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM324878 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM324878 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM324878 target RNA into GAM324878 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6180 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6180 gene: GAM77178 target protein, GAM237701 target protein and GAM324878 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM77178, GAM237701 and GAM324878

GR6181 AW205896 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6181(GR6181) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6181 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6181 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6181 gene encodes GR6181 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6181 precursor RNA folds spatially, forming GR6181 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6181 folded precursor RNA comprises a plurality of what is known in the

art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6181 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6181 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM29490 precursor RNA, GAM49987 precursor RNA and GAM278341 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM29490 RNA, GAM49987 RNA and GAM278341 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM29490 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM29490 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM29490 target RNA into GAM29490 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM49987 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM49987 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM49987 target RNA into GAM49987 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM278341 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM278341 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM278341 target RNA into GAM278341 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6181 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6181 gene: GAM29490 target protein, GAM49987 target protein and GAM278341 target protein, herein

schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM29490, GAM49987 and GAM278341

GR6182 BG474441 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6182(GR6182) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6182 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6182 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6182 gene encodes GR6182 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6182 precursor RNA folds spatially, forming GR6182 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6182 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6182 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6182 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM91740 precursor RNA, GAM223283 precursor RNA and GAM277855 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM91740 RNA, GAM223283 RNA and GAM277855 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM91740 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM91740 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM91740 target RNA into GAM91740 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM223283 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM223283 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM223283 target RNA into GAM223283 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM277855 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM277855 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM277855 target RNA into GAM277855 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6182 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6182 gene: GAM91740 target protein, GAM223283 target protein and GAM277855 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM91740, GAM223283 and GAM277855

GR6183 AI952711 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6183(GR6183) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6183 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6183 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6183 gene encodes GR6183 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6183 precursor RNA folds spatially, forming GR6183 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6183 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6183 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR6183 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2047 precursor RNA, GAM148319 precursor RNA and GAM328676 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2047 RNA, GAM148319 RNA and GAM328676 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2047 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2047 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2047 target RNA into GAM2047 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM148319 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM148319 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM148319 target RNA into GAM148319 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM328676 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM328676 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM328676 target RNA into GAM328676 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6183 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6183 gene: GAM2047 target protein, GAM148319 target protein and GAM328676 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2047, GAM148319 and GAM328676

GR6184 BF307055 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6184(GR6184) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6184 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6184 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6184 gene encodes GR6184 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6184 precursor RNA folds spatially, forming GR6184 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6184 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6184 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6184 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5265 precursor RNA and GAM224812 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5265 RNA and GAM224812 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5265 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5265 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5265 target RNA into GAM5265 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM224812 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM224812 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM224812 target RNA into GAM224812 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6184 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6184 gene: GAM5265 target protein and GAM224812 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5265 and GAM224812

GR6185 BI262352 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6185(GR6185) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6185 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6185 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6185 gene encodes GR6185 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6185 precursor RNA folds spatially, forming GR6185 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6185 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6185 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6185 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM3999 precursor RNA, GAM116573 precursor RNA, GAM134925 precursor RNA and GAM150698 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3999 RNA, GAM116573 RNA, GAM134925 RNA and GAM150698 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of

which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3999 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3999 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3999 target RNA into GAM3999 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM116573 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM116573 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM116573 target RNA into GAM116573 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM134925 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM134925 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM134925 target RNA into GAM134925 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM150698 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM150698 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM150698 target RNA into GAM150698 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6185 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6185 gene: GAM3999 target protein, GAM116573 target protein, GAM134925 target protein and GAM150698 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3999, GAM116573, GAM134925 and GAM150698

GR6186 BM807694 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6186(GR6186) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR6186 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6186 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6186 gene encodes GR6186 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6186 precursor RNA folds spatially, forming GR6186 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6186 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6186 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6186 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM7047 precursor RNA, GAM278337 precursor RNA and GAM319284 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7047 RNA, GAM278337 RNA and GAM319284 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7047 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7047 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7047 target RNA into GAM7047 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM278337 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM278337 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM278337 target RNA into GAM278337 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM319284 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM319284 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM319284 target RNA into GAM319284 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6186 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6186 gene: GAM7047 target protein, GAM278337 target protein and GAM319284 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7047, GAM278337 and GAM319284

GR6187 AV725411 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6187(GR6187) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6187 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6187 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6187 gene encodes GR6187 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6187 precursor RNA folds spatially, forming GR6187 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6187 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6187 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6187 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM5643 precursor RNA, GAM44307 precursor RNA and GAM133174 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5643 RNA, GAM44307 RNA and GAM133174 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5643 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5643 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5643 target RNA into GAM5643 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM44307 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM44307 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM44307 target RNA into GAM44307 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM133174 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM133174 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM133174 target RNA into GAM133174 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6187 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6187 gene: GAM5643 target protein, GAM44307 target protein and GAM133174 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5643, GAM44307 and GAM133174

GR6188 AW291580 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6188(GR6188) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6188 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6188

gene was detected is described hereinabove with reference to Figs. 8-18.

GR6188 gene encodes GR6188 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6188 precursor RNA folds spatially, forming GR6188 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6188 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6188 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6188 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM220912 precursor RNA and GAM240127 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM220912 RNA and GAM240127 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM220912 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM220912 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM220912 target RNA into GAM220912 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM240127 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM240127 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM240127 target RNA into GAM240127 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6188 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6188 gene: GAM220912 target protein and GAM240127 target protein, herein schematically represented by GAM1

TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM220912 and GAM240127

GR6189 BM847626 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6189(GR6189) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6189 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6189 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6189 gene encodes GR6189 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6189 precursor RNA folds spatially, forming GR6189 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6189 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6189 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6189 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4822 precursor RNA, GAM20359 precursor RNA and GAM171912 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4822 RNA, GAM20359 RNA and GAM171912 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4822 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4822 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4822 target RNA into GAM4822 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM20359 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM20359 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM20359 target RNA into GAM20359 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM171912 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM171912 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM171912 target RNA into GAM171912 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6189 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6189 gene: GAM4822 target protein, GAM20359 target protein and GAM171912 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4822, GAM20359 and GAM171912

GR6190 BF757294 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6190(GR6190) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6190 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6190 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6190 gene encodes GR6190 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6190 precursor RNA folds spatially, forming GR6190 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6190 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6190 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6190 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3703 precursor RNA, GAM13365 precursor RNA and GAM319120 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3703 RNA, GAM13365 RNA and GAM319120 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3703 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3703 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3703 target RNA into GAM3703 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM13365 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM13365 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM13365 target RNA into GAM13365 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM319120 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM319120 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM319120 target RNA into GAM319120 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6190 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6190 gene: GAM3703 target protein, GAM13365 target protein and GAM319120 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3703, GAM13365 and GAM319120

GR6191 BF930733 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6191 (GR6191) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6191 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6191 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6191 gene encodes GR6191 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6191 precursor RNA folds spatially, forming GR6191 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6191 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6191 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6191 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM6901 precursor RNA, GAM33905 precursor RNA and GAM306979 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6901 RNA, GAM33905 RNA and GAM306979 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6901 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6901 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6901 target RNA into GAM6901 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM33905 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM33905 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM33905 target RNA into GAM33905 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM306979 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM306979 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM306979 target RNA into GAM306979 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6191 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6191 gene: GAM6901 target protein, GAM33905 target protein and GAM306979 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6901, GAM33905 and GAM306979

GR6192 BI008186 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6192(GR6192) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6192 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6192 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6192 gene encodes GR6192 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6192 precursor RNA folds spatially, forming GR6192 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6192 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6192 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6192 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM159447 precursor RNA, GAM163808 precursor RNA,

GAM173432 precursor RNA and GAM189409 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM159447 RNA, GAM163808 RNA, GAM173432 RNA and GAM189409 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM159447 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM159447 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM159447 target RNA into GAM159447 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM163808 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM163808 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM163808 target RNA into GAM163808 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM173432 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM173432 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM173432 target RNA into GAM173432 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM189409 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM189409 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM189409 target RNA into GAM189409 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6192 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6192 gene: GAM159447 target protein, GAM163808 target protein, GAM173432 target protein and GAM189409 target protein, herein schematically represented by GAM1 TARGET PROTEIN

through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM159447, GAM163808, GAM173432 and GAM189409

GR6193 BQ021077 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6193(GR6193) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6193 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6193 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6193 gene encodes GR6193 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6193 precursor RNA folds spatially, forming GR6193 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6193 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6193 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6193 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM314443 precursor RNA and GAM336053 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM314443 RNA and GAM336053 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM314443 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM314443 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM314443 target RNA into GAM314443 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336053 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336053 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336053 target RNA into GAM336053 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6193 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6193 gene: GAM314443 target protein and GAM336053 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM314443 and GAM336053

GR6194 BI495684 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6194(GR6194) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6194 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6194 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6194 gene encodes GR6194 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6194 precursor RNA folds spatially, forming GR6194 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6194 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6194 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6194 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6734 precursor RNA and GAM91848 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM6734 RNA and GAM91848 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6734 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6734 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6734 target RNA into GAM6734 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM91848 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM91848 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM91848 target RNA into GAM91848 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6194 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6194 gene: GAM6734 target protein and GAM91848 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6734 and GAM91848

GR6195 BE567868 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6195(GR6195) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6195 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6195 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6195 gene encodes GR6195 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6195 precursor RNA folds spatially, forming GR6195 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6195 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6195 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6195 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8553 precursor RNA and GAM314530 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8553 RNA and GAM314530 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8553 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8553 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8553 target RNA into GAM8553 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM314530 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM314530 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM314530 target RNA into GAM314530 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6195 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6195 gene: GAM8553 target protein and GAM314530 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8553 and GAM314530

GR6196 BF889248 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6196(GR6196) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6196 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6196 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6196 gene encodes GR6196 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6196 precursor RNA folds spatially, forming GR6196 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6196 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6196 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6196 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM64339 precursor RNA and GAM320869 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM64339 RNA and GAM320869 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM64339 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM64339 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM64339 target RNA into GAM64339 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM320869 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM320869 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM320869 target RNA into GAM320869 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6196 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR6196 gene: GAM64339 target protein and GAM320869 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM64339 and GAM320869

GR6197 BM016243 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6197(GR6197) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6197 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6197 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6197 gene encodes GR6197 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6197 precursor RNA folds spatially, forming GR6197 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6197 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6197 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6197 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM64062 precursor RNA and GAM146261 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM64062 RNA and GAM146261 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM64062 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM64062 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM64062 target RNA into GAM64062 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM146261 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM146261 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM146261 target RNA into GAM146261 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6197 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6197 gene: GAM64062 target protein and GAM146261 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM64062 and GAM146261

GR6198 BF694959 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6198(GR6198) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6198 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6198 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6198 gene encodes GR6198 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6198 precursor RNA folds spatially, forming GR6198 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6198 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6198 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6198 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1466 precursor RNA and GAM319036 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1466 RNA and GAM319036 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1466 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1466 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1466 target RNA into GAM1466 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM319036 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM319036 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM319036 target RNA into GAM319036 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6198 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6198 gene: GAM1466 target protein and GAM319036 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1466 and GAM319036

GR6199 BI825559 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6199(GR6199) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6199 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6199 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6199 gene encodes GR6199 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6199 precursor RNA folds spatially, forming GR6199 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6199 folded precursor RNA comprises a plurality of what is known in the

art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6199 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6199 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM83990 precursor RNA, GAM224595 precursor RNA and GAM327437 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM83990 RNA, GAM224595 RNA and GAM327437 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM83990 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM83990 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM83990 target RNA into GAM83990 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM224595 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM224595 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM224595 target RNA into GAM224595 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM327437 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM327437 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM327437 target RNA into GAM327437 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6199 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6199 gene: GAM83990 target protein, GAM224595 target protein and GAM327437 target protein, herein

schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM83990, GAM224595 and GAM327437

GR6200 BG118685 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6200(GR6200) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6200 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6200 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6200 gene encodes GR6200 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6200 precursor RNA folds spatially, forming GR6200 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6200 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6200 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6200 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM18040 precursor RNA and GAM188730 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM18040 RNA and GAM188730 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM18040 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM18040 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM18040 target RNA into GAM18040 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM188730 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM188730 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM188730 target RNA into GAM188730 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6200 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6200 gene: GAM18040 target protein and GAM188730 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM18040 and GAM188730

GR6201 AI741608 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6201 (GR6201) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6201 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6201 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6201 gene encodes GR6201 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6201 precursor RNA folds spatially, forming GR6201 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6201 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6201 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6201 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7686 precursor RNA and GAM160753 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7686 RNA and GAM160753 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7686 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7686 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7686 target RNA into GAM7686 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM160753 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM160753 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM160753 target RNA into GAM160753 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6201 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6201 gene: GAM7686 target protein and GAM160753 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7686 and GAM160753

GR6202 BG488903 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6202(GR6202) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6202 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6202 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6202 gene encodes GR6202 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6202 precursor RNA folds spatially, forming GR6202 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6202 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR6202 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6202 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1030 precursor RNA and GAM213865 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1030 RNA and GAM213865 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1030 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1030 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1030 target RNA into GAM1030 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM213865 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM213865 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM213865 target RNA into GAM213865 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6202 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6202 gene: GAM1030 target protein and GAM213865 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1030 and GAM213865

GR6203 BE260052 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6203(GR6203) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6203 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6203 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6203 gene encodes GR6203 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6203 precursor RNA folds spatially, forming GR6203 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6203 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6203 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6203 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM181083 precursor RNA and GAM224839 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM181083 RNA and GAM224839 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM181083 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM181083 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM181083 target RNA into GAM181083 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM224839 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM224839 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM224839 target RNA into GAM224839 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6203 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6203 gene: GAM181083 target protein and GAM224839 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM181083 and GAM224839

GR6204 R14503 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6204(GR6204) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6204 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6204 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6204 gene encodes GR6204 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6204 precursor RNA folds spatially, forming GR6204 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6204 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6204 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6204 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM18428 precursor RNA, GAM208396 precursor RNA and GAM233012 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM18428 RNA, GAM208396 RNA and GAM233012 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM18428 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM18428 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM18428 target RNA into GAM18428 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM208396 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM208396 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM208396 target RNA into GAM208396 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM233012 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM233012 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM233012 target RNA into GAM233012 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6204 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6204 gene: GAM18428 target protein, GAM208396 target protein and GAM233012 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM18428, GAM208396 and GAM233012

GR6205 AV711769 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6205(GR6205) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6205 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6205 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6205 gene encodes GR6205 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6205 precursor RNA folds spatially, forming GR6205 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6205 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6205 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6205 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM18177 precursor RNA, GAM214736 precursor RNA and GAM304947 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM18177 RNA, GAM214736 RNA and GAM304947 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM18177 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM18177 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM18177 target RNA into GAM18177 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM214736 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM214736 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM214736 target RNA into GAM214736 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM304947 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM304947 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM304947 target RNA into GAM304947 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6205 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6205 gene: GAM18177 target protein, GAM214736 target protein and GAM304947 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6,

hereby incorporated by reference, with references to GAM18177, GAM214736 and GAM304947

GR6206 BI255456 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6206(GR6206) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6206 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6206 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6206 gene encodes GR6206 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6206 precursor RNA folds spatially, forming GR6206 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6206 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6206 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6206 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM5638 precursor RNA, GAM91068 precursor RNA, GAM100353 precursor RNA and GAM151907 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5638 RNA, GAM91068 RNA, GAM100353 RNA and GAM151907 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5638 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5638 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5638 target RNA into GAM5638 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM91068 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM91068 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM91068 target RNA into GAM91068 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM100353 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM100353 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM100353 target RNA into GAM100353 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM151907 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM151907 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM151907 target RNA into GAM151907 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6206 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6206 gene: GAM5638 target protein, GAM91068 target protein, GAM100353 target protein and GAM151907 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5638, GAM91068, GAM100353 and GAM151907

GR6207 BQ003799 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6207(GR6207) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6207 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6207 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6207 gene encodes GR6207 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6207 precursor RNA folds spatially, forming GR6207 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6207 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6207 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6207 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM64736 precursor RNA, GAM101263 precursor RNA and GAM216040 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM64736 RNA, GAM101263 RNA and GAM216040 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM64736 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM64736 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM64736 target RNA into GAM64736 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM101263 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM101263 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM101263 target RNA into GAM101263 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM216040 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM216040 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM216040 target RNA into GAM216040 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6207 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR6207 gene: GAM64736 target protein, GAM101263 target protein and GAM216040 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM64736, GAM101263 and GAM216040

GR6208 BG678227 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6208(GR6208) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6208 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6208 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6208 gene encodes GR6208 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6208 precursor RNA folds spatially, forming GR6208 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6208 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6208 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6208 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6009 precursor RNA and GAM41871 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6009 RNA and GAM41871 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6009 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6009 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6009 target RNA into

GAM6009 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM41871 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM41871 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM41871 target RNA into GAM41871 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6208 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6208 gene: GAM6009 target protein and GAM41871 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6009 and GAM41871

GR6209 BG461044 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6209(GR6209) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6209 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6209 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6209 gene encodes GR6209 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6209 precursor RNA folds spatially, forming GR6209 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6209 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6209 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6209 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM739 precursor RNA and GAM173082 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM739 RNA and GAM173082 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM739 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM739 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM739 target RNA into GAM739 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM173082 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM173082 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM173082 target RNA into GAM173082 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6209 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6209 gene: GAM739 target protein and GAM173082 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM739 and GAM173082

GR6210 BE540498 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6210(GR6210) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6210 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6210 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6210 gene encodes GR6210 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6210 precursor RNA folds spatially, forming GR6210 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated

that GR6210 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6210 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6210 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM60212 precursor RNA and GAM283406 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM60212 RNA and GAM283406 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM60212 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM60212 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM60212 target RNA into GAM60212 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM283406 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM283406 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM283406 target RNA into GAM283406 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6210 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6210 gene: GAM60212 target protein and GAM283406 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM60212 and GAM283406

GR6211 BE813308 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6211(GR6211) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR6211 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6211 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6211 gene encodes GR6211 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6211 precursor RNA folds spatially, forming GR6211 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6211 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6211 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6211 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM82337 precursor RNA, GAM230026 precursor RNA and GAM295844 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM82337 RNA, GAM230026 RNA and GAM295844 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM82337 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM82337 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM82337 target RNA into GAM82337 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM230026 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM230026 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM230026 target RNA into GAM230026 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM295844 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM295844 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM295844 target RNA into GAM295844 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6211 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6211 gene: GAM82337 target protein, GAM230026 target protein and GAM295844 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM82337, GAM230026 and GAM295844

GR6212 AU127870 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6212(GR6212) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6212 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6212 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6212 gene encodes GR6212 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6212 precursor RNA folds spatially, forming GR6212 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6212 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6212 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6212 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM51709 precursor RNA, GAM120111 precursor RNA and GAM324632 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM51709 RNA, GAM120111 RNA and GAM324632 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM51709 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM51709 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM51709 target RNA into GAM51709 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM120111 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM120111 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM120111 target RNA into GAM120111 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM324632 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM324632 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM324632 target RNA into GAM324632 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6212 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6212 gene: GAM51709 target protein, GAM120111 target protein and GAM324632 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM51709, GAM120111 and GAM324632

GR6213 BF130941 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6213(GR6213) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6213 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR6213 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6213 gene encodes GR6213 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6213 precursor RNA folds spatially, forming GR6213 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6213 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6213 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6213 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM277 precursor RNA, GAM7655 precursor RNA, GAM41665 precursor RNA and GAM235188 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM277 RNA, GAM7655 RNA, GAM41665 RNA and GAM235188 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM277 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM277 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM277 target RNA into GAM277 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7655 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7655 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7655 target RNA into GAM7655 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM41665 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM41665 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM41665 target RNA into GAM41665 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM235188 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM235188 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM235188 target RNA into GAM235188 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6213 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6213 gene: GAM277 target protein, GAM7655 target protein, GAM41665 target protein and GAM235188 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM277, GAM7655, GAM41665 and GAM235188

GR6214 BF310820 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6214(GR6214) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6214 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6214 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6214 gene encodes GR6214 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6214 precursor RNA folds spatially, forming GR6214 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6214 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6214 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6214 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM118410 precursor RNA and GAM148192 precursor

RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM118410 RNA and GAM148192 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM118410 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM118410 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM118410 target RNA into GAM118410 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM148192 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM148192 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM148192 target RNA into GAM148192 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6214 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6214 gene: GAM118410 target protein and GAM148192 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM118410 and GAM148192

GR6215 AW582435 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6215(GR6215) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6215 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6215 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6215 gene encodes GR6215 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6215 precursor RNA folds spatially, forming GR6215 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6215 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6215 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6215 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM49558 precursor RNA and GAM200060 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM49558 RNA and GAM200060 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM49558 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM49558 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM49558 target RNA into GAM49558 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM200060 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM200060 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM200060 target RNA into GAM200060 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6215 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6215 gene: GAM49558 target protein and GAM200060 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM49558 and GAM200060

bioinformatically detected regulatory gene, referred to here as Genomic Record 6216(GR6216) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6216 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6216 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6216 gene encodes GR6216 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6216 precursor RNA folds spatially, forming GR6216 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6216 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6216 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6216 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM99559 precursor RNA, GAM132237 precursor RNA, GAM137296 precursor RNA and GAM308410 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM99559 RNA, GAM132237 RNA, GAM137296 RNA and GAM308410 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM99559 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM99559 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM99559 target RNA into GAM99559 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM132237 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM132237 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM132237 target RNA into GAM132237 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM137296 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM137296 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM137296 target RNA into GAM137296 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM308410 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM308410 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM308410 target RNA into GAM308410 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6216 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6216 gene: GAM99559 target protein, GAM132237 target protein, GAM137296 target protein and GAM308410 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM99559, GAM132237, GAM137296 and GAM308410

GR6217 AV750121 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6217(GR6217) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6217 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6217 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6217 gene encodes GR6217 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6217 precursor RNA folds spatially, forming GR6217 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6217 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6217 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6217 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1851 precursor RNA and GAM308418 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1851 RNA and GAM308418 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1851 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1851 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1851 target RNA into GAM1851 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM308418 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM308418 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM308418 target RNA into GAM308418 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6217 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6217 gene: GAM1851 target protein and GAM308418 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1851 and GAM308418

GR6218 N51413 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6218(GR6218) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6218 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6218 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6218 gene encodes GR6218 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6218 precursor RNA folds spatially, forming GR6218 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6218 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6218 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6218 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3417 precursor RNA and GAM171421 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3417 RNA and GAM171421 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3417 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3417 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3417 target RNA into GAM3417 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM171421 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM171421 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM171421 target RNA into GAM171421 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6218 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR6218 gene: GAM3417 target protein and GAM171421 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3417 and GAM171421

GR6219 BM678660 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6219 (GR6219) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6219 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6219 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6219 gene encodes GR6219 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6219 precursor RNA folds spatially, forming GR6219 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6219 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6219 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6219 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM137568 precursor RNA, GAM209841 precursor RNA and GAM250507 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM137568 RNA, GAM209841 RNA and GAM250507 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM137568 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM137568 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM137568

target RNA into GAM137568 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM209841 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM209841 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM209841 target RNA into GAM209841 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM250507 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM250507 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM250507 target RNA into GAM250507 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6219 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6219 gene: GAM137568 target protein, GAM209841 target protein and GAM250507 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM137568, GAM209841 and GAM250507

GR6220 BM704003 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6220(GR6220) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6220 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6220 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6220 gene encodes GR6220 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6220 precursor RNA folds spatially, forming GR6220 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6220 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6220 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6220 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM40353 precursor RNA and GAM263509 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM40353 RNA and GAM263509 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM40353 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM40353 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM40353 target RNA into GAM40353 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM263509 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM263509 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM263509 target RNA into GAM263509 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6220 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6220 gene: GAM40353 target protein and GAM263509 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM40353 and GAM263509

GR6221 BF512557 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6221 (GR6221) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6221 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR6221 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6221 gene encodes GR6221 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6221 precursor RNA folds spatially, forming GR6221 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6221 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6221 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6221 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6290 precursor RNA and GAM330503 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6290 RNA and GAM330503 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6290 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6290 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6290 target RNA into GAM6290 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM330503 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM330503 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM330503 target RNA into GAM330503 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6221 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6221 gene: GAM6290 target

protein and GAM330503 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6290 and GAM330503

GR6222 BF241482 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6222(GR6222) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6222 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6222 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6222 gene encodes GR6222 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6222 precursor RNA folds spatially, forming GR6222 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6222 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6222 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6222 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4587 precursor RNA, GAM31129 precursor RNA and GAM251154 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4587 RNA, GAM31129 RNA and GAM251154 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4587 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4587 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4587 target RNA into GAM4587 target protein, herein schematically represented by GAM1 TARGET

PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM31129 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM31129 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM31129 target RNA into GAM31129 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM251154 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM251154 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM251154 target RNA into GAM251154 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6222 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6222 gene: GAM4587 target protein, GAM31129 target protein and GAM251154 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4587, GAM31129 and GAM251154

GR6223 BM129159 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6223(GR6223) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6223 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6223 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6223 gene encodes GR6223 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6223 precursor RNA folds spatially, forming GR6223 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6223 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6223 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR6223 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1494 precursor RNA, GAM277024 precursor RNA and GAM305349 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1494 RNA, GAM277024 RNA and GAM305349 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1494 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1494 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1494 target RNA into GAM1494 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM277024 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM277024 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM277024 target RNA into GAM277024 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM305349 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM305349 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM305349 target RNA into GAM305349 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6223 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6223 gene: GAM1494 target protein, GAM277024 target protein and GAM305349 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1494, GAM277024 and GAM305349

GR6224 AW961824 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6224(GR6224) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6224 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6224 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6224 gene encodes GR6224 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6224 precursor RNA folds spatially, forming GR6224 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6224 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6224 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6224 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM128609 precursor RNA and GAM295830 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM128609 RNA and GAM295830 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM128609 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM128609 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM128609 target RNA into GAM128609 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM295830 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM295830 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM295830 target RNA into GAM295830 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6224 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6224 gene: GAM128609 target protein and GAM295830 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM128609 and GAM295830

GR6225 BG288011 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6225(GR6225) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6225 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6225 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6225 gene encodes GR6225 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6225 precursor RNA folds spatially, forming GR6225 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6225 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6225 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6225 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6322 precursor RNA and GAM275471 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6322 RNA and GAM275471 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6322 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6322 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6322 target RNA into GAM6322 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM275471 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM275471 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM275471 target RNA into GAM275471 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6225 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6225 gene: GAM6322 target protein and GAM275471 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6322 and GAM275471

GR6226 AA099518 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6226(GR6226) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6226 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6226 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6226 gene encodes GR6226 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6226 precursor RNA folds spatially, forming GR6226 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6226 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6226 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6226 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM90572 precursor RNA and GAM258724 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM90572 RNA and GAM258724 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM90572 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM90572 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM90572 target RNA into GAM90572 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM258724 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM258724 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM258724 target RNA into GAM258724 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6226 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6226 gene: GAM90572 target protein and GAM258724 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM90572 and GAM258724

GR6227 BE005276 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6227(GR6227) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6227 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6227 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6227 gene encodes GR6227 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6227 precursor RNA folds spatially, forming GR6227 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6227 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6227 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6227 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5832 precursor RNA and GAM226279 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5832 RNA and GAM226279 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5832 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5832 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5832 target RNA into GAM5832 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM226279 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM226279 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM226279 target RNA into GAM226279 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6227 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6227 gene: GAM5832 target protein and GAM226279 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes

is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5832 and GAM226279

GR6228 R99941 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6228(GR6228) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6228 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6228 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6228 gene encodes GR6228 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6228 precursor RNA folds spatially, forming GR6228 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6228 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6228 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6228 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM266239 precursor RNA and GAM286688 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM266239 RNA and GAM286688 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM266239 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM266239 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM266239 target RNA into GAM266239 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM286688 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM286688 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM286688 target RNA into GAM286688 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6228 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6228 gene: GAM266239 target protein and GAM286688 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM266239 and GAM286688

GR6229 AI560154 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6229(GR6229) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6229 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6229 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6229 gene encodes GR6229 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6229 precursor RNA folds spatially, forming GR6229 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6229 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6229 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6229 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM6176 precursor RNA, GAM163698 precursor RNA and GAM336014 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM6176 RNA, GAM163698 RNA and GAM336014 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6176 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6176 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6176 target RNA into GAM6176 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM163698 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM163698 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM163698 target RNA into GAM163698 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336014 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336014 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336014 target RNA into GAM336014 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6229 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6229 gene: GAM6176 target protein, GAM163698 target protein and GAM336014 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6176, GAM163698 and GAM336014

GR6230 AI131180 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6230(GR6230) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6230 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6230 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6230 gene encodes GR6230 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6230 precursor RNA folds spatially, forming GR6230 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6230 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6230 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6230 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM35929 precursor RNA and GAM220358 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM35929 RNA and GAM220358 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM35929 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM35929 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM35929 target RNA into GAM35929 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM220358 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM220358 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM220358 target RNA into GAM220358 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6230 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6230 gene: GAM35929 target protein and GAM220358 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference,

with references to GAM35929 and GAM220358

GR6231 BM795442 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6231 (GR6231) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6231 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6231 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6231 gene encodes GR6231 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6231 precursor RNA folds spatially, forming GR6231 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6231 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6231 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6231 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2066 precursor RNA and GAM5439 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2066 RNA and GAM5439 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2066 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2066 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2066 target RNA into GAM2066 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5439 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5439 target RNA, herein schematically represented by

GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5439 target RNA into GAM5439 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6231 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6231 gene: GAM2066 target protein and GAM5439 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2066 and GAM5439

GR6232 BI225419 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6232(GR6232) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6232 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6232 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6232 gene encodes GR6232 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6232 precursor RNA folds spatially, forming GR6232 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6232 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6232 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6232 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM70689 precursor RNA and GAM288282 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM70689 RNA and GAM288282 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding

to GAM RNA of Fig. 8.

GAM70689 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM70689 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM70689 target RNA into GAM70689 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM288282 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM288282 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM288282 target RNA into GAM288282 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6232 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6232 gene: GAM70689 target protein and GAM288282 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM70689 and GAM288282

GR6233 BI520884 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6233(GR6233) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6233 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6233 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6233 gene encodes GR6233 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6233 precursor RNA folds spatially, forming GR6233 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6233 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6233 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR6233 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM101686 precursor RNA, GAM109716 precursor RNA and GAM256271 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM101686 RNA, GAM109716 RNA and GAM256271 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM101686 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM101686 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM101686 target RNA into GAM101686 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM109716 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM109716 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM109716 target RNA into GAM109716 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM256271 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM256271 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM256271 target RNA into GAM256271 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6233 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6233 gene: GAM101686 target protein, GAM109716 target protein and GAM256271 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM101686, GAM109716 and GAM256271

GR6234 BE503149 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6234(GR6234) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6234 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6234 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6234 gene encodes GR6234 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6234 precursor RNA folds spatially, forming GR6234 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6234 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6234 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6234 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM261659 precursor RNA and GAM305361 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM261659 RNA and GAM305361 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM261659 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM261659 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM261659 target RNA into GAM261659 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM305361 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM305361 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM305361 target RNA into GAM305361 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6234 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6234 gene: GAM261659 target protein and GAM305361 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM261659 and GAM305361

GR6235 BM723500 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6235(GR6235) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6235 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6235 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6235 gene encodes GR6235 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6235 precursor RNA folds spatially, forming GR6235 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6235 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6235 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6235 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM229689 precursor RNA and GAM258202 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM229689 RNA and GAM258202 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM229689 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM229689 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM229689 target RNA into GAM229689 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM258202 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM258202 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM258202 target RNA into GAM258202 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6235 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6235 gene: GAM229689 target protein and GAM258202 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM229689 and GAM258202

GR6236 AW936516 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6236(GR6236) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6236 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6236 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6236 gene encodes GR6236 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6236 precursor RNA folds spatially, forming GR6236 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6236 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6236 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6236 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM93188 precursor RNA, GAM130701 precursor RNA and GAM220650 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM93188 RNA, GAM130701 RNA and GAM220650 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM93188 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM93188 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM93188 target RNA into GAM93188 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM130701 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM130701 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM130701 target RNA into GAM130701 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM220650 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM220650 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM220650 target RNA into GAM220650 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6236 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6236 gene: GAM93188 target protein, GAM130701 target protein and GAM220650 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM93188, GAM130701 and GAM220650

GR6237 BF105148 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6237(GR6237) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6237 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6237 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6237 gene encodes GR6237 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6237 precursor RNA folds spatially, forming GR6237 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6237 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6237 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6237 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1727 precursor RNA and GAM331941 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1727 RNA and GAM331941 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1727 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1727 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1727 target RNA into GAM1727 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM331941 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM331941 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM331941 target RNA into GAM331941 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6237 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6237 gene: GAM1727 target protein and GAM331941 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1727 and GAM331941

GR6238 BM671654 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6238(GR6238) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6238 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6238 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6238 gene encodes GR6238 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6238 precursor RNA folds spatially, forming GR6238 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6238 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6238 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6238 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM175737 precursor RNA, GAM303377 precursor RNA and GAM326338 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM175737 RNA, GAM303377 RNA and GAM326338 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM175737 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM175737 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM175737 target RNA into GAM175737 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM303377 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM303377 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM303377 target RNA into GAM303377 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM326338 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM326338 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM326338 target RNA into GAM326338 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6238 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6238 gene: GAM175737 target protein, GAM303377 target protein and GAM326338 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM175737, GAM303377 and GAM326338

GR6239 BI964145 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6239(GR6239) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6239 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6239 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6239 gene encodes GR6239 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6239 precursor RNA folds spatially, forming GR6239 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6239 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6239 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6239 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM258792 precursor RNA, GAM264849 precursor RNA and GAM322490 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM258792 RNA, GAM264849 RNA and GAM322490 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM258792 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM258792 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM258792 target RNA into GAM258792 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM264849 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM264849 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM264849 target RNA into GAM264849 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM322490 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM322490 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM322490 target RNA into GAM322490 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly

utilities, of GR6239 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6239 gene: GAM258792 target protein, GAM264849 target protein and GAM322490 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM258792, GAM264849 and GAM322490

GR6240 AA679384 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6240(GR6240) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6240 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6240 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6240 gene encodes GR6240 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6240 precursor RNA folds spatially, forming GR6240 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6240 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6240 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6240 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2307 precursor RNA and GAM51833 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2307 RNA and GAM51833 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2307 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2307 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds

to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2307 target RNA into GAM2307 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM51833 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM51833 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM51833 target RNA into GAM51833 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6240 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6240 gene: GAM2307 target protein and GAM51833 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2307 and GAM51833

GR6241 AW504354 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6241 (GR6241) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6241 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6241 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6241 gene encodes GR6241 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6241 precursor RNA folds spatially, forming GR6241 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6241 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6241 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6241 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4985 precursor RNA and GAM240056 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3

FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4985 RNA and GAM240056 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4985 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4985 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4985 target RNA into GAM4985 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM240056 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM240056 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM240056 target RNA into GAM240056 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6241 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6241 gene: GAM4985 target protein and GAM240056 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4985 and GAM240056

GR6242 BG761082 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6242(GR6242) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6242 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6242 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6242 gene encodes GR6242 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6242 precursor RNA folds spatially, forming GR6242 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6242 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6242 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6242 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6881 precursor RNA and GAM17528 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6881 RNA and GAM17528 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6881 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6881 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6881 target RNA into GAM6881 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM17528 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM17528 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM17528 target RNA into GAM17528 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6242 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6242 gene: GAM6881 target protein and GAM17528 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6881 and GAM17528

6243(GR6243) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6243 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6243 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6243 gene encodes GR6243 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6243 precursor RNA folds spatially, forming GR6243 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6243 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6243 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6243 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5876 precursor RNA and GAM334296 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5876 RNA and GAM334296 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5876 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5876 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5876 target RNA into GAM5876 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM334296 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM334296 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM334296 target RNA into GAM334296 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6243 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6243 gene: GAM5876 target protein and GAM334296 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5876 and GAM334296

GR6244 BE895610 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6244(GR6244) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6244 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6244 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6244 gene encodes GR6244 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6244 precursor RNA folds spatially, forming GR6244 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6244 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6244 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6244 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3623 precursor RNA, GAM6565 precursor RNA and GAM169110 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3623 RNA, GAM6565 RNA and GAM169110 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3623 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3623 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3623 target RNA into GAM3623 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6565 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6565 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6565 target RNA into GAM6565 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM169110 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM169110 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM169110 target RNA into GAM169110 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6244 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6244 gene: GAM3623 target protein, GAM6565 target protein and GAM169110 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3623, GAM6565 and GAM169110

GR6245 H00513 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6245(GR6245) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6245 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6245 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6245 gene encodes GR6245 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6245 precursor RNA folds spatially, forming GR6245 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6245 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6245 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6245 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM202440 precursor RNA and GAM300462 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM202440 RNA and GAM300462 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM202440 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM202440 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM202440 target RNA into GAM202440 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM300462 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM300462 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM300462 target RNA into GAM300462 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6245 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6245 gene: GAM202440 target protein and GAM300462 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM202440 and GAM300462

GR6246 AL049134 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6246(GR6246) gene, which encodes an `operon-like` cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6246 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6246 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6246 gene encodes GR6246 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6246 precursor RNA folds spatially, forming GR6246 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6246 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6246 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6246 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4134 precursor RNA and GAM116816 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4134 RNA and GAM116816 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4134 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4134 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4134 target RNA into GAM4134 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM116816 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM116816 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM116816 target RNA into GAM116816 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6246 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6246 gene: GAM4134 target protein and GAM116816 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4134 and GAM116816

GR6247 BQ052990 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6247(GR6247) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6247 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6247 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6247 gene encodes GR6247 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6247 precursor RNA folds spatially, forming GR6247 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6247 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6247 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6247 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2711 precursor RNA and GAM312614 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2711 RNA and GAM312614 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2711 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2711 target RNA, herein schematically represented by

GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2711 target RNA into GAM2711 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM312614 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM312614 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM312614 target RNA into GAM312614 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6247 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6247 gene: GAM2711 target protein and GAM312614 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2711 and GAM312614

GR6248 BM011121 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6248(GR6248) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6248 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6248 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6248 gene encodes GR6248 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6248 precursor RNA folds spatially, forming GR6248 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6248 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6248 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6248 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM151519 precursor RNA and GAM214328 precursor

RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM151519 RNA and GAM214328 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM151519 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM151519 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM151519 target RNA into GAM151519 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM214328 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM214328 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM214328 target RNA into GAM214328 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6248 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6248 gene: GAM151519 target protein and GAM214328 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM151519 and GAM214328

GR6249 AI040152 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6249(GR6249) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6249 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6249 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6249 gene encodes GR6249 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6249 precursor RNA folds spatially, forming GR6249 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6249 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6249 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6249 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM11870 precursor RNA, GAM17903 precursor RNA, GAM173247 precursor RNA and GAM335952 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM11870 RNA, GAM17903 RNA, GAM173247 RNA and GAM335952 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM11870 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM11870 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM11870 target RNA into GAM11870 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM17903 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM17903 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM17903 target RNA into GAM17903 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM173247 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM173247 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM173247 target RNA into GAM173247 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM335952 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM335952 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM335952 target RNA into GAM335952 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6249 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6249 gene: GAM11870 target protein, GAM17903 target protein, GAM173247 target protein and GAM335952 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM11870, GAM17903, GAM173247 and GAM335952

GR6250 BE616369 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6250(GR6250) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6250 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6250 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6250 gene encodes GR6250 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6250 precursor RNA folds spatially, forming GR6250 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6250 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6250 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6250 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1655 precursor RNA, GAM56362 precursor RNA and GAM60825 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1655 RNA, GAM56362 RNA and GAM60825 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1655 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1655 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1655 target RNA into GAM1655 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM56362 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM56362 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM56362 target RNA into GAM56362 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM60825 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM60825 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM60825 target RNA into GAM60825 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6250 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6250 gene: GAM1655 target protein, GAM56362 target protein and GAM60825 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1655, GAM56362 and GAM60825

GR6251 BI043552 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6251(GR6251) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6251 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6251 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6251 gene encodes GR6251 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6251 precursor RNA folds spatially, forming GR6251 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6251 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6251 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6251 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM82073 precursor RNA and GAM321091 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM82073 RNA and GAM321091 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM82073 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM82073 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM82073 target RNA into GAM82073 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM321091 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM321091 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM321091 target RNA into GAM321091 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6251 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6251 gene: GAM82073 target protein and GAM321091 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes

is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM82073 and GAM321091

GR6252 BI028444 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6252(GR6252) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6252 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6252 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6252 gene encodes GR6252 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6252 precursor RNA folds spatially, forming GR6252 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6252 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6252 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6252 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5326 precursor RNA and GAM62978 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5326 RNA and GAM62978 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5326 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5326 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5326 target RNA into GAM5326 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM62978 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM62978 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM62978 target RNA into GAM62978 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6252 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6252 gene: GAM5326 target protein and GAM62978 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5326 and GAM62978

GR6253 BI198137 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6253(GR6253) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6253 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6253 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6253 gene encodes GR6253 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6253 precursor RNA folds spatially, forming GR6253 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6253 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6253 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6253 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2547 precursor RNA and GAM62684 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2547 RNA and GAM62684 RNA, herein schematically

represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2547 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2547 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2547 target RNA into GAM2547 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM62684 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM62684 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM62684 target RNA into GAM62684 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6253 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6253 gene: GAM2547 target protein and GAM62684 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2547 and GAM62684

GR6254 AA772752 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6254(GR6254) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6254 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6254 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6254 gene encodes GR6254 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6254 precursor RNA folds spatially, forming GR6254 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6254 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6254 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6254 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2654 precursor RNA, GAM96812 precursor RNA and GAM309213 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2654 RNA, GAM96812 RNA and GAM309213 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2654 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2654 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2654 target RNA into GAM2654 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM96812 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM96812 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM96812 target RNA into GAM96812 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM309213 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM309213 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM309213 target RNA into GAM309213 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6254 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6254 gene: GAM2654 target protein, GAM96812 target protein and GAM309213 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2654, GAM96812 and

GR6255 BE790109 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6255(GR6255) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6255 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6255 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6255 gene encodes GR6255 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6255 precursor RNA folds spatially, forming GR6255 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6255 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6255 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6255 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM9316 precursor RNA, GAM10094 precursor RNA and GAM283415 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM9316 RNA, GAM10094 RNA and GAM283415 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM9316 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM9316 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM9316 target RNA into GAM9316 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM10094 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM10094 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM10094 target RNA into GAM10094 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM283415 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM283415 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM283415 target RNA into GAM283415 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6255 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6255 gene: GAM9316 target protein, GAM10094 target protein and GAM283415 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM9316, GAM10094 and GAM283415

GR6256 H11249 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6256(GR6256) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6256 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6256 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6256 gene encodes GR6256 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6256 precursor RNA folds spatially, forming GR6256 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6256 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6256 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6256 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM171712 precursor RNA, GAM222521 precursor RNA and GAM308185 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM171712 RNA, GAM222521 RNA and GAM308185 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM171712 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM171712 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM171712 target RNA into GAM171712 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM222521 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM222521 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM222521 target RNA into GAM222521 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM308185 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM308185 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM308185 target RNA into GAM308185 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6256 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6256 gene: GAM171712 target protein, GAM222521 target protein and GAM308185 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM171712, GAM222521 and GAM308185

6257(GR6257) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6257 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6257 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6257 gene encodes GR6257 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6257 precursor RNA folds spatially, forming GR6257 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6257 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6257 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6257 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6099 precursor RNA and GAM219099 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6099 RNA and GAM219099 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6099 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6099 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6099 target RNA into GAM6099 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM219099 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM219099 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM219099 target RNA into GAM219099 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6257 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6257 gene: GAM6099 target protein and GAM219099 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6099 and GAM219099

GR6258 AV759594 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6258(GR6258) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6258 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6258 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6258 gene encodes GR6258 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6258 precursor RNA folds spatially, forming GR6258 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6258 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6258 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6258 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM10073 precursor RNA and GAM275951 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM10073 RNA and GAM275951 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM10073 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM10073 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM10073 target RNA into GAM10073 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM275951 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM275951 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM275951 target RNA into GAM275951 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6258 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6258 gene: GAM10073 target protein and GAM275951 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM10073 and GAM275951

GR6259 BG769935 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6259(GR6259) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6259 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6259 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6259 gene encodes GR6259 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6259 precursor RNA folds spatially, forming GR6259 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6259 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6259 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6259 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4

separate GAM precursor RNAs, GAM92582 precursor RNA, GAM122121 precursor RNA, GAM242037 precursor RNA and GAM264733 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM92582 RNA, GAM122121 RNA, GAM242037 RNA and GAM264733 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM92582 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM92582 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM92582 target RNA into GAM92582 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM122121 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM122121 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM122121 target RNA into GAM122121 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM242037 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM242037 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM242037 target RNA into GAM242037 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM264733 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM264733 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM264733 target RNA into GAM264733 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6259 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6259 gene: GAM92582 target protein, GAM122121 target protein, GAM242037 target protein and GAM264733

target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM92582, GAM122121, GAM242037 and GAM264733

GR6260 BM312377 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6260(GR6260) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6260 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6260 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6260 gene encodes GR6260 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6260 precursor RNA folds spatially, forming GR6260 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6260 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6260 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6260 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM36461 precursor RNA, GAM64054 precursor RNA and GAM191661 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM36461 RNA, GAM64054 RNA and GAM191661 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM36461 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM36461 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM36461 target RNA into GAM36461 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM64054 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM64054 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM64054 target RNA into GAM64054 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM191661 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM191661 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM191661 target RNA into GAM191661 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6260 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6260 gene: GAM36461 target protein, GAM64054 target protein and GAM191661 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM36461, GAM64054 and GAM191661

GR6261 AI912375 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6261 (GR6261) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6261 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6261 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6261 gene encodes GR6261 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6261 precursor RNA folds spatially, forming GR6261 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6261 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6261 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR6261 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5126 precursor RNA and GAM335990 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5126 RNA and GAM335990 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5126 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5126 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5126 target RNA into GAM5126 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM335990 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM335990 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM335990 target RNA into GAM335990 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6261 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6261 gene: GAM5126 target protein and GAM335990 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5126 and GAM335990

GR6262 BM997388 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6262(GR6262) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6262 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6262

gene was detected is described hereinabove with reference to Figs. 8-18.

GR6262 gene encodes GR6262 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6262 precursor RNA folds spatially, forming GR6262 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6262 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6262 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6262 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1916 precursor RNA and GAM81154 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1916 RNA and GAM81154 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1916 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1916 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1916 target RNA into GAM1916 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM81154 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM81154 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM81154 target RNA into GAM81154 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6262 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6262 gene: GAM1916 target protein and GAM81154 target protein, herein schematically represented by GAM1

TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1916 and GAM81154

GR6263 BI712750 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6263(GR6263) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6263 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6263 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6263 gene encodes GR6263 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6263 precursor RNA folds spatially, forming GR6263 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6263 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6263 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6263 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM57498 precursor RNA and GAM65919 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM57498 RNA and GAM65919 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM57498 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM57498 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM57498 target RNA into GAM57498 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM65919 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM65919 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM65919 target RNA into GAM65919 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6263 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6263 gene: GAM57498 target protein and GAM65919 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM57498 and GAM65919

GR6264 AV763988 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6264(GR6264) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6264 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6264 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6264 gene encodes GR6264 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6264 precursor RNA folds spatially, forming GR6264 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6264 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6264 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6264 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6056 precursor RNA and GAM241999 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM6056 RNA and GAM241999 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6056 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6056 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6056 target RNA into GAM6056 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM241999 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM241999 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM241999 target RNA into GAM241999 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6264 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6264 gene: GAM6056 target protein and GAM241999 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6056 and GAM241999

GR6265 AI672974 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6265(GR6265) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6265 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6265 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6265 gene encodes GR6265 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6265 precursor RNA folds spatially, forming GR6265 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6265 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6265 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6265 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM108845 precursor RNA and GAM265533 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM108845 RNA and GAM265533 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM108845 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM108845 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM108845 target RNA into GAM108845 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM265533 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM265533 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM265533 target RNA into GAM265533 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6265 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6265 gene: GAM108845 target protein and GAM265533 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM108845 and GAM265533

GR6266 BF115247 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6266(GR6266) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6266 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6266 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6266 gene encodes GR6266 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6266 precursor RNA folds spatially, forming GR6266 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6266 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6266 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6266 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM114818 precursor RNA and GAM222584 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM114818 RNA and GAM222584 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM114818 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM114818 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM114818 target RNA into GAM114818 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM222584 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM222584 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM222584 target RNA into GAM222584 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6266 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR6266 gene: GAM114818 target protein and GAM222584 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM114818 and GAM222584

GR6267 AI347928 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6267(GR6267) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6267 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6267 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6267 gene encodes GR6267 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6267 precursor RNA folds spatially, forming GR6267 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6267 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6267 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6267 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM74320 precursor RNA, GAM269290 precursor RNA and GAM310330 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM74320 RNA, GAM269290 RNA and GAM310330 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM74320 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM74320 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM74320

target RNA into GAM74320 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM269290 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM269290 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM269290 target RNA into GAM269290 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM310330 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM310330 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM310330 target RNA into GAM310330 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6267 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6267 gene: GAM74320 target protein, GAM269290 target protein and GAM310330 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM74320, GAM269290 and GAM310330

GR6268 AU142540 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6268(GR6268) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6268 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6268 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6268 gene encodes GR6268 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6268 precursor RNA folds spatially, forming GR6268 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6268 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6268 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6268 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM114998 precursor RNA and GAM132306 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM114998 RNA and GAM132306 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM114998 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM114998 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM114998 target RNA into GAM114998 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM132306 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM132306 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM132306 target RNA into GAM132306 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6268 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6268 gene: GAM114998 target protein and GAM132306 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM114998 and GAM132306

GR6269 AW952479 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6269 (GR6269) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6269 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR6269 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6269 gene encodes GR6269 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6269 precursor RNA folds spatially, forming GR6269 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6269 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6269 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6269 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM88368 precursor RNA, GAM123966 precursor RNA, GAM176719 precursor RNA and GAM216540 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM88368 RNA, GAM123966 RNA, GAM176719 RNA and GAM216540 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM88368 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM88368 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM88368 target RNA into GAM88368 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM123966 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM123966 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM123966 target RNA into GAM123966 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM176719 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM176719 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM176719 target RNA into GAM176719 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM216540 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM216540 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM216540 target RNA into GAM216540 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6269 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6269 gene: GAM88368 target protein, GAM123966 target protein, GAM176719 target protein and GAM216540 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM88368, GAM123966, GAM176719 and GAM216540

GR6270 N71050 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6270(GR6270) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6270 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6270 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6270 gene encodes GR6270 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6270 precursor RNA folds spatially, forming GR6270 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6270 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6270 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6270 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM273945 precursor RNA and GAM277535 precursor

RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM273945 RNA and GAM277535 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM273945 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM273945 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM273945 target RNA into GAM273945 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM277535 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM277535 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM277535 target RNA into GAM277535 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6270 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6270 gene: GAM273945 target protein and GAM277535 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM273945 and GAM277535

GR6271 AA442399 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6271 (GR6271) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6271 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6271 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6271 gene encodes GR6271 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6271 precursor RNA folds spatially, forming GR6271 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6271 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6271 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6271 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7752 precursor RNA and GAM111848 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7752 RNA and GAM111848 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7752 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7752 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7752 target RNA into GAM7752 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM111848 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM111848 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM111848 target RNA into GAM111848 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6271 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6271 gene: GAM7752 target protein and GAM111848 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7752 and GAM111848

bioinformatically detected regulatory gene, referred to here as Genomic Record 6272(GR6272) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6272 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6272 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6272 gene encodes GR6272 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6272 precursor RNA folds spatially, forming GR6272 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6272 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6272 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6272 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM115410 precursor RNA and GAM313592 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM115410 RNA and GAM313592 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM115410 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM115410 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM115410 target RNA into GAM115410 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM313592 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM313592 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM313592

target RNA into GAM313592 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6272 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6272 gene: GAM115410 target protein and GAM313592 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM115410 and GAM313592

GR6273 BM172418 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6273(GR6273) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6273 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6273 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6273 gene encodes GR6273 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6273 precursor RNA folds spatially, forming GR6273 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6273 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6273 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6273 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM99430 precursor RNA and GAM297825 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM99430 RNA and GAM297825 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM99430 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM99430 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM99430 target RNA into GAM99430 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM297825 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM297825 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM297825 target RNA into GAM297825 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6273 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6273 gene: GAM99430 target protein and GAM297825 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM99430 and GAM297825

GR6274 BF674140 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6274(GR6274) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6274 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6274 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6274 gene encodes GR6274 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6274 precursor RNA folds spatially, forming GR6274 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6274 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6274 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6274 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3036 precursor RNA and GAM330079 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3036 RNA and GAM330079 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3036 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3036 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3036 target RNA into GAM3036 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM330079 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM330079 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM330079 target RNA into GAM330079 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6274 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6274 gene: GAM3036 target protein and GAM330079 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3036 and GAM330079

GR6275 BE906622 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6275(GR6275) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6275 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6275 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6275 gene encodes GR6275 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6275 precursor RNA folds spatially, forming GR6275 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6275 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6275 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6275 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM70937 precursor RNA, GAM257452 precursor RNA and GAM288288 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM70937 RNA, GAM257452 RNA and GAM288288 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM70937 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM70937 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM70937 target RNA into GAM70937 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM257452 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM257452 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM257452 target RNA into GAM257452 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM288288 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM288288 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM288288 target RNA into GAM288288 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6275 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6275 gene: GAM70937 target protein, GAM257452 target protein and GAM288288 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM70937, GAM257452 and GAM288288

GR6276 BI602664 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6276(GR6276) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6276 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6276 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6276 gene encodes GR6276 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6276 precursor RNA folds spatially, forming GR6276 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6276 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6276 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6276 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 5 separate GAM precursor RNAs, GAM4101 precursor RNA, GAM40027 precursor RNA, GAM122442 precursor RNA, GAM244773 precursor RNA and GAM307254 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4101 RNA, GAM40027 RNA, GAM122442 RNA, GAM244773 RNA and GAM307254 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4101 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4101 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4101 target RNA into GAM4101 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM40027 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM40027 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM40027 target RNA into GAM40027 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM122442 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM122442 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM122442 target RNA into GAM122442 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM244773 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM244773 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM244773 target RNA into GAM244773 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM307254 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM307254 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM307254 target RNA into GAM307254 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6276 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6276 gene: GAM4101 target protein, GAM40027 target protein, GAM122442 target protein, GAM244773 target protein and GAM307254 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4101, GAM40027, GAM122442, GAM244773 and GAM307254

GR6277 AV700377 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6277(GR6277) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6277 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6277 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6277 gene encodes GR6277 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6277 precursor RNA folds spatially, forming GR6277 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6277 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6277 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6277 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM305069 precursor RNA and GAM330947 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM305069 RNA and GAM330947 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM305069 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM305069 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM305069 target RNA into GAM305069 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM330947 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM330947 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM330947 target RNA into GAM330947 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6277 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6277 gene: GAM305069 target protein and GAM330947 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM305069 and GAM330947

GR6278 BM990306 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6278(GR6278) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6278 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6278 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6278 gene encodes GR6278 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6278 precursor RNA folds spatially, forming GR6278 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6278 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6278 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6278 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6906 precursor RNA and GAM13641 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6906 RNA and GAM13641 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6906 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6906 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6906 target RNA into GAM6906 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM13641 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM13641 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM13641 target RNA into GAM13641 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6278 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6278 gene: GAM6906 target protein and GAM13641 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6906 and GAM13641

GR6279 BE255770 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6279(GR6279) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6279 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6279 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6279 gene encodes GR6279 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6279 precursor RNA folds spatially, forming GR6279 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6279 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6279 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6279 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8827 precursor RNA and GAM115503 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8827 RNA and GAM115503 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8827 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8827 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8827 target RNA into GAM8827 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM115503 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM115503 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM115503 target RNA into GAM115503 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6279 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6279 gene: GAM8827 target protein and GAM115503 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8827 and GAM115503

GR6280 AW157463 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6280(GR6280) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6280 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6280 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6280 gene encodes GR6280 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6280 precursor RNA folds spatially, forming GR6280 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6280 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6280 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6280 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4197 precursor RNA and GAM74583 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4197 RNA and GAM74583 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4197 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4197 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4197 target RNA into GAM4197 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM74583 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM74583 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM74583 target RNA into GAM74583 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6280 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6280 gene: GAM4197 target protein and GAM74583 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes

is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4197 and GAM74583

GR6281 BF737811 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6281 (GR6281) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6281 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6281 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6281 gene encodes GR6281 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6281 precursor RNA folds spatially, forming GR6281 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6281 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6281 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6281 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM36034 precursor RNA, GAM92020 precursor RNA and GAM184740 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM36034 RNA, GAM92020 RNA and GAM184740 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM36034 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM36034 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM36034 target RNA into GAM36034 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM92020 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM92020 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM92020 target RNA into GAM92020 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM184740 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM184740 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM184740 target RNA into GAM184740 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6281 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6281 gene: GAM36034 target protein, GAM92020 target protein and GAM184740 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM36034, GAM92020 and GAM184740

GR6282 AA654640 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6282(GR6282) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6282 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6282 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6282 gene encodes GR6282 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6282 precursor RNA folds spatially, forming GR6282 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6282 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6282 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6282 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3084 precursor RNA and GAM81504 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3084 RNA and GAM81504 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3084 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3084 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3084 target RNA into GAM3084 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM81504 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM81504 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM81504 target RNA into GAM81504 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6282 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6282 gene: GAM3084 target protein and GAM81504 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3084 and GAM81504

GR6283 AI768033 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6283(GR6283) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6283 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6283 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6283 gene encodes GR6283 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6283 precursor RNA folds spatially, forming GR6283 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6283 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6283 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6283 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM7568 precursor RNA, GAM8666 precursor RNA and GAM190531 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7568 RNA, GAM8666 RNA and GAM190531 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7568 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7568 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7568 target RNA into GAM7568 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8666 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8666 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8666 target RNA into GAM8666 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM190531 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM190531 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM190531 target RNA into GAM190531 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6283 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6283 gene: GAM7568 target protein, GAM8666 target protein and GAM190531 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7568, GAM8666 and GAM190531

GR6284 AA531444 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6284(GR6284) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6284 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6284 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6284 gene encodes GR6284 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6284 precursor RNA folds spatially, forming GR6284 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6284 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6284 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6284 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM277011 precursor RNA and GAM297410 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM277011 RNA and GAM297410 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM277011 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM277011 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM277011 target RNA into GAM277011 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM297410 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM297410 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM297410 target RNA into GAM297410 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6284 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6284 gene: GAM277011 target protein and GAM297410 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM277011 and GAM297410

GR6285 BG623144 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6285(GR6285) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6285 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6285 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6285 gene encodes GR6285 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6285 precursor RNA folds spatially, forming GR6285 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6285 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6285 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6285 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2901 precursor RNA and GAM133595 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2901 RNA and GAM133595 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2901 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2901 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2901 target RNA into GAM2901 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM133595 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM133595 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM133595 target RNA into GAM133595 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6285 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6285 gene: GAM2901 target protein and GAM133595 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2901 and GAM133595

GR6286 BF914328 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6286(GR6286) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6286 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6286 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6286 gene encodes GR6286 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6286 precursor RNA folds spatially, forming GR6286 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6286 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6286 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6286 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM221372 precursor RNA and GAM221664 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM221372 RNA and GAM221664 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM221372 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM221372 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM221372 target RNA into GAM221372 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM221664 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM221664 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM221664 target RNA into GAM221664 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6286 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6286 gene: GAM221372 target protein and GAM221664 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM221372 and GAM221664

GR6287 BQ028180 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6287(GR6287) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6287 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6287 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6287 gene encodes GR6287 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6287 precursor RNA folds spatially, forming GR6287 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6287 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6287 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6287 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2546 precursor RNA, GAM3801 precursor RNA and GAM67609 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2546 RNA, GAM3801 RNA and GAM67609 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2546 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2546 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2546 target RNA into GAM2546 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM3801 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3801 target RNA, herein schematically represented by

GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3801 target RNA into GAM3801 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM67609 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM67609 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM67609 target RNA into GAM67609 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6287 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6287 gene: GAM2546 target protein, GAM3801 target protein and GAM67609 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2546, GAM3801 and GAM67609

GR6288 AI289420 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6288(GR6288) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6288 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6288 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6288 gene encodes GR6288 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6288 precursor RNA folds spatially, forming GR6288 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6288 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6288 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6288 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2

separate GAM precursor RNAs, GAM16007 precursor RNA and GAM234138 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM16007 RNA and GAM234138 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM16007 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM16007 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM16007 target RNA into GAM16007 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM234138 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM234138 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM234138 target RNA into GAM234138 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6288 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6288 gene: GAM16007 target protein and GAM234138 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM16007 and GAM234138

GR6289 AW385459 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6289(GR6289) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6289 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6289 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6289 gene encodes GR6289 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR6289 precursor RNA folds spatially, forming GR6289 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6289 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6289 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6289 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM5892 precursor RNA, GAM6695 precursor RNA and GAM31609 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5892 RNA, GAM6695 RNA and GAM31609 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5892 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5892 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5892 target RNA into GAM5892 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6695 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6695 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6695 target RNA into GAM6695 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM31609 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM31609 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM31609 target RNA into GAM31609 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6289 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6289 gene: GAM5892 target protein, GAM6695 target protein and GAM31609 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5892, GAM6695 and GAM31609

GR6290 W86682 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6290(GR6290) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6290 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6290 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6290 gene encodes GR6290 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6290 precursor RNA folds spatially, forming GR6290 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6290 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6290 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6290 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5762 precursor RNA and GAM111292 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5762 RNA and GAM111292 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5762 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5762 target RNA, herein schematically represented by

GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5762 target RNA into GAM5762 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM111292 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM111292 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM111292 target RNA into GAM111292 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6290 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6290 gene: GAM5762 target protein and GAM111292 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5762 and GAM111292

GR6291 BF031816 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6291(GR6291) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6291 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6291 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6291 gene encodes GR6291 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6291 precursor RNA folds spatially, forming GR6291 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6291 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6291 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6291 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM53616 precursor RNA and GAM81014 precursor

RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM53616 RNA and GAM81014 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM53616 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM53616 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM53616 target RNA into GAM53616 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM81014 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM81014 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM81014 target RNA into GAM81014 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6291 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6291 gene: GAM53616 target protein and GAM81014 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM53616 and GAM81014

GR6292 AA732676 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6292(GR6292) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6292 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6292 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6292 gene encodes GR6292 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6292 precursor RNA folds spatially, forming GR6292 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6292 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6292 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6292 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM683 precursor RNA, GAM8290 precursor RNA and GAM147752 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM683 RNA, GAM8290 RNA and GAM147752 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM683 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM683 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM683 target RNA into GAM683 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8290 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8290 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8290 target RNA into GAM8290 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM147752 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM147752 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM147752 target RNA into GAM147752 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly

utilities, of GR6292 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6292 gene: GAM683 target protein, GAM8290 target protein and GAM147752 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM683, GAM8290 and GAM147752

GR6293 AA251399 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6293(GR6293) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6293 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6293 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6293 gene encodes GR6293 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6293 precursor RNA folds spatially, forming GR6293 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6293 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6293 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6293 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1371 precursor RNA, GAM160001 precursor RNA and GAM172839 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1371 RNA, GAM160001 RNA and GAM172839 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1371 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1371 target RNA, herein schematically represented by

GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1371 target RNA into GAM1371 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM160001 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM160001 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM160001 target RNA into GAM160001 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM172839 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM172839 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM172839 target RNA into GAM172839 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6293 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6293 gene: GAM1371 target protein, GAM160001 target protein and GAM172839 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1371, GAM160001 and GAM172839

GR6294 BI911695 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6294(GR6294) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6294 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6294 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6294 gene encodes GR6294 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6294 precursor RNA folds spatially, forming GR6294 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6294 folded precursor RNA comprises a plurality of what is known in the

art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6294 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6294 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM320 precursor RNA, GAM6790 precursor RNA and GAM297284 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM320 RNA, GAM6790 RNA and GAM297284 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM320 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM320 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM320 target RNA into GAM320 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6790 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6790 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6790 target RNA into GAM6790 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM297284 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM297284 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM297284 target RNA into GAM297284 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6294 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6294 gene: GAM320 target protein, GAM6790 target protein and GAM297284 target protein, herein

schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM320, GAM6790 and GAM297284

GR6295 BG192700 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6295(GR6295) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6295 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6295 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6295 gene encodes GR6295 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6295 precursor RNA folds spatially, forming GR6295 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6295 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6295 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6295 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM37680 precursor RNA, GAM214622 precursor RNA and GAM264980 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM37680 RNA, GAM214622 RNA and GAM264980 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM37680 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM37680 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM37680 target RNA into GAM37680 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM214622 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM214622 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM214622 target RNA into GAM214622 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM264980 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM264980 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM264980 target RNA into GAM264980 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6295 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6295 gene: GAM37680 target protein, GAM214622 target protein and GAM264980 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM37680, GAM214622 and GAM264980

GR6296 BG722468 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6296 (GR6296) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6296 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6296 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6296 gene encodes GR6296 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6296 precursor RNA folds spatially, forming GR6296 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6296 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6296 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR6296 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM6091 precursor RNA, GAM6726 precursor RNA and GAM66944 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6091 RNA, GAM6726 RNA and GAM66944 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6091 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6091 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6091 target RNA into GAM6091 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6726 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6726 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6726 target RNA into GAM6726 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM66944 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM66944 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM66944 target RNA into GAM66944 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6296 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6296 gene: GAM6091 target protein, GAM6726 target protein and GAM66944 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6091, GAM6726 and GAM66944

GR6297 BF342579 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6297(GR6297) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6297 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6297 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6297 gene encodes GR6297 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6297 precursor RNA folds spatially, forming GR6297 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6297 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6297 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6297 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6042 precursor RNA and GAM148262 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6042 RNA and GAM148262 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6042 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6042 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6042 target RNA into GAM6042 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM148262 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM148262 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM148262 target RNA into GAM148262 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6297 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6297 gene: GAM6042 target protein and GAM148262 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6042 and GAM148262

GR6298 AW022106 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6298(GR6298) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6298 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6298 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6298 gene encodes GR6298 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6298 precursor RNA folds spatially, forming GR6298 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6298 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6298 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6298 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM137713 precursor RNA, GAM279246 precursor RNA and GAM331768 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM137713 RNA, GAM279246 RNA and GAM331768 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs

corresponding to GAM RNA of Fig. 8.

GAM137713 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM137713 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM137713 target RNA into GAM137713 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM279246 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM279246 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM279246 target RNA into GAM279246 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM331768 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM331768 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM331768 target RNA into GAM331768 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6298 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6298 gene: GAM137713 target protein, GAM279246 target protein and GAM331768 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM137713, GAM279246 and GAM331768

GR6299 BF984626 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6299(GR6299) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6299 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6299 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6299 gene encodes GR6299 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR6299 precursor RNA folds spatially, forming GR6299 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6299 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6299 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6299 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8701 precursor RNA and GAM186217 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8701 RNA and GAM186217 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8701 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8701 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8701 target RNA into GAM8701 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM186217 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM186217 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM186217 target RNA into GAM186217 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6299 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6299 gene: GAM8701 target protein and GAM186217 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8701 and GAM186217

GR6300 AL713287 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6300(GR6300) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6300 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6300 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6300 gene encodes GR6300 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6300 precursor RNA folds spatially, forming GR6300 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6300 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6300 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6300 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2357 precursor RNA, GAM290962 precursor RNA and GAM320275 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2357 RNA, GAM290962 RNA and GAM320275 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2357 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2357 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2357 target RNA into GAM2357 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM290962 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM290962 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM290962 target RNA into GAM290962 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM320275 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM320275 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM320275 target RNA into GAM320275 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6300 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6300 gene: GAM2357 target protein, GAM290962 target protein and GAM320275 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2357, GAM290962 and GAM320275

GR6301 BG829445 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6301 (GR6301) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6301 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6301 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6301 gene encodes GR6301 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6301 precursor RNA folds spatially, forming GR6301 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6301 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6301 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6301 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4438 precursor RNA, GAM94791 precursor RNA and

GAM276089 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4438 RNA, GAM94791 RNA and GAM276089 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4438 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4438 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4438 target RNA into GAM4438 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM94791 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM94791 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM94791 target RNA into GAM94791 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM276089 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM276089 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM276089 target RNA into GAM276089 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6301 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6301 gene: GAM4438 target protein, GAM94791 target protein and GAM276089 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4438, GAM94791 and GAM276089

GR6302 AI636380 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6302(GR6302) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR6302 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6302 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6302 gene encodes GR6302 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6302 precursor RNA folds spatially, forming GR6302 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6302 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6302 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6302 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1235 precursor RNA and GAM152175 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1235 RNA and GAM152175 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1235 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1235 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1235 target RNA into GAM1235 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM152175 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM152175 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM152175 target RNA into GAM152175 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6302 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6302 gene: GAM1235 target protein and GAM152175 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1235 and GAM152175

GR6303 AA495958 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6303(GR6303) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6303 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6303 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6303 gene encodes GR6303 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6303 precursor RNA folds spatially, forming GR6303 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6303 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6303 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6303 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM22645 precursor RNA and GAM36815 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM22645 RNA and GAM36815 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM22645 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM22645 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM22645 target RNA into GAM22645 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM36815 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM36815 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM36815 target RNA into GAM36815 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6303 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6303 gene: GAM22645 target protein and GAM36815 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM22645 and GAM36815

GR6304 AA508528 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6304(GR6304) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6304 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6304 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6304 gene encodes GR6304 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6304 precursor RNA folds spatially, forming GR6304 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6304 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6304 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6304 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2354 precursor RNA and GAM137014 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3

FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2354 RNA and GAM137014 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2354 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2354 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2354 target RNA into GAM2354 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM137014 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM137014 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM137014 target RNA into GAM137014 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6304 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6304 gene: GAM2354 target protein and GAM137014 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2354 and GAM137014

GR6305 BG392814 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6305(GR6305) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6305 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6305 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6305 gene encodes GR6305 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6305 precursor RNA folds spatially, forming GR6305 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6305 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6305 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6305 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3134 precursor RNA and GAM95009 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3134 RNA and GAM95009 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3134 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3134 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3134 target RNA into GAM3134 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM95009 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM95009 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM95009 target RNA into GAM95009 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6305 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6305 gene: GAM3134 target protein and GAM95009 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3134 and GAM95009

6306(GR6306) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6306 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6306 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6306 gene encodes GR6306 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6306 precursor RNA folds spatially, forming GR6306 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6306 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6306 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6306 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM51471 precursor RNA and GAM68187 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM51471 RNA and GAM68187 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM51471 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM51471 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM51471 target RNA into GAM51471 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM68187 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM68187 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM68187 target RNA into GAM68187 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6306 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6306 gene: GAM51471 target protein and GAM68187 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM51471 and GAM68187

GR6307 BF841022 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6307(GR6307) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6307 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6307 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6307 gene encodes GR6307 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6307 precursor RNA folds spatially, forming GR6307 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6307 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6307 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6307 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM776 precursor RNA and GAM3556 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM776 RNA and GAM3556 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM776 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM776 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM776 target RNA into GAM776 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM3556 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3556 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3556 target RNA into GAM3556 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6307 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6307 gene: GAM776 target protein and GAM3556 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM776 and GAM3556

GR6308 BM548971 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6308(GR6308) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6308 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6308 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6308 gene encodes GR6308 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6308 precursor RNA folds spatially, forming GR6308 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6308 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6308 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6308 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4

separate GAM precursor RNAs, GAM11235 precursor RNA, GAM91683 precursor RNA, GAM271794 precursor RNA and GAM277643 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM11235 RNA, GAM91683 RNA, GAM271794 RNA and GAM277643 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM11235 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM11235 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM11235 target RNA into GAM11235 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM91683 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM91683 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM91683 target RNA into GAM91683 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM271794 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM271794 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM271794 target RNA into GAM271794 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM277643 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM277643 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM277643 target RNA into GAM277643 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6308 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6308 gene: GAM11235 target protein, GAM91683 target protein, GAM271794 target protein and GAM277643

target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM11235, GAM91683, GAM271794 and GAM277643

GR6309 AI277488 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6309(GR6309) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6309 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6309 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6309 gene encodes GR6309 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6309 precursor RNA folds spatially, forming GR6309 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6309 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6309 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6309 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM149131 precursor RNA and GAM315983 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM149131 RNA and GAM315983 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM149131 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM149131 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM149131 target RNA into GAM149131 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM315983 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM315983 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM315983 target RNA into GAM315983 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6309 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6309 gene: GAM149131 target protein and GAM315983 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM149131 and GAM315983

GR6310 BM920880 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6310(GR6310) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6310 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6310 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6310 gene encodes GR6310 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6310 precursor RNA folds spatially, forming GR6310 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6310 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6310 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6310 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM399 precursor RNA and GAM7190 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM399 RNA and GAM7190 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM399 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM399 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM399 target RNA into GAM399 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7190 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7190 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7190 target RNA into GAM7190 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6310 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6310 gene: GAM399 target protein and GAM7190 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM399 and GAM7190

GR6311 BG505631 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6311 (GR6311) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6311 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6311 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6311 gene encodes GR6311 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6311 precursor RNA folds spatially, forming GR6311 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6311 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR6311 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6311 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM153458 precursor RNA and GAM180467 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM153458 RNA and GAM180467 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM153458 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM153458 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM153458 target RNA into GAM153458 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM180467 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM180467 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM180467 target RNA into GAM180467 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6311 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6311 gene: GAM153458 target protein and GAM180467 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM153458 and GAM180467

GR6312 R38117 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6312(GR6312) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6312 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6312 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6312 gene encodes GR6312 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6312 precursor RNA folds spatially, forming GR6312 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6312 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6312 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6312 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8664 precursor RNA and GAM69222 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8664 RNA and GAM69222 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8664 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8664 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8664 target RNA into GAM8664 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM69222 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM69222 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM69222 target RNA into GAM69222 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6312 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6312 gene: GAM8664 target protein and GAM69222 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8664 and GAM69222

GR6313 AW004048 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6313(GR6313) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6313 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6313 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6313 gene encodes GR6313 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6313 precursor RNA folds spatially, forming GR6313 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6313 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6313 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6313 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM13331 precursor RNA and GAM117872 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM13331 RNA and GAM117872 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM13331 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM13331 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM13331

target RNA into GAM13331 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM117872 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM117872 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM117872 target RNA into GAM117872 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6313 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6313 gene: GAM13331 target protein and GAM117872 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM13331 and GAM117872

GR6314 BF203990 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6314(GR6314) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6314 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6314 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6314 gene encodes GR6314 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6314 precursor RNA folds spatially, forming GR6314 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6314 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6314 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6314 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM87261 precursor RNA and GAM312250 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM87261 RNA and GAM312250 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM87261 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM87261 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM87261 target RNA into GAM87261 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM312250 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM312250 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM312250 target RNA into GAM312250 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6314 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6314 gene: GAM87261 target protein and GAM312250 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM87261 and GAM312250

GR6315 BI915436 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6315(GR6315) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6315 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6315 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6315 gene encodes GR6315 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6315 precursor RNA folds spatially, forming GR6315 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated

that GR6315 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6315 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6315 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7427 precursor RNA and GAM28070 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7427 RNA and GAM28070 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7427 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7427 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7427 target RNA into GAM7427 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM28070 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM28070 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM28070 target RNA into GAM28070 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6315 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6315 gene: GAM7427 target protein and GAM28070 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7427 and GAM28070

GR6316 BG424283 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6316(GR6316) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR6316 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6316 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6316 gene encodes GR6316 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6316 precursor RNA folds spatially, forming GR6316 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6316 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6316 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6316 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM45578 precursor RNA, GAM186749 precursor RNA and GAM316273 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM45578 RNA, GAM186749 RNA and GAM316273 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM45578 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM45578 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM45578 target RNA into GAM45578 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM186749 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM186749 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM186749 target RNA into GAM186749 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM316273 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM316273 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM316273 target RNA into GAM316273 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6316 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6316 gene: GAM45578 target protein, GAM186749 target protein and GAM316273 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM45578, GAM186749 and GAM316273

GR6317 BM461566 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6317 (GR6317) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6317 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6317 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6317 gene encodes GR6317 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6317 precursor RNA folds spatially, forming GR6317 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6317 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6317 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6317 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM57297 precursor RNA, GAM255476 precursor RNA and GAM263475 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM57297 RNA, GAM255476 RNA and GAM263475 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM57297 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM57297 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM57297 target RNA into GAM57297 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM255476 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM255476 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM255476 target RNA into GAM255476 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM263475 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM263475 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM263475 target RNA into GAM263475 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6317 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6317 gene: GAM57297 target protein, GAM255476 target protein and GAM263475 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM57297, GAM255476 and GAM263475

GR6318 BG202178 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6318(GR6318) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6318 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR6318 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6318 gene encodes GR6318 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6318 precursor RNA folds spatially, forming GR6318 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6318 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6318 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6318 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM145610 precursor RNA, GAM196460 precursor RNA, GAM296655 precursor RNA and GAM326988 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM145610 RNA, GAM196460 RNA, GAM296655 RNA and GAM326988 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM145610 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM145610 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM145610 target RNA into GAM145610 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM196460 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM196460 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM196460 target RNA into GAM196460 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM296655 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM296655 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM296655 target RNA into GAM296655 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM326988 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM326988 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM326988 target RNA into GAM326988 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6318 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6318 gene: GAM145610 target protein, GAM196460 target protein, GAM296655 target protein and GAM326988 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM145610, GAM196460, GAM296655 and GAM326988

GR6319 BI561465 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6319 (GR6319) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6319 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6319 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6319 gene encodes GR6319 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6319 precursor RNA folds spatially, forming GR6319 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6319 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6319 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6319 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM64896 precursor RNA, GAM73898 precursor RNA

and GAM300978 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM64896 RNA, GAM73898 RNA and GAM300978 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM64896 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM64896 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM64896 target RNA into GAM64896 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM73898 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM73898 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM73898 target RNA into GAM73898 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM300978 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM300978 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM300978 target RNA into GAM300978 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6319 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6319 gene: GAM64896 target protein, GAM73898 target protein and GAM300978 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM64896, GAM73898 and GAM300978

GR6320 BF379459 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6320(GR6320) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR6320 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6320 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6320 gene encodes GR6320 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6320 precursor RNA folds spatially, forming GR6320 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6320 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6320 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6320 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2833 precursor RNA and GAM284998 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2833 RNA and GAM284998 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2833 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2833 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2833 target RNA into GAM2833 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM284998 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM284998 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM284998 target RNA into GAM284998 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6320 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6320 gene: GAM2833 target protein and GAM284998 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2833 and GAM284998

GR6321 BF799745 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6321 (GR6321) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6321 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6321 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6321 gene encodes GR6321 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6321 precursor RNA folds spatially, forming GR6321 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6321 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6321 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6321 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM64518 precursor RNA and GAM212400 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM64518 RNA and GAM212400 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM64518 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM64518 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM64518 target RNA into GAM64518 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM212400 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM212400 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM212400 target RNA into GAM212400 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6321 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6321 gene: GAM64518 target protein and GAM212400 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM64518 and GAM212400

GR6322 BG774621 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6322(GR6322) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6322 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6322 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6322 gene encodes GR6322 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6322 precursor RNA folds spatially, forming GR6322 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6322 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6322 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6322 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM122433 precursor RNA and GAM275989 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3

FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM122433 RNA and GAM275989 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM122433 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM122433 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM122433 target RNA into GAM122433 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM275989 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM275989 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM275989 target RNA into GAM275989 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6322 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6322 gene: GAM122433 target protein and GAM275989 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM122433 and GAM275989

GR6323 BE738716 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6323(GR6323) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6323 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6323 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6323 gene encodes GR6323 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6323 precursor RNA folds spatially, forming GR6323 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6323 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6323 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6323 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM7231 precursor RNA, GAM224049 precursor RNA and GAM235473 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7231 RNA, GAM224049 RNA and GAM235473 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7231 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7231 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7231 target RNA into GAM7231 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM224049 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM224049 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM224049 target RNA into GAM224049 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM235473 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM235473 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM235473 target RNA into GAM235473 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6323 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6323 gene: GAM7231 target protein, GAM224049 target protein and GAM235473 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7231, GAM224049 and GAM235473

GR6324 BG876843 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6324(GR6324) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6324 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6324 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6324 gene encodes GR6324 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6324 precursor RNA folds spatially, forming GR6324 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6324 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6324 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6324 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1329 precursor RNA and GAM230965 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1329 RNA and GAM230965 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1329 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1329 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig. 8, thereby inhibiting translation of GAM1329 target RNA into GAM1329 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM230965 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM230965 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM230965 target RNA into GAM230965 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6324 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6324 gene: GAM1329 target protein and GAM230965 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1329 and GAM230965

GR6325 AW373597 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6325(GR6325) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6325 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6325 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6325 gene encodes GR6325 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6325 precursor RNA folds spatially, forming GR6325 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6325 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6325 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6325 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM316888 precursor RNA, GAM324973 precursor RNA and GAM325457 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded

precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM316888 RNA, GAM324973 RNA and GAM325457 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM316888 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM316888 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM316888 target RNA into GAM316888 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM324973 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM324973 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM324973 target RNA into GAM324973 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM325457 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM325457 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM325457 target RNA into GAM325457 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6325 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6325 gene: GAM316888 target protein, GAM324973 target protein and GAM325457 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM316888, GAM324973 and GAM325457

GR6326 BG002862 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6326(GR6326) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6326 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6326 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6326 gene encodes GR6326 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6326 precursor RNA folds spatially, forming GR6326 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6326 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6326 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6326 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM4000 precursor RNA, GAM6756 precursor RNA, GAM32238 precursor RNA and GAM184876 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4000 RNA, GAM6756 RNA, GAM32238 RNA and GAM184876 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4000 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4000 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4000 target RNA into GAM4000 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6756 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6756 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6756 target RNA into GAM6756 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM32238 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM32238 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM32238 target RNA into GAM32238 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM184876 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM184876 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM184876 target RNA into GAM184876 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6326 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6326 gene: GAM4000 target protein, GAM6756 target protein, GAM32238 target protein and GAM184876 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4000, GAM6756, GAM32238 and GAM184876

GR6327 BI085792 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6327(GR6327) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6327 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6327 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6327 gene encodes GR6327 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6327 precursor RNA folds spatially, forming GR6327 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6327 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6327 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6327 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5158 precursor RNA and GAM193680 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5158 RNA and GAM193680 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5158 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5158 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5158 target RNA into GAM5158 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM193680 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM193680 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM193680 target RNA into GAM193680 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6327 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6327 gene: GAM5158 target protein and GAM193680 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5158 and GAM193680

GR6328 BI161357 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6328(GR6328) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6328 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6328 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6328 gene encodes GR6328 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6328 precursor RNA folds spatially, forming GR6328 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6328 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6328 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6328 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4288 precursor RNA, GAM71538 precursor RNA and GAM261021 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4288 RNA, GAM71538 RNA and GAM261021 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4288 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4288 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4288 target RNA into GAM4288 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM71538 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM71538 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM71538 target RNA into GAM71538 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM261021 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM261021 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM261021 target RNA into GAM261021 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6328 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6328 gene: GAM4288 target protein, GAM71538 target protein and GAM261021 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4288, GAM71538 and GAM261021

GR6329 BF856008 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6329(GR6329) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6329 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6329 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6329 gene encodes GR6329 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6329 precursor RNA folds spatially, forming GR6329 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6329 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6329 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6329 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM16188 precursor RNA and GAM27928 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM16188 RNA and GAM27928 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM16188 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM16188 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM16188 target RNA into GAM16188 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM27928 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM27928 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM27928 target RNA into GAM27928 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6329 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6329 gene: GAM16188 target protein and GAM27928 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM16188 and GAM27928

GR6330 BI544867 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6330(GR6330) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6330 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6330 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6330 gene encodes GR6330 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6330 precursor RNA folds spatially, forming GR6330 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6330 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6330 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6330 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2

separate GAM precursor RNAs, GAM5096 precursor RNA and GAM306188 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5096 RNA and GAM306188 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5096 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5096 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5096 target RNA into GAM5096 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM306188 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM306188 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM306188 target RNA into GAM306188 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6330 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6330 gene: GAM5096 target protein and GAM306188 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5096 and GAM306188

GR6331 BM562221 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6331 (GR6331) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6331 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6331 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6331 gene encodes GR6331 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR6331 precursor RNA folds spatially, forming GR6331 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6331 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6331 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6331 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4646 precursor RNA and GAM273342 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4646 RNA and GAM273342 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4646 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4646 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4646 target RNA into GAM4646 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM273342 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM273342 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM273342 target RNA into GAM273342 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6331 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6331 gene: GAM4646 target protein and GAM273342 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4646 and GAM273342

GR6332 BE674963 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6332(GR6332) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6332 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6332 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6332 gene encodes GR6332 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6332 precursor RNA folds spatially, forming GR6332 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6332 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6332 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6332 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1517 precursor RNA, GAM32175 precursor RNA and GAM85149 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1517 RNA, GAM32175 RNA and GAM85149 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1517 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1517 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1517 target RNA into GAM1517 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM32175 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM32175 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM32175 target RNA into GAM32175 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM85149 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM85149 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM85149 target RNA into GAM85149 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6332 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6332 gene: GAM1517 target protein, GAM32175 target protein and GAM85149 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1517, GAM32175 and GAM85149

GR6333 BE085410 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6333(GR6333) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6333 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6333 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6333 gene encodes GR6333 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6333 precursor RNA folds spatially, forming GR6333 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6333 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6333 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6333 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM79943 precursor RNA and GAM235171 precursor

RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM79943 RNA and GAM235171 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM79943 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM79943 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM79943 target RNA into GAM79943 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM235171 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM235171 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM235171 target RNA into GAM235171 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6333 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6333 gene: GAM79943 target protein and GAM235171 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM79943 and GAM235171

GR6334 AI369800 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6334(GR6334) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6334 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6334 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6334 gene encodes GR6334 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6334 precursor RNA folds spatially, forming GR6334 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6334 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6334 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6334 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5437 precursor RNA and GAM15263 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5437 RNA and GAM15263 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5437 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5437 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5437 target RNA into GAM5437 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM15263 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM15263 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM15263 target RNA into GAM15263 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6334 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6334 gene: GAM5437 target protein and GAM15263 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5437 and GAM15263

bioinformatically detected regulatory gene, referred to here as Genomic Record 6335(GR6335) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6335 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6335 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6335 gene encodes GR6335 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6335 precursor RNA folds spatially, forming GR6335 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6335 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6335 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6335 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6838 precursor RNA and GAM42270 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6838 RNA and GAM42270 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6838 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6838 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6838 target RNA into GAM6838 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM42270 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM42270 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM42270

target RNA into GAM42270 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6335 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6335 gene: GAM6838 target protein and GAM42270 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6838 and GAM42270

GR6336 R67777 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6336(GR6336) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6336 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6336 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6336 gene encodes GR6336 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6336 precursor RNA folds spatially, forming GR6336 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6336 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6336 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6336 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2219 precursor RNA and GAM85381 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2219 RNA and GAM85381 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2219 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2219 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2219 target RNA into GAM2219 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM85381 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM85381 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM85381 target RNA into GAM85381 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6336 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6336 gene: GAM2219 target protein and GAM85381 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2219 and GAM85381

GR6337 AI860267 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6337(GR6337) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6337 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6337 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6337 gene encodes GR6337 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6337 precursor RNA folds spatially, forming GR6337 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6337 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6337 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6337 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM8214 precursor RNA, GAM219826 precursor RNA and GAM256611 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8214 RNA, GAM219826 RNA and GAM256611 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8214 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8214 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8214 target RNA into GAM8214 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM219826 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM219826 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM219826 target RNA into GAM219826 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM256611 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM256611 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM256611 target RNA into GAM256611 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6337 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6337 gene: GAM8214 target protein, GAM219826 target protein and GAM256611 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8214, GAM219826 and GAM256611

6338(GR6338) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6338 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6338 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6338 gene encodes GR6338 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6338 precursor RNA folds spatially, forming GR6338 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6338 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6338 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6338 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6825 precursor RNA and GAM168644 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6825 RNA and GAM168644 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6825 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6825 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6825 target RNA into GAM6825 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM168644 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM168644 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM168644 target RNA into GAM168644 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6338 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6338 gene: GAM6825 target protein and GAM168644 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6825 and GAM168644

GR6339 BM974566 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6339(GR6339) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6339 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6339 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6339 gene encodes GR6339 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6339 precursor RNA folds spatially, forming GR6339 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6339 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6339 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6339 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7816 precursor RNA and GAM275731 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7816 RNA and GAM275731 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7816 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM7816 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7816 target RNA into GAM7816 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM275731 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM275731 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM275731 target RNA into GAM275731 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6339 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6339 gene: GAM7816 target protein and GAM275731 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7816 and GAM275731

GR6340 AL708087 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6340(GR6340) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6340 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6340 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6340 gene encodes GR6340 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6340 precursor RNA folds spatially, forming GR6340 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6340 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6340 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6340 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2

separate GAM precursor RNAs, GAM172932 precursor RNA and GAM279746 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM172932 RNA and GAM279746 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM172932 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM172932 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM172932 target RNA into GAM172932 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM279746 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM279746 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM279746 target RNA into GAM279746 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6340 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6340 gene: GAM172932 target protein and GAM279746 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM172932 and GAM279746

GR6341 AU145362 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6341 (GR6341) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6341 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6341 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6341 gene encodes GR6341 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR6341 precursor RNA folds spatially, forming GR6341 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6341 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6341 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6341 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2023 precursor RNA and GAM246465 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2023 RNA and GAM246465 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2023 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2023 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2023 target RNA into GAM2023 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM246465 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM246465 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM246465 target RNA into GAM246465 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6341 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6341 gene: GAM2023 target protein and GAM246465 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2023 and GAM246465

GR6342 BF978599 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6342(GR6342) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6342 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6342 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6342 gene encodes GR6342 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6342 precursor RNA folds spatially, forming GR6342 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6342 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6342 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6342 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5570 precursor RNA and GAM103705 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5570 RNA and GAM103705 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5570 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5570 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5570 target RNA into GAM5570 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM103705 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM103705 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM103705 target RNA into GAM103705 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6342 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6342 gene: GAM5570 target protein and GAM103705 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5570 and GAM103705

GR6343 F12184 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6343(GR6343) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6343 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6343 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6343 gene encodes GR6343 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6343 precursor RNA folds spatially, forming GR6343 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6343 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6343 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6343 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM6416 precursor RNA, GAM41867 precursor RNA and GAM186451 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6416 RNA, GAM41867 RNA and GAM186451 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6416 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6416 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6416 target RNA into GAM6416 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM41867 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM41867 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM41867 target RNA into GAM41867 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM186451 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM186451 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM186451 target RNA into GAM186451 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6343 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6343 gene: GAM6416 target protein, GAM41867 target protein and GAM186451 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6416, GAM41867 and GAM186451

GR6344 BQ060978 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6344(GR6344) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6344 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6344 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6344 gene encodes GR6344 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6344 precursor RNA folds spatially, forming GR6344 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6344 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6344 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6344 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1534 precursor RNA and GAM217690 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1534 RNA and GAM217690 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1534 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1534 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1534 target RNA into GAM1534 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM217690 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM217690 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM217690 target RNA into GAM217690 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6344 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6344 gene: GAM1534 target protein and GAM217690 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1534 and GAM217690

bioinformatically detected regulatory gene, referred to here as Genomic Record 6345(GR6345) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6345 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6345 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6345 gene encodes GR6345 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6345 precursor RNA folds spatially, forming GR6345 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6345 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6345 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6345 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM167200 precursor RNA and GAM290784 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM167200 RNA and GAM290784 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM167200 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM167200 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM167200 target RNA into GAM167200 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM290784 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM290784 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM290784

target RNA into GAM290784 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6345 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6345 gene: GAM167200 target protein and GAM290784 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM167200 and GAM290784

GR6346 AA577708 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6346(GR6346) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6346 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6346 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6346 gene encodes GR6346 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6346 precursor RNA folds spatially, forming GR6346 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6346 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6346 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6346 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM76054 precursor RNA and GAM277993 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM76054 RNA and GAM277993 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM76054 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM76054 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM76054 target RNA into GAM76054 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM277993 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM277993 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM277993 target RNA into GAM277993 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6346 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6346 gene: GAM76054 target protein and GAM277993 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM76054 and GAM277993

GR6347 BF090159 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6347(GR6347) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6347 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6347 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6347 gene encodes GR6347 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6347 precursor RNA folds spatially, forming GR6347 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6347 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6347 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6347 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM206110 precursor RNA, GAM283321 precursor RNA and GAM324429 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM206110 RNA, GAM283321 RNA and GAM324429 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM206110 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM206110 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM206110 target RNA into GAM206110 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM283321 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM283321 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM283321 target RNA into GAM283321 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM324429 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM324429 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM324429 target RNA into GAM324429 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6347 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6347 gene: GAM206110 target protein, GAM283321 target protein and GAM324429 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM206110, GAM283321 and GAM324429

6348(GR6348) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6348 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6348 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6348 gene encodes GR6348 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6348 precursor RNA folds spatially, forming GR6348 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6348 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6348 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6348 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM11444 precursor RNA and GAM166124 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM11444 RNA and GAM166124 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM11444 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM11444 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM11444 target RNA into GAM11444 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM166124 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM166124 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM166124 target RNA into GAM166124 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6348 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6348 gene: GAM11444 target protein and GAM166124 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM11444 and GAM166124

GR6349 BG122873 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6349(GR6349) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6349 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6349 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6349 gene encodes GR6349 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6349 precursor RNA folds spatially, forming GR6349 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6349 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6349 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6349 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM1315 precursor RNA, GAM4252 precursor RNA, GAM8025 precursor RNA and GAM116107 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1315 RNA, GAM4252 RNA, GAM8025 RNA and GAM116107 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1315 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1315 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1315 target RNA into GAM1315 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM4252 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4252 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4252 target RNA into GAM4252 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8025 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8025 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8025 target RNA into GAM8025 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM116107 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM116107 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM116107 target RNA into GAM116107 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6349 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6349 gene: GAM1315 target protein, GAM4252 target protein, GAM8025 target protein and GAM116107 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1315, GAM4252, GAM8025 and GAM116107

GR6350 R92469 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6350(GR6350) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6350 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR6350 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6350 gene encodes GR6350 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6350 precursor RNA folds spatially, forming GR6350 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6350 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6350 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6350 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM75509 precursor RNA and GAM263487 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM75509 RNA and GAM263487 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM75509 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM75509 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM75509 target RNA into GAM75509 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM263487 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM263487 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM263487 target RNA into GAM263487 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6350 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6350 gene: GAM75509 target

protein and GAM263487 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM75509 and GAM263487

GR6351 BG570212 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6351 (GR6351) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6351 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6351 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6351 gene encodes GR6351 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6351 precursor RNA folds spatially, forming GR6351 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6351 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6351 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6351 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM32481 precursor RNA, GAM95039 precursor RNA, GAM215689 precursor RNA and GAM304143 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM32481 RNA, GAM95039 RNA, GAM215689 RNA and GAM304143 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM32481 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM32481 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM32481 target RNA into GAM32481 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM95039 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM95039 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM95039 target RNA into GAM95039 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM215689 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM215689 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM215689 target RNA into GAM215689 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM304143 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM304143 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM304143 target RNA into GAM304143 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6351 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6351 gene: GAM32481 target protein, GAM95039 target protein, GAM215689 target protein and GAM304143 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM32481, GAM95039, GAM215689 and GAM304143

GR6352 BF317432 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6352(GR6352) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6352 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6352 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6352 gene encodes GR6352 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6352 precursor RNA folds spatially, forming GR6352 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6352 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6352 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6352 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM104373 precursor RNA, GAM223742 precursor RNA and GAM286862 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM104373 RNA, GAM223742 RNA and GAM286862 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM104373 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM104373 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM104373 target RNA into GAM104373 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM223742 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM223742 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM223742 target RNA into GAM223742 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM286862 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM286862 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM286862 target RNA into GAM286862 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly

utilities, of GR6352 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6352 gene: GAM104373 target protein, GAM223742 target protein and GAM286862 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM104373, GAM223742 and GAM286862

GR6353 BF881251 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6353(GR6353) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6353 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6353 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6353 gene encodes GR6353 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6353 precursor RNA folds spatially, forming GR6353 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6353 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6353 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6353 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM26611 precursor RNA, GAM41354 precursor RNA and GAM72389 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM26611 RNA, GAM41354 RNA and GAM72389 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM26611 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM26611 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM26611 target RNA into GAM26611 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM41354 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM41354 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM41354 target RNA into GAM41354 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM72389 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM72389 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM72389 target RNA into GAM72389 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6353 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6353 gene: GAM26611 target protein, GAM41354 target protein and GAM72389 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM26611, GAM41354 and GAM72389

GR6354 AI084024 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6354(GR6354) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6354 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6354 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6354 gene encodes GR6354 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6354 precursor RNA folds spatially, forming GR6354 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6354 folded precursor RNA comprises a plurality of what is known in the

art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6354 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6354 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1529 precursor RNA, GAM38893 precursor RNA and GAM142115 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1529 RNA, GAM38893 RNA and GAM142115 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1529 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1529 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1529 target RNA into GAM1529 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM38893 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM38893 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM38893 target RNA into GAM38893 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM142115 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM142115 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM142115 target RNA into GAM142115 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6354 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6354 gene: GAM1529 target protein, GAM38893 target protein and GAM142115 target protein, herein

schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1529, GAM38893 and GAM142115

GR6355 AI222749 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6355(GR6355) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6355 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6355 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6355 gene encodes GR6355 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6355 precursor RNA folds spatially, forming GR6355 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6355 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6355 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6355 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM184102 precursor RNA and GAM223580 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM184102 RNA and GAM223580 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM184102 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM184102 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM184102 target RNA into GAM184102 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM223580 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM223580 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM223580 target RNA into GAM223580 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6355 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6355 gene: GAM184102 target protein and GAM223580 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM184102 and GAM223580

GR6356 BG498052 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6356(GR6356) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6356 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6356 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6356 gene encodes GR6356 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6356 precursor RNA folds spatially, forming GR6356 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6356 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6356 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6356 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM170841 precursor RNA and GAM290939 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM170841 RNA and GAM290939 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM170841 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM170841 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM170841 target RNA into GAM170841 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM290939 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM290939 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM290939 target RNA into GAM290939 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6356 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6356 gene: GAM170841 target protein and GAM290939 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM170841 and GAM290939

GR6357 AA021394 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6357(GR6357) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6357 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6357 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6357 gene encodes GR6357 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6357 precursor RNA folds spatially, forming GR6357 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6357 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR6357 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6357 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM248865 precursor RNA and GAM302510 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM248865 RNA and GAM302510 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM248865 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM248865 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM248865 target RNA into GAM248865 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM302510 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM302510 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM302510 target RNA into GAM302510 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6357 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6357 gene: GAM248865 target protein and GAM302510 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM248865 and GAM302510

GR6358 AI921837 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6358(GR6358) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6358 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6358 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6358 gene encodes GR6358 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6358 precursor RNA folds spatially, forming GR6358 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6358 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6358 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6358 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM130 precursor RNA and GAM18283 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM130 RNA and GAM18283 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM130 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM130 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM130 target RNA into GAM130 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM18283 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM18283 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM18283 target RNA into GAM18283 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6358 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6358 gene: GAM130 target protein and GAM18283 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM130 and GAM18283

GR6359 BG214516 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6359(GR6359) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6359 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6359 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6359 gene encodes GR6359 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6359 precursor RNA folds spatially, forming GR6359 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6359 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6359 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6359 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM176595 precursor RNA and GAM316332 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM176595 RNA and GAM316332 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM176595 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM176595 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM176595

target RNA into GAM176595 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM316332 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM316332 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM316332 target RNA into GAM316332 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6359 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6359 gene: GAM176595 target protein and GAM316332 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM176595 and GAM316332

GR6360 BG430878 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6360(GR6360) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6360 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6360 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6360 gene encodes GR6360 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6360 precursor RNA folds spatially, forming GR6360 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6360 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6360 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6360 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3196 precursor RNA and GAM100265 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3196 RNA and GAM100265 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3196 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3196 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3196 target RNA into GAM3196 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM100265 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM100265 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM100265 target RNA into GAM100265 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6360 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6360 gene: GAM3196 target protein and GAM100265 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3196 and GAM100265

GR6361 BF686353 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6361(GR6361) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6361 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6361 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6361 gene encodes GR6361 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6361 precursor RNA folds spatially, forming GR6361 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated

that GR6361 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6361 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6361 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM113002 precursor RNA, GAM174002 precursor RNA and GAM213680 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM113002 RNA, GAM174002 RNA and GAM213680 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM113002 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM113002 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM113002 target RNA into GAM113002 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM174002 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM174002 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM174002 target RNA into GAM174002 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM213680 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM213680 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM213680 target RNA into GAM213680 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6361 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6361 gene: GAM113002 target

protein, GAM174002 target protein and GAM213680 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM113002, GAM174002 and GAM213680

GR6362 BG024480 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6362(GR6362) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6362 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6362 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6362 gene encodes GR6362 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6362 precursor RNA folds spatially, forming GR6362 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6362 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6362 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6362 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2845 precursor RNA and GAM148272 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2845 RNA and GAM148272 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2845 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2845 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2845 target RNA into GAM2845 target protein, herein schematically represented by GAM1 TARGET

PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM148272 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM148272 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM148272 target RNA into GAM148272 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6362 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6362 gene: GAM2845 target protein and GAM148272 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2845 and GAM148272

GR6363 BF574610 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6363(GR6363) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6363 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6363 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6363 gene encodes GR6363 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6363 precursor RNA folds spatially, forming GR6363 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6363 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6363 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6363 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM363 precursor RNA, GAM33314 precursor RNA and GAM75003 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM363 RNA, GAM33314 RNA and GAM75003 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM363 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM363 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM363 target RNA into GAM363 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM33314 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM33314 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM33314 target RNA into GAM33314 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM75003 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM75003 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM75003 target RNA into GAM75003 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6363 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6363 gene: GAM363 target protein, GAM33314 target protein and GAM75003 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM363, GAM33314 and GAM75003

GR6364 BG324292 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6364(GR6364) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6364 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR6364 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6364 gene encodes GR6364 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6364 precursor RNA folds spatially, forming GR6364 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6364 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6364 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6364 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM4941 precursor RNA, GAM5599 precursor RNA, GAM169796 precursor RNA and GAM283560 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4941 RNA, GAM5599 RNA, GAM169796 RNA and GAM283560 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4941 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4941 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4941 target RNA into GAM4941 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5599 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5599 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5599 target RNA into GAM5599 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM169796 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM169796 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM169796 target RNA into GAM169796 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM283560 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM283560 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM283560 target RNA into GAM283560 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6364 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6364 gene: GAM4941 target protein, GAM5599 target protein, GAM169796 target protein and GAM283560 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4941, GAM5599, GAM169796 and GAM283560

GR6365 BG208555 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6365(GR6365) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6365 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6365 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6365 gene encodes GR6365 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6365 precursor RNA folds spatially, forming GR6365 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6365 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6365 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6365 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4855 precursor RNA and GAM85608 precursor

RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4855 RNA and GAM85608 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4855 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4855 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4855 target RNA into GAM4855 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM85608 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM85608 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM85608 target RNA into GAM85608 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6365 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6365 gene: GAM4855 target protein and GAM85608 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4855 and GAM85608

GR6366 BF973440 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6366(GR6366) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6366 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6366 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6366 gene encodes GR6366 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6366 precursor RNA folds spatially, forming GR6366 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6366 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6366 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6366 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1679 precursor RNA and GAM206627 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1679 RNA and GAM206627 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1679 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1679 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1679 target RNA into GAM1679 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM206627 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM206627 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM206627 target RNA into GAM206627 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6366 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6366 gene: GAM1679 target protein and GAM206627 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1679 and GAM206627

bioinformatically detected regulatory gene, referred to here as Genomic Record 6367(GR6367) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6367 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6367 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6367 gene encodes GR6367 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6367 precursor RNA folds spatially, forming GR6367 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6367 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6367 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6367 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM6166 precursor RNA, GAM25737 precursor RNA, GAM177515 precursor RNA and GAM200005 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6166 RNA, GAM25737 RNA, GAM177515 RNA and GAM200005 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6166 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6166 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6166 target RNA into GAM6166 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM25737 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM25737 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM25737 target RNA into GAM25737 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM177515 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM177515 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM177515 target RNA into GAM177515 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM200005 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM200005 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM200005 target RNA into GAM200005 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6367 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6367 gene: GAM6166 target protein, GAM25737 target protein, GAM177515 target protein and GAM200005 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6166, GAM25737, GAM177515 and GAM200005

GR6368 BF691534 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6368(GR6368) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6368 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6368 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6368 gene encodes GR6368 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6368 precursor RNA folds spatially, forming GR6368 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6368 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6368 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6368 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM5895 precursor RNA, GAM8435 precursor RNA and GAM60324 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5895 RNA, GAM8435 RNA and GAM60324 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5895 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5895 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5895 target RNA into GAM5895 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8435 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8435 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8435 target RNA into GAM8435 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM60324 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM60324 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM60324 target RNA into GAM60324 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6368 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6368 gene: GAM5895 target protein, GAM8435 target protein and GAM60324 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6,

hereby incorporated by reference, with references to GAM5895, GAM8435 and GAM60324

GR6369 AI815218 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6369 (GR6369) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6369 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6369 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6369 gene encodes GR6369 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6369 precursor RNA folds spatially, forming GR6369 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6369 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6369 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6369 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM139687 precursor RNA and GAM247224 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM139687 RNA and GAM247224 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM139687 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM139687 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM139687 target RNA into GAM139687 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM247224 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM247224 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM247224 target RNA into GAM247224 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6369 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6369 gene: GAM139687 target protein and GAM247224 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM139687 and GAM247224

GR6370 AV651771 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6370(GR6370) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6370 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6370 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6370 gene encodes GR6370 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6370 precursor RNA folds spatially, forming GR6370 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6370 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6370 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6370 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM6986 precursor RNA, GAM140857 precursor RNA and GAM206236 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM6986 RNA, GAM140857 RNA and GAM206236 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6986 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6986 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6986 target RNA into GAM6986 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM140857 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM140857 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM140857 target RNA into GAM140857 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM206236 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM206236 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM206236 target RNA into GAM206236 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6370 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6370 gene: GAM6986 target protein, GAM140857 target protein and GAM206236 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6986, GAM140857 and GAM206236

GR6371 BF338008 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6371 (GR6371) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6371 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6371 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6371 gene encodes GR6371 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6371 precursor RNA folds spatially, forming GR6371 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6371 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6371 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6371 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM262234 precursor RNA and GAM306215 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM262234 RNA and GAM306215 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM262234 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM262234 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM262234 target RNA into GAM262234 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM306215 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM306215 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM306215 target RNA into GAM306215 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6371 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6371 gene: GAM262234 target protein and GAM306215 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference,

with references to GAM262234 and GAM306215

GR6372 AA335417 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6372(GR6372) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6372 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6372 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6372 gene encodes GR6372 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6372 precursor RNA folds spatially, forming GR6372 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6372 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6372 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6372 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM100619 precursor RNA and GAM276219 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM100619 RNA and GAM276219 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM100619 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM100619 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM100619 target RNA into GAM100619 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM276219 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM276219 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM276219 target RNA into GAM276219 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6372 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6372 gene: GAM100619 target protein and GAM276219 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM100619 and GAM276219

GR6373 AA062950 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6373(GR6373) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6373 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6373 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6373 gene encodes GR6373 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6373 precursor RNA folds spatially, forming GR6373 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6373 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6373 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6373 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8649 precursor RNA and GAM229470 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8649 RNA and GAM229470 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding

to GAM RNA of Fig. 8.

GAM8649 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8649 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8649 target RNA into GAM8649 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM229470 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM229470 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM229470 target RNA into GAM229470 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6373 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6373 gene: GAM8649 target protein and GAM229470 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8649 and GAM229470

GR6374 BE179027 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6374(GR6374) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6374 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6374 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6374 gene encodes GR6374 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6374 precursor RNA folds spatially, forming GR6374 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6374 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6374 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR6374 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1004 precursor RNA and GAM31015 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1004 RNA and GAM31015 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1004 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1004 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1004 target RNA into GAM1004 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM31015 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM31015 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM31015 target RNA into GAM31015 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6374 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6374 gene: GAM1004 target protein and GAM31015 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1004 and GAM31015

GR6375 AI732450 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6375(GR6375) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6375 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6375

gene was detected is described hereinabove with reference to Figs. 8-18.

GR6375 gene encodes GR6375 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6375 precursor RNA folds spatially, forming GR6375 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6375 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6375 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6375 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM31262 precursor RNA and GAM304699 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM31262 RNA and GAM304699 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM31262 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM31262 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM31262 target RNA into GAM31262 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM304699 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM304699 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM304699 target RNA into GAM304699 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6375 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6375 gene: GAM31262 target protein and GAM304699 target protein, herein schematically represented by GAM1

TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM31262 and GAM304699

GR6376 R78101 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6376(GR6376) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6376 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6376 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6376 gene encodes GR6376 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6376 precursor RNA folds spatially, forming GR6376 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6376 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6376 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6376 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6907 precursor RNA and GAM15261 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6907 RNA and GAM15261 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6907 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6907 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6907 target RNA into GAM6907 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM15261 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM15261 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM15261 target RNA into GAM15261 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6376 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6376 gene: GAM6907 target protein and GAM15261 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6907 and GAM15261

GR6377 AA196425 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6377(GR6377) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6377 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6377 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6377 gene encodes GR6377 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6377 precursor RNA folds spatially, forming GR6377 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6377 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6377 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6377 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3790 precursor RNA and GAM126591 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM3790 RNA and GAM126591 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3790 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3790 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3790 target RNA into GAM3790 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM126591 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM126591 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM126591 target RNA into GAM126591 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6377 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6377 gene: GAM3790 target protein and GAM126591 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3790 and GAM126591

GR6378 AA984849 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6378(GR6378) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6378 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6378 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6378 gene encodes GR6378 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6378 precursor RNA folds spatially, forming GR6378 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6378 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6378 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6378 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7793 precursor RNA and GAM69698 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7793 RNA and GAM69698 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7793 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7793 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7793 target RNA into GAM7793 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM69698 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM69698 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM69698 target RNA into GAM69698 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6378 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6378 gene: GAM7793 target protein and GAM69698 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7793 and GAM69698

GR6379 BE271420 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6379(GR6379) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6379 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6379 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6379 gene encodes GR6379 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6379 precursor RNA folds spatially, forming GR6379 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6379 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6379 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6379 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM119023 precursor RNA, GAM200357 precursor RNA, GAM210474 precursor RNA and GAM294848 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM119023 RNA, GAM200357 RNA, GAM210474 RNA and GAM294848 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM119023 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM119023 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM119023 target RNA into GAM119023 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM200357 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM200357 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM200357 target RNA into GAM200357 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM210474 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM210474 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM210474 target RNA into GAM210474 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM294848 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM294848 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM294848 target RNA into GAM294848 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6379 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6379 gene: GAM119023 target protein, GAM200357 target protein, GAM210474 target protein and GAM294848 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM119023, GAM200357, GAM210474 and GAM294848

GR6380 BQ068796 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6380 (GR6380) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6380 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6380 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6380 gene encodes GR6380 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6380 precursor RNA folds spatially, forming GR6380 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6380 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6380 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6380 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2

separate GAM precursor RNAs, GAM6655 precursor RNA and GAM6777 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6655 RNA and GAM6777 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6655 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6655 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6655 target RNA into GAM6655 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6777 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6777 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6777 target RNA into GAM6777 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6380 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6380 gene: GAM6655 target protein and GAM6777 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6655 and GAM6777

GR6381 AV732209 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6381 (GR6381) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6381 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6381 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6381 gene encodes GR6381 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR6381 precursor RNA folds spatially, forming GR6381 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6381 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6381 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6381 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM229602 precursor RNA, GAM300413 precursor RNA and GAM300809 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM229602 RNA, GAM300413 RNA and GAM300809 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM229602 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM229602 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM229602 target RNA into GAM229602 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM300413 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM300413 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM300413 target RNA into GAM300413 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM300809 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM300809 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM300809 target RNA into GAM300809 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6381 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6381 gene: GAM229602 target protein, GAM300413 target protein and GAM300809 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM229602, GAM300413 and GAM300809

GR6382 AI247210 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6382(GR6382) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6382 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6382 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6382 gene encodes GR6382 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6382 precursor RNA folds spatially, forming GR6382 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6382 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6382 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6382 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4974 precursor RNA, GAM144105 precursor RNA and GAM218835 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4974 RNA, GAM144105 RNA and GAM218835 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4974 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM4974 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4974 target RNA into GAM4974 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM144105 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM144105 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM144105 target RNA into GAM144105 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM218835 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM218835 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM218835 target RNA into GAM218835 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6382 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6382 gene: GAM4974 target protein, GAM144105 target protein and GAM218835 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4974, GAM144105 and GAM218835

GR6383 AW867166 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6383(GR6383) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6383 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6383 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6383 gene encodes GR6383 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6383 precursor RNA folds spatially, forming GR6383 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated

that GR6383 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6383 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6383 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1966 precursor RNA and GAM236168 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1966 RNA and GAM236168 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1966 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1966 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1966 target RNA into GAM1966 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM236168 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM236168 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM236168 target RNA into GAM236168 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6383 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6383 gene: GAM1966 target protein and GAM236168 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1966 and GAM236168

GR6384 BF508133 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6384(GR6384) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR6384 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6384 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6384 gene encodes GR6384 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6384 precursor RNA folds spatially, forming GR6384 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6384 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6384 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6384 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM171374 precursor RNA and GAM288345 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM171374 RNA and GAM288345 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM171374 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM171374 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM171374 target RNA into GAM171374 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM288345 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM288345 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM288345 target RNA into GAM288345 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6384 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6384 gene: GAM171374 target protein and GAM288345 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM171374 and GAM288345

GR6385 AW972300 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6385(GR6385) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6385 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6385 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6385 gene encodes GR6385 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6385 precursor RNA folds spatially, forming GR6385 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6385 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6385 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6385 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM157366 precursor RNA and GAM255576 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM157366 RNA and GAM255576 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM157366 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM157366 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM157366 target RNA into GAM157366 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM255576 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM255576 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM255576 target RNA into GAM255576 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6385 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6385 gene: GAM157366 target protein and GAM255576 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM157366 and GAM255576

GR6386 BF792442 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6386(GR6386) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6386 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6386 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6386 gene encodes GR6386 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6386 precursor RNA folds spatially, forming GR6386 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6386 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6386 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6386 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5391 precursor RNA and GAM267686 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3

FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5391 RNA and GAM267686 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5391 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5391 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5391 target RNA into GAM5391 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM267686 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM267686 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM267686 target RNA into GAM267686 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6386 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6386 gene: GAM5391 target protein and GAM267686 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5391 and GAM267686

GR6387 BM478999 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6387(GR6387) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6387 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6387 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6387 gene encodes GR6387 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6387 precursor RNA folds spatially, forming GR6387 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6387 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6387 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6387 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM205717 precursor RNA and GAM288432 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM205717 RNA and GAM288432 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM205717 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM205717 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM205717 target RNA into GAM205717 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM288432 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM288432 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM288432 target RNA into GAM288432 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6387 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6387 gene: GAM205717 target protein and GAM288432 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM205717 and GAM288432

6388(GR6388) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6388 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6388 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6388 gene encodes GR6388 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6388 precursor RNA folds spatially, forming GR6388 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6388 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6388 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6388 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM669 precursor RNA, GAM30598 precursor RNA, GAM75566 precursor RNA and GAM287056 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM669 RNA, GAM30598 RNA, GAM75566 RNA and GAM287056 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM669 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM669 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM669 target RNA into GAM669 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM30598 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM30598 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM30598

target RNA into GAM30598 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM75566 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM75566 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM75566 target RNA into GAM75566 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM287056 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM287056 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM287056 target RNA into GAM287056 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6388 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6388 gene: GAM669 target protein, GAM30598 target protein, GAM75566 target protein and GAM287056 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM669, GAM30598, GAM75566 and GAM287056

GR6389 AW406383 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6389(GR6389) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6389 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6389 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6389 gene encodes GR6389 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6389 precursor RNA folds spatially, forming GR6389 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6389 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6389 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6389 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM10620 precursor RNA and GAM328733 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM10620 RNA and GAM328733 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM10620 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM10620 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM10620 target RNA into GAM10620 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM328733 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM328733 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM328733 target RNA into GAM328733 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6389 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6389 gene: GAM10620 target protein and GAM328733 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM10620 and GAM328733

GR6390 AI933107 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6390 (GR6390) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6390 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR6390 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6390 gene encodes GR6390 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6390 precursor RNA folds spatially, forming GR6390 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6390 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6390 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6390 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3866 precursor RNA and GAM335973 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3866 RNA and GAM335973 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3866 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3866 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3866 target RNA into GAM3866 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM335973 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM335973 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM335973 target RNA into GAM335973 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6390 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6390 gene: GAM3866 target

protein and GAM335973 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3866 and GAM335973

GR6391 AI620792 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6391 (GR6391) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6391 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6391 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6391 gene encodes GR6391 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6391 precursor RNA folds spatially, forming GR6391 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6391 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6391 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6391 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM10714 precursor RNA and GAM42362 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM10714 RNA and GAM42362 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM10714 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM10714 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM10714 target RNA into GAM10714 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM42362 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM42362 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM42362 target RNA into GAM42362 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6391 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6391 gene: GAM10714 target protein and GAM42362 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM10714 and GAM42362

GR6392 BI767822 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6392(GR6392) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6392 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6392 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6392 gene encodes GR6392 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6392 precursor RNA folds spatially, forming GR6392 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6392 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6392 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6392 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM130109 precursor RNA and GAM331320 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM130109 RNA and GAM331320 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM130109 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM130109 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM130109 target RNA into GAM130109 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM331320 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM331320 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM331320 target RNA into GAM331320 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6392 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6392 gene: GAM130109 target protein and GAM331320 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM130109 and GAM331320

GR6393 AA481149 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6393(GR6393) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6393 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6393 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6393 gene encodes GR6393 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6393 precursor RNA folds spatially, forming GR6393 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6393 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR6393 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6393 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM258992 precursor RNA and GAM297196 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM258992 RNA and GAM297196 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM258992 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM258992 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM258992 target RNA into GAM258992 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM297196 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM297196 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM297196 target RNA into GAM297196 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6393 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6393 gene: GAM258992 target protein and GAM297196 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM258992 and GAM297196

GR6394 BF184859 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6394(GR6394) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6394 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6394 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6394 gene encodes GR6394 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6394 precursor RNA folds spatially, forming GR6394 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6394 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6394 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6394 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4122 precursor RNA and GAM13271 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4122 RNA and GAM13271 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4122 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4122 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4122 target RNA into GAM4122 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM13271 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM13271 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM13271 target RNA into GAM13271 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6394 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6394 gene: GAM4122 target protein and GAM13271 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4122 and GAM13271

GR6395 BE395137 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6395(GR6395) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6395 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6395 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6395 gene encodes GR6395 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6395 precursor RNA folds spatially, forming GR6395 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6395 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6395 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6395 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8633 precursor RNA and GAM155847 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8633 RNA and GAM155847 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8633 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8633 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8633 target RNA into

GAM8633 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM155847 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM155847 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM155847 target RNA into GAM155847 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6395 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6395 gene: GAM8633 target protein and GAM155847 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8633 and GAM155847

GR6396 BI094257 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6396(GR6396) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6396 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6396 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6396 gene encodes GR6396 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6396 precursor RNA folds spatially, forming GR6396 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6396 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6396 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6396 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM5926 precursor RNA, GAM40018 precursor RNA and GAM187659 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED

PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5926 RNA, GAM40018 RNA and GAM187659 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5926 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5926 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5926 target RNA into GAM5926 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM40018 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM40018 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM40018 target RNA into GAM40018 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM187659 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM187659 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM187659 target RNA into GAM187659 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6396 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6396 gene: GAM5926 target protein, GAM40018 target protein and GAM187659 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5926, GAM40018 and GAM187659

GR6397 AA609325 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6397(GR6397) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6397 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6397 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6397 gene encodes GR6397 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6397 precursor RNA folds spatially, forming GR6397 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6397 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6397 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6397 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1641 precursor RNA and GAM242400 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1641 RNA and GAM242400 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1641 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1641 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1641 target RNA into GAM1641 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM242400 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM242400 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM242400 target RNA into GAM242400 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6397 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR6397 gene: GAM1641 target protein and GAM242400 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1641 and GAM242400

GR6398 BF513608 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6398(GR6398) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6398 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6398 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6398 gene encodes GR6398 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6398 precursor RNA folds spatially, forming GR6398 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6398 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6398 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6398 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM89198 precursor RNA and GAM274390 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM89198 RNA and GAM274390 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM89198 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM89198 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM89198 target RNA into GAM89198 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM274390 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM274390 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM274390 target RNA into GAM274390 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6398 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6398 gene: GAM89198 target protein and GAM274390 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM89198 and GAM274390

GR6399 N75148 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6399(GR6399) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6399 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6399 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6399 gene encodes GR6399 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6399 precursor RNA folds spatially, forming GR6399 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6399 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6399 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6399 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7141 precursor RNA and GAM203725 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7141 RNA and GAM203725 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7141 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7141 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7141 target RNA into GAM7141 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM203725 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM203725 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM203725 target RNA into GAM203725 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6399 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6399 gene: GAM7141 target protein and GAM203725 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7141 and GAM203725

GR6400 BM263587 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6400(GR6400) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6400 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6400 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6400 gene encodes GR6400 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6400 precursor RNA folds spatially, forming GR6400 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6400 folded precursor RNA comprises a plurality of what is known in the

art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6400 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6400 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8070 precursor RNA and GAM137693 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8070 RNA and GAM137693 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8070 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8070 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8070 target RNA into GAM8070 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM137693 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM137693 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM137693 target RNA into GAM137693 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6400 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6400 gene: GAM8070 target protein and GAM137693 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8070 and GAM137693

GR6401 AL711070 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6401(GR6401) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR6401 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6401 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6401 gene encodes GR6401 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6401 precursor RNA folds spatially, forming GR6401 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6401 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6401 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6401 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM246342 precursor RNA and GAM250877 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM246342 RNA and GAM250877 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM246342 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM246342 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM246342 target RNA into GAM246342 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM250877 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM250877 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM250877 target RNA into GAM250877 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly

utilities, of GR6401 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6401 gene: GAM246342 target protein and GAM250877 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM246342 and GAM250877

GR6402 AA369588 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6402(GR6402) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6402 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6402 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6402 gene encodes GR6402 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6402 precursor RNA folds spatially, forming GR6402 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6402 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6402 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6402 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1564 precursor RNA, GAM184334 precursor RNA and GAM322978 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1564 RNA, GAM184334 RNA and GAM322978 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1564 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1564 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds

to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1564 target RNA into GAM1564 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM184334 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM184334 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM184334 target RNA into GAM184334 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM322978 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM322978 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM322978 target RNA into GAM322978 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6402 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6402 gene: GAM1564 target protein, GAM184334 target protein and GAM322978 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1564, GAM184334 and GAM322978

GR6403 T39189 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6403(GR6403) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6403 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6403 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6403 gene encodes GR6403 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6403 precursor RNA folds spatially, forming GR6403 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6403 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR6403 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6403 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM33281 precursor RNA and GAM106814 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM33281 RNA and GAM106814 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM33281 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM33281 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM33281 target RNA into GAM33281 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM106814 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM106814 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM106814 target RNA into GAM106814 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6403 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6403 gene: GAM33281 target protein and GAM106814 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM33281 and GAM106814

GR6404 AI878948 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6404(GR6404) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6404 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6404 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6404 gene encodes GR6404 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6404 precursor RNA folds spatially, forming GR6404 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6404 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6404 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6404 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM6276 precursor RNA, GAM24242 precursor RNA, GAM113185 precursor RNA and GAM279690 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6276 RNA, GAM24242 RNA, GAM113185 RNA and GAM279690 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6276 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6276 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6276 target RNA into GAM6276 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM24242 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM24242 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM24242 target RNA into GAM24242 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM113185 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM113185 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM113185 target RNA into GAM113185 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM279690 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM279690 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM279690 target RNA into GAM279690 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6404 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6404 gene: GAM6276 target protein, GAM24242 target protein, GAM113185 target protein and GAM279690 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6276, GAM24242, GAM113185 and GAM279690

GR6405 BE018217 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6405(GR6405) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6405 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6405 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6405 gene encodes GR6405 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6405 precursor RNA folds spatially, forming GR6405 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6405 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6405 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6405 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM75154 precursor RNA and GAM306925 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM75154 RNA and GAM306925 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM75154 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM75154 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM75154 target RNA into GAM75154 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM306925 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM306925 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM306925 target RNA into GAM306925 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6405 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6405 gene: GAM75154 target protein and GAM306925 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM75154 and GAM306925

GR6406 AI083512 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6406(GR6406) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6406 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6406 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6406 gene encodes GR6406 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6406 precursor RNA folds spatially, forming GR6406 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6406 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6406 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6406 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM25197 precursor RNA and GAM67961 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM25197 RNA and GAM67961 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM25197 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM25197 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM25197 target RNA into GAM25197 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM67961 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM67961 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM67961 target RNA into GAM67961 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6406 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6406 gene: GAM25197 target protein and GAM67961 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM25197 and GAM67961

GR6407 BF887843 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6407(GR6407) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6407 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6407 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6407 gene encodes GR6407 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6407 precursor RNA folds spatially, forming GR6407 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6407 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6407 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6407 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM119828 precursor RNA, GAM209815 precursor RNA and GAM269720 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM119828 RNA, GAM209815 RNA and GAM269720 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM119828 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM119828 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM119828 target RNA into GAM119828 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM209815 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM209815 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM209815 target RNA into GAM209815 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM269720 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM269720 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM269720 target RNA into GAM269720 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6407 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6407 gene: GAM119828 target protein, GAM209815 target protein and GAM269720 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM119828, GAM209815 and GAM269720

GR6408 BG202500 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6408(GR6408) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6408 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6408 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6408 gene encodes GR6408 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6408 precursor RNA folds spatially, forming GR6408 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6408 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6408 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6408 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2

separate GAM precursor RNAs, GAM80893 precursor RNA and GAM102254 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM80893 RNA and GAM102254 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM80893 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM80893 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM80893 target RNA into GAM80893 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM102254 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM102254 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM102254 target RNA into GAM102254 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6408 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6408 gene: GAM80893 target protein and GAM102254 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM80893 and GAM102254

GR6409 BG823328 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6409(GR6409) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6409 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6409 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6409 gene encodes GR6409 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR6409 precursor RNA folds spatially, forming GR6409 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6409 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6409 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6409 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5332 precursor RNA and GAM277662 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5332 RNA and GAM277662 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5332 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5332 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5332 target RNA into GAM5332 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM277662 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM277662 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM277662 target RNA into GAM277662 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6409 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6409 gene: GAM5332 target protein and GAM277662 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5332 and GAM277662

GR6410 BI544260 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6410 (GR6410) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6410 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6410 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6410 gene encodes GR6410 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6410 precursor RNA folds spatially, forming GR6410 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6410 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6410 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6410 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM226852 precursor RNA and GAM244292 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM226852 RNA and GAM244292 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM226852 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM226852 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM226852 target RNA into GAM226852 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM244292 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM244292 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM244292 target RNA into GAM244292 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6410 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6410 gene: GAM226852 target protein and GAM244292 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM226852 and GAM244292

GR6411 BE565660 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6411 (GR6411) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6411 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6411 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6411 gene encodes GR6411 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6411 precursor RNA folds spatially, forming GR6411 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6411 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6411 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6411 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7877 precursor RNA and GAM89505 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7877 RNA and GAM89505 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7877 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7877 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7877 target RNA into GAM7877 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM89505 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM89505 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM89505 target RNA into GAM89505 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6411 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6411 gene: GAM7877 target protein and GAM89505 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7877 and GAM89505

GR6412 AW371741 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6412(GR6412) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6412 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6412 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6412 gene encodes GR6412 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6412 precursor RNA folds spatially, forming GR6412 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6412 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6412 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6412 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2940 precursor RNA and GAM282013 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2940 RNA and GAM282013 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2940 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2940 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2940 target RNA into GAM2940 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM282013 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM282013 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM282013 target RNA into GAM282013 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6412 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6412 gene: GAM2940 target protein and GAM282013 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2940 and GAM282013

GR6413 BI837151 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6413(GR6413) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6413 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6413 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6413 gene encodes GR6413 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6413 precursor RNA folds spatially, forming GR6413 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6413 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6413 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6413 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM293106 precursor RNA and GAM322192 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM293106 RNA and GAM322192 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM293106 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM293106 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM293106 target RNA into GAM293106 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM322192 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM322192 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM322192 target RNA into GAM322192 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6413 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6413 gene: GAM293106 target protein and GAM322192 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference,

with references to GAM293106 and GAM322192

GR6414 AI056472 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6414 (GR6414) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6414 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6414 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6414 gene encodes GR6414 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6414 precursor RNA folds spatially, forming GR6414 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6414 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6414 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6414 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM44587 precursor RNA and GAM220691 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM44587 RNA and GAM220691 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM44587 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM44587 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM44587 target RNA into GAM44587 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM220691 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM220691 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM220691 target RNA into GAM220691 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6414 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6414 gene: GAM44587 target protein and GAM220691 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM44587 and GAM220691

GR6415 AW001829 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6415(GR6415) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6415 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6415 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6415 gene encodes GR6415 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6415 precursor RNA folds spatially, forming GR6415 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6415 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6415 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6415 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM28 precursor RNA and GAM6398 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM28 RNA and GAM6398 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding

to GAM RNA of Fig. 8.

GAM28 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM28 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM28 target RNA into GAM28 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6398 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6398 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6398 target RNA into GAM6398 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6415 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6415 gene: GAM28 target protein and GAM6398 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM28 and GAM6398

GR6416 BE835966 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6416(GR6416) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6416 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6416 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6416 gene encodes GR6416 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6416 precursor RNA folds spatially, forming GR6416 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6416 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6416 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR6416 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1601 precursor RNA and GAM3068 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1601 RNA and GAM3068 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1601 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1601 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1601 target RNA into GAM1601 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM3068 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3068 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3068 target RNA into GAM3068 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6416 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6416 gene: GAM1601 target protein and GAM3068 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1601 and GAM3068

GR6417 AA404708 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6417(GR6417) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6417 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6417

gene was detected is described hereinabove with reference to Figs. 8-18.

GR6417 gene encodes GR6417 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6417 precursor RNA folds spatially, forming GR6417 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6417 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6417 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6417 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM85420 precursor RNA and GAM163066 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM85420 RNA and GAM163066 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM85420 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM85420 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM85420 target RNA into GAM85420 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM163066 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM163066 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM163066 target RNA into GAM163066 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6417 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6417 gene: GAM85420 target protein and GAM163066 target protein, herein schematically represented by GAM1

TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM85420 and GAM163066

GR6418 BF688936 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6418(GR6418) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6418 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6418 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6418 gene encodes GR6418 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6418 precursor RNA folds spatially, forming GR6418 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6418 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6418 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6418 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5250 precursor RNA and GAM71293 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5250 RNA and GAM71293 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5250 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5250 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5250 target RNA into GAM5250 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM71293 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM71293 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM71293 target RNA into GAM71293 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6418 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6418 gene: GAM5250 target protein and GAM71293 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5250 and GAM71293

GR6419 AI351503 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6419(GR6419) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6419 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6419 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6419 gene encodes GR6419 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6419 precursor RNA folds spatially, forming GR6419 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6419 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6419 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6419 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM48318 precursor RNA and GAM240657 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM48318 RNA and GAM240657 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM48318 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM48318 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM48318 target RNA into GAM48318 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM240657 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM240657 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM240657 target RNA into GAM240657 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6419 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6419 gene: GAM48318 target protein and GAM240657 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM48318 and GAM240657

GR6420 AW015958 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6420 (GR6420) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6420 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6420 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6420 gene encodes GR6420 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6420 precursor RNA folds spatially, forming GR6420 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6420 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6420 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6420 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM264355 precursor RNA and GAM336064 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM264355 RNA and GAM336064 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM264355 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM264355 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM264355 target RNA into GAM264355 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336064 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336064 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336064 target RNA into GAM336064 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6420 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6420 gene: GAM264355 target protein and GAM336064 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM264355 and GAM336064

GR6421 BE272976 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6421(GR6421) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6421 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6421 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6421 gene encodes GR6421 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6421 precursor RNA folds spatially, forming GR6421 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6421 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6421 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6421 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3546 precursor RNA, GAM8608 precursor RNA and GAM118095 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3546 RNA, GAM8608 RNA and GAM118095 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3546 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3546 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3546 target RNA into GAM3546 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8608 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8608 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8608 target RNA into GAM8608 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM118095 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM118095 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM118095 target RNA into GAM118095 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6421 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6421 gene: GAM3546 target protein, GAM8608 target protein and GAM118095 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3546, GAM8608 and GAM118095

GR6422 BG720019 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6422(GR6422) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6422 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6422 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6422 gene encodes GR6422 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6422 precursor RNA folds spatially, forming GR6422 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6422 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6422 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6422 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4433 precursor RNA and GAM163676 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4433 RNA and GAM163676 RNA, herein schematically

represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4433 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4433 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4433 target RNA into GAM4433 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM163676 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM163676 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM163676 target RNA into GAM163676 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6422 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6422 gene: GAM4433 target protein and GAM163676 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4433 and GAM163676

GR6423 AW363590 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6423(GR6423) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6423 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6423 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6423 gene encodes GR6423 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6423 precursor RNA folds spatially, forming GR6423 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6423 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6423 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6423 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM7822 precursor RNA, GAM7982 precursor RNA and GAM104805 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7822 RNA, GAM7982 RNA and GAM104805 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7822 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7822 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7822 target RNA into GAM7822 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7982 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7982 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7982 target RNA into GAM7982 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM104805 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM104805 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM104805 target RNA into GAM104805 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6423 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6423 gene: GAM7822 target protein, GAM7982 target protein and GAM104805 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7822, GAM7982 and

GR6424 AU148279 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6424 (GR6424) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6424 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6424 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6424 gene encodes GR6424 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6424 precursor RNA folds spatially, forming GR6424 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6424 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6424 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6424 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM49164 precursor RNA and GAM128185 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM49164 RNA and GAM128185 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM49164 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM49164 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM49164 target RNA into GAM49164 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM128185 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM128185 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM128185 target RNA into GAM128185 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6424 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6424 gene: GAM49164 target protein and GAM128185 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM49164 and GAM128185

GR6425 BI083844 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6425(GR6425) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6425 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6425 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6425 gene encodes GR6425 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6425 precursor RNA folds spatially, forming GR6425 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6425 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6425 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6425 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2974 precursor RNA and GAM208398 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2974 RNA and GAM208398 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding

to GAM RNA of Fig. 8.

GAM2974 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2974 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2974 target RNA into GAM2974 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM208398 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM208398 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM208398 target RNA into GAM208398 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6425 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6425 gene: GAM2974 target protein and GAM208398 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2974 and GAM208398

GR6426 BF242411 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6426(GR6426) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6426 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6426 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6426 gene encodes GR6426 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6426 precursor RNA folds spatially, forming GR6426 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6426 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6426 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR6426 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM63463 precursor RNA, GAM184381 precursor RNA and GAM304895 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM63463 RNA, GAM184381 RNA and GAM304895 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM63463 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM63463 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM63463 target RNA into GAM63463 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM184381 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM184381 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM184381 target RNA into GAM184381 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM304895 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM304895 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM304895 target RNA into GAM304895 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6426 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6426 gene: GAM63463 target protein, GAM184381 target protein and GAM304895 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM63463, GAM184381 and GAM304895

GR6427 AA811027 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6427(GR6427) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6427 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6427 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6427 gene encodes GR6427 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6427 precursor RNA folds spatially, forming GR6427 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6427 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6427 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6427 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM379 precursor RNA and GAM7355 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM379 RNA and GAM7355 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM379 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM379 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM379 target RNA into GAM379 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7355 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7355 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds

to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7355 target RNA into GAM7355 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6427 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6427 gene: GAM379 target protein and GAM7355 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM379 and GAM7355

GR6428 BE559959 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6428(GR6428) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6428 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6428 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6428 gene encodes GR6428 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6428 precursor RNA folds spatially, forming GR6428 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6428 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6428 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6428 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1802 precursor RNA, GAM5387 precursor RNA and GAM7951 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1802 RNA, GAM5387 RNA and GAM7951 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs

corresponding to GAM RNA of Fig. 8.

GAM1802 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1802 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1802 target RNA into GAM1802 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5387 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5387 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5387 target RNA into GAM5387 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7951 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7951 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7951 target RNA into GAM7951 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6428 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6428 gene: GAM1802 target protein, GAM5387 target protein and GAM7951 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1802, GAM5387 and GAM7951

GR6429 BG775965 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6429(GR6429) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6429 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6429 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6429 gene encodes GR6429 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR6429 precursor RNA folds spatially, forming GR6429 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6429 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6429 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6429 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM151 precursor RNA and GAM262603 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM151 RNA and GAM262603 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM151 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM151 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM151 target RNA into GAM151 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM262603 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM262603 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM262603 target RNA into GAM262603 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6429 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6429 gene: GAM151 target protein and GAM262603 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM151 and GAM262603

GR6430 AI674390 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6430 (GR6430) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6430 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6430 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6430 gene encodes GR6430 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6430 precursor RNA folds spatially, forming GR6430 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6430 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6430 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6430 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6349 precursor RNA and GAM70407 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6349 RNA and GAM70407 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6349 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6349 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6349 target RNA into GAM6349 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM70407 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM70407 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM70407 target RNA into GAM70407 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6430 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6430 gene: GAM6349 target protein and GAM70407 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6349 and GAM70407

GR6431 AI656727 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6431 (GR6431) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6431 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6431 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6431 gene encodes GR6431 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6431 precursor RNA folds spatially, forming GR6431 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6431 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6431 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6431 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM27896 precursor RNA and GAM300895 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM27896 RNA and GAM300895 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM27896 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM27896 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM27896 target RNA into GAM27896 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM300895 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM300895 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM300895 target RNA into GAM300895 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6431 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6431 gene: GAM27896 target protein and GAM300895 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM27896 and GAM300895

GR6432 BE890381 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6432(GR6432) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6432 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6432 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6432 gene encodes GR6432 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6432 precursor RNA folds spatially, forming GR6432 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6432 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6432 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6432 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM15614 precursor RNA, GAM168837 precursor RNA and GAM285157 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM15614 RNA, GAM168837 RNA and GAM285157 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM15614 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM15614 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM15614 target RNA into GAM15614 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM168837 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM168837 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM168837 target RNA into GAM168837 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM285157 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM285157 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM285157 target RNA into GAM285157 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6432 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6432 gene: GAM15614 target protein, GAM168837 target protein and GAM285157 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM15614, GAM168837 and GAM285157

bioinformatically detected regulatory gene, referred to here as Genomic Record 6433(GR6433) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6433 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6433 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6433 gene encodes GR6433 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6433 precursor RNA folds spatially, forming GR6433 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6433 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6433 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6433 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1619 precursor RNA and GAM36221 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1619 RNA and GAM36221 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1619 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1619 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1619 target RNA into GAM1619 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM36221 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM36221 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM36221

target RNA into GAM36221 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6433 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6433 gene: GAM1619 target protein and GAM36221 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1619 and GAM36221

GR6434 BI049720 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6434(GR6434) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6434 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6434 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6434 gene encodes GR6434 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6434 precursor RNA folds spatially, forming GR6434 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6434 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6434 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6434 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5903 precursor RNA and GAM33381 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5903 RNA and GAM33381 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5903 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5903 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5903 target RNA into GAM5903 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM33381 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM33381 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM33381 target RNA into GAM33381 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6434 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6434 gene: GAM5903 target protein and GAM33381 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5903 and GAM33381

GR6435 AI333631 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6435(GR6435) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6435 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6435 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6435 gene encodes GR6435 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6435 precursor RNA folds spatially, forming GR6435 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6435 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6435 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6435 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4712 precursor RNA and GAM5531 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4712 RNA and GAM5531 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4712 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4712 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4712 target RNA into GAM4712 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5531 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5531 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5531 target RNA into GAM5531 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6435 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6435 gene: GAM4712 target protein and GAM5531 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4712 and GAM5531

GR6436 AA830025 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6436(GR6436) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6436 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6436 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6436 gene encodes GR6436 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6436 precursor RNA folds spatially, forming GR6436 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6436 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6436 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6436 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM41227 precursor RNA and GAM180868 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM41227 RNA and GAM180868 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM41227 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM41227 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM41227 target RNA into GAM41227 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM180868 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM180868 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM180868 target RNA into GAM180868 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6436 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6436 gene: GAM41227 target protein and GAM180868 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM41227 and GAM180868

GR6437 AI689086 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6437(GR6437) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6437 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6437 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6437 gene encodes GR6437 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6437 precursor RNA folds spatially, forming GR6437 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6437 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6437 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6437 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6187 precursor RNA and GAM144990 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6187 RNA and GAM144990 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6187 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6187 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6187 target RNA into GAM6187 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM144990 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM144990 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM144990 target RNA into GAM144990 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6437 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6437 gene: GAM6187 target protein and GAM144990 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6187 and GAM144990

GR6438 BI520228 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6438(GR6438) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6438 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6438 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6438 gene encodes GR6438 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6438 precursor RNA folds spatially, forming GR6438 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6438 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6438 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6438 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM28651 precursor RNA and GAM217949 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM28651 RNA and GAM217949 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM28651 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM28651 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM28651 target RNA into GAM28651 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM217949 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM217949 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM217949 target RNA into GAM217949 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6438 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6438 gene: GAM28651 target protein and GAM217949 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM28651 and GAM217949

GR6439 BE545749 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6439(GR6439) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6439 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6439 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6439 gene encodes GR6439 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6439 precursor RNA folds spatially, forming GR6439 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6439 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6439 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6439 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM283471 precursor RNA and GAM305159 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM283471 RNA and GAM305159 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM283471 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM283471 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM283471 target RNA into GAM283471 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM305159 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM305159 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM305159 target RNA into GAM305159 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6439 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6439 gene: GAM283471 target protein and GAM305159 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM283471 and GAM305159

GR6440 BF509048 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6440(GR6440) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6440 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6440 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6440 gene encodes GR6440 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6440 precursor RNA folds spatially, forming GR6440 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6440 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6440 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6440 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1376 precursor RNA, GAM4629 precursor RNA and GAM95099 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1376 RNA, GAM4629 RNA and GAM95099 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1376 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1376 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1376 target RNA into GAM1376 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM4629 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4629 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4629 target RNA into GAM4629 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM95099 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM95099 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM95099

target RNA into GAM95099 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6440 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6440 gene: GAM1376 target protein, GAM4629 target protein and GAM95099 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1376, GAM4629 and GAM95099

GR6441 BG771742 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6441 (GR6441) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6441 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6441 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6441 gene encodes GR6441 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6441 precursor RNA folds spatially, forming GR6441 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6441 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6441 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6441 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 5 separate GAM precursor RNAs, GAM2714 precursor RNA, GAM7580 precursor RNA, GAM257772 precursor RNA, GAM258036 precursor RNA and GAM322238 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2714 RNA, GAM7580 RNA, GAM257772 RNA, GAM258036 RNA and GAM322238 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2714 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2714 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2714 target RNA into GAM2714 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7580 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7580 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7580 target RNA into GAM7580 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM257772 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM257772 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM257772 target RNA into GAM257772 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM258036 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM258036 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM258036 target RNA into GAM258036 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM322238 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM322238 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM322238 target RNA into GAM322238 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6441 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6441 gene: GAM2714 target protein, GAM7580 target protein, GAM257772 target protein, GAM258036 target protein and GAM322238 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference,

with references to GAM2714, GAM7580, GAM257772, GAM258036 and GAM322238

GR6442 BI116840 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6442(GR6442) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6442 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6442 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6442 gene encodes GR6442 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6442 precursor RNA folds spatially, forming GR6442 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6442 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6442 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6442 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 5 separate GAM precursor RNAs, GAM1536 precursor RNA, GAM5032 precursor RNA, GAM17481 precursor RNA, GAM119185 precursor RNA and GAM272836 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1536 RNA, GAM5032 RNA, GAM17481 RNA, GAM119185 RNA and GAM272836 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1536 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1536 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1536 target RNA into GAM1536 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5032 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM5032 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5032 target RNA into GAM5032 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM17481 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM17481 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM17481 target RNA into GAM17481 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM119185 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM119185 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM119185 target RNA into GAM119185 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM272836 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM272836 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM272836 target RNA into GAM272836 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6442 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6442 gene: GAM1536 target protein, GAM5032 target protein, GAM17481 target protein, GAM119185 target protein and GAM272836 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1536, GAM5032, GAM17481, GAM119185 and GAM272836

GR6443 BF224401 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6443(GR6443) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6443 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6443

gene was detected is described hereinabove with reference to Figs. 8-18.

GR6443 gene encodes GR6443 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6443 precursor RNA folds spatially, forming GR6443 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6443 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6443 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6443 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8172 precursor RNA and GAM8530 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8172 RNA and GAM8530 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8172 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8172 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8172 target RNA into GAM8172 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8530 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8530 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8530 target RNA into GAM8530 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6443 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6443 gene: GAM8172 target protein and GAM8530 target protein, herein schematically represented by GAM1

TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8172 and GAM8530

GR6444 AI866040 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6444(GR6444) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6444 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6444 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6444 gene encodes GR6444 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6444 precursor RNA folds spatially, forming GR6444 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6444 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6444 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6444 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM217731 precursor RNA and GAM223132 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM217731 RNA and GAM223132 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM217731 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM217731 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM217731 target RNA into GAM217731 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM223132 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM223132 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM223132 target RNA into GAM223132 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6444 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6444 gene: GAM217731 target protein and GAM223132 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM217731 and GAM223132

GR6445 AA625193 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6445(GR6445) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6445 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6445 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6445 gene encodes GR6445 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6445 precursor RNA folds spatially, forming GR6445 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6445 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6445 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6445 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM94742 precursor RNA, GAM11693 precursor RNA and GAM155015 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM94742 RNA, GAM111693 RNA and GAM155015 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM94742 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM94742 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM94742 target RNA into GAM94742 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM111693 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM111693 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM111693 target RNA into GAM111693 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM155015 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM155015 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM155015 target RNA into GAM155015 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6445 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6445 gene: GAM94742 target protein, GAM111693 target protein and GAM155015 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM94742, GAM111693 and GAM155015

GR6446 BE798958 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6446(GR6446) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6446 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6446 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6446 gene encodes GR6446 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6446 precursor RNA folds spatially, forming GR6446 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6446 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6446 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6446 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM66998 precursor RNA and GAM286353 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM66998 RNA and GAM286353 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM66998 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM66998 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM66998 target RNA into GAM66998 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM286353 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM286353 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM286353 target RNA into GAM286353 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6446 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6446 gene: GAM66998 target protein and GAM286353 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes

is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM66998 and GAM286353

GR6447 BG519706 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6447(GR6447) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6447 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6447 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6447 gene encodes GR6447 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6447 precursor RNA folds spatially, forming GR6447 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6447 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6447 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6447 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4349 precursor RNA and GAM159629 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4349 RNA and GAM159629 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4349 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4349 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4349 target RNA into GAM4349 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM159629 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM159629 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM159629 target RNA into GAM159629 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6447 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6447 gene: GAM4349 target protein and GAM159629 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4349 and GAM159629

GR6448 BF568673 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6448(GR6448) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6448 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6448 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6448 gene encodes GR6448 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6448 precursor RNA folds spatially, forming GR6448 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6448 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6448 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6448 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6535 precursor RNA and GAM100030 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6535 RNA and GAM100030 RNA, herein schematically

represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6535 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6535 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6535 target RNA into GAM6535 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM100030 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM100030 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM100030 target RNA into GAM100030 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6448 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6448 gene: GAM6535 target protein and GAM100030 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6535 and GAM100030

GR6449 BG209684 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6449(GR6449) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6449 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6449 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6449 gene encodes GR6449 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6449 precursor RNA folds spatially, forming GR6449 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6449 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6449 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6449 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1437 precursor RNA and GAM1696 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1437 RNA and GAM1696 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1437 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1437 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1437 target RNA into GAM1437 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM1696 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1696 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1696 target RNA into GAM1696 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6449 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6449 gene: GAM1437 target protein and GAM1696 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1437 and GAM1696

GR6450 N41751 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6450(GR6450) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6450 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR6450 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6450 gene encodes GR6450 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6450 precursor RNA folds spatially, forming GR6450 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6450 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6450 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6450 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM104091 precursor RNA and GAM287421 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM104091 RNA and GAM287421 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM104091 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM104091 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM104091 target RNA into GAM104091 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM287421 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM287421 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM287421 target RNA into GAM287421 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6450 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6450 gene: GAM104091 target

protein and GAM287421 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM104091 and GAM287421

GR6451 BG426830 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6451 (GR6451) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6451 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6451 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6451 gene encodes GR6451 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6451 precursor RNA folds spatially, forming GR6451 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6451 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6451 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6451 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM8456 precursor RNA, GAM36590 precursor RNA and GAM237232 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8456 RNA, GAM36590 RNA and GAM237232 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8456 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8456 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8456 target RNA into GAM8456 target protein, herein schematically represented by GAM1 TARGET

PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM36590 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM36590 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM36590 target RNA into GAM36590 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM237232 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM237232 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM237232 target RNA into GAM237232 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6451 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6451 gene: GAM8456 target protein, GAM36590 target protein and GAM237232 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8456, GAM36590 and GAM237232

GR6452 AW805533 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6452 (GR6452) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6452 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6452 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6452 gene encodes GR6452 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6452 precursor RNA folds spatially, forming GR6452 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6452 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6452 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR6452 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM31486 precursor RNA and GAM238375 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM31486 RNA and GAM238375 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM31486 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM31486 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM31486 target RNA into GAM31486 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM238375 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM238375 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM238375 target RNA into GAM238375 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6452 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6452 gene: GAM31486 target protein and GAM238375 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM31486 and GAM238375

GR6453 BG394333 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6453(GR6453) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6453 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6453

gene was detected is described hereinabove with reference to Figs. 8-18.

GR6453 gene encodes GR6453 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6453 precursor RNA folds spatially, forming GR6453 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6453 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6453 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6453 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM40144 precursor RNA and GAM230438 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM40144 RNA and GAM230438 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM40144 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM40144 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM40144 target RNA into GAM40144 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM230438 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM230438 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM230438 target RNA into GAM230438 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6453 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6453 gene: GAM40144 target protein and GAM230438 target protein, herein schematically represented by GAM1

TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM40144 and GAM230438

GR6454 AV654189 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6454(GR6454) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6454 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6454 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6454 gene encodes GR6454 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6454 precursor RNA folds spatially, forming GR6454 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6454 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6454 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6454 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3475 precursor RNA and GAM27855 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3475 RNA and GAM27855 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3475 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3475 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3475 target RNA into GAM3475 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM27855 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM27855 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM27855 target RNA into GAM27855 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6454 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6454 gene: GAM3475 target protein and GAM27855 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3475 and GAM27855

GR6455 AW614347 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6455(GR6455) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6455 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6455 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6455 gene encodes GR6455 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6455 precursor RNA folds spatially, forming GR6455 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6455 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6455 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6455 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2823 precursor RNA and GAM54193 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM2823 RNA and GAM54193 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2823 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2823 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2823 target RNA into GAM2823 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM54193 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM54193 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM54193 target RNA into GAM54193 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6455 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6455 gene: GAM2823 target protein and GAM54193 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2823 and GAM54193

GR6456 BE061737 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6456(GR6456) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6456 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6456 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6456 gene encodes GR6456 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6456 precursor RNA folds spatially, forming GR6456 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6456 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6456 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6456 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM150426 precursor RNA and GAM284829 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM150426 RNA and GAM284829 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM150426 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM150426 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM150426 target RNA into GAM150426 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM284829 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM284829 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM284829 target RNA into GAM284829 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6456 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6456 gene: GAM150426 target protein and GAM284829 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM150426 and GAM284829

GR6457 BG546883 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6457(GR6457) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6457 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6457 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6457 gene encodes GR6457 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6457 precursor RNA folds spatially, forming GR6457 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6457 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6457 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6457 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6286 precursor RNA and GAM8030 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6286 RNA and GAM8030 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6286 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6286 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6286 target RNA into GAM6286 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8030 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8030 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8030 target RNA into GAM8030 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6457 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR6457 gene: GAM6286 target protein and GAM8030 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6286 and GAM8030

GR6458 BF307863 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6458(GR6458) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6458 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6458 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6458 gene encodes GR6458 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6458 precursor RNA folds spatially, forming GR6458 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6458 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6458 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6458 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM73260 precursor RNA and GAM274687 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM73260 RNA and GAM274687 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM73260 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM73260 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM73260 target RNA into GAM73260 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM274687 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM274687 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM274687 target RNA into GAM274687 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6458 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6458 gene: GAM73260 target protein and GAM274687 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM73260 and GAM274687

GR6459 BG028892 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6459(GR6459) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6459 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6459 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6459 gene encodes GR6459 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6459 precursor RNA folds spatially, forming GR6459 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6459 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6459 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6459 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3909 precursor RNA and GAM119047 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3909 RNA and GAM119047 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3909 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3909 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3909 target RNA into GAM3909 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM119047 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM119047 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM119047 target RNA into GAM119047 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6459 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6459 gene: GAM3909 target protein and GAM119047 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3909 and GAM119047

GR6460 BG186906 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6460(GR6460) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6460 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6460 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6460 gene encodes GR6460 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6460 precursor RNA folds spatially, forming GR6460 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6460 folded precursor RNA comprises a plurality of what is known in the

art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6460 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6460 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7798 precursor RNA and GAM141887 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7798 RNA and GAM141887 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7798 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7798 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7798 target RNA into GAM7798 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM141887 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM141887 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM141887 target RNA into GAM141887 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6460 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6460 gene: GAM7798 target protein and GAM141887 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7798 and GAM141887

GR6461 BM844456 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6461 (GR6461) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR6461 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6461 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6461 gene encodes GR6461 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6461 precursor RNA folds spatially, forming GR6461 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6461 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6461 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6461 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM5196 precursor RNA, GAM5347 precursor RNA and GAM269346 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5196 RNA, GAM5347 RNA and GAM269346 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5196 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5196 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5196 target RNA into GAM5196 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5347 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5347 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5347 target RNA into GAM5347 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM269346 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM269346 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM269346 target RNA into GAM269346 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6461 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6461 gene: GAM5196 target protein, GAM5347 target protein and GAM269346 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5196, GAM5347 and GAM269346

GR6462 BM719452 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6462(GR6462) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6462 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6462 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6462 gene encodes GR6462 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6462 precursor RNA folds spatially, forming GR6462 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6462 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6462 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6462 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5488 precursor RNA and GAM318313 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5488 RNA and GAM318313 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5488 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5488 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5488 target RNA into GAM5488 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM318313 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM318313 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM318313 target RNA into GAM318313 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6462 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6462 gene: GAM5488 target protein and GAM318313 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5488 and GAM318313

GR6463 AA769214 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6463(GR6463) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6463 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6463 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6463 gene encodes GR6463 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6463 precursor RNA folds spatially, forming GR6463 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6463 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR6463 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6463 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM18347 precursor RNA, GAM83271 precursor RNA, GAM93822 precursor RNA and GAM176254 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM18347 RNA, GAM83271 RNA, GAM93822 RNA and GAM176254 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM18347 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM18347 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM18347 target RNA into GAM18347 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM83271 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM83271 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM83271 target RNA into GAM83271 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM93822 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM93822 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM93822 target RNA into GAM93822 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM176254 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM176254 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM176254 target RNA into GAM176254 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6463 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6463 gene: GAM18347 target protein, GAM83271 target protein, GAM93822 target protein and GAM176254 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM18347, GAM83271, GAM93822 and GAM176254

GR6464 BF991253 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6464(GR6464) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6464 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6464 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6464 gene encodes GR6464 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6464 precursor RNA folds spatially, forming GR6464 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6464 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6464 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6464 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM17987 precursor RNA and GAM151856 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM17987 RNA and GAM151856 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM17987 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM17987 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM17987 target RNA into GAM17987 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM151856 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM151856 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM151856 target RNA into GAM151856 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6464 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6464 gene: GAM17987 target protein and GAM151856 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM17987 and GAM151856

GR6465 BE304716 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6465(GR6465) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6465 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6465 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6465 gene encodes GR6465 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6465 precursor RNA folds spatially, forming GR6465 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6465 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6465 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6465 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8570 precursor RNA and GAM290168 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8570 RNA and GAM290168 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8570 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8570 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8570 target RNA into GAM8570 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM290168 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM290168 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM290168 target RNA into GAM290168 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6465 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6465 gene: GAM8570 target protein and GAM290168 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8570 and GAM290168

GR6466 AW851603 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6466(GR6466) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6466 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6466 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6466 gene encodes GR6466 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6466 precursor RNA folds spatially, forming GR6466 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6466 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6466 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6466 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3033 precursor RNA, GAM89274 precursor RNA and GAM307105 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3033 RNA, GAM89274 RNA and GAM307105 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3033 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3033 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3033 target RNA into GAM3033 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM89274 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM89274 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM89274 target RNA into GAM89274 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM307105 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM307105 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM307105 target RNA into GAM307105 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6466 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6466 gene: GAM3033 target protein, GAM89274 target protein and GAM307105 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3033, GAM89274 and GAM307105

GR6467 BG436462 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6467(GR6467) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6467 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6467 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6467 gene encodes GR6467 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6467 precursor RNA folds spatially, forming GR6467 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6467 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6467 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6467 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3450 precursor RNA and GAM202504 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3450 RNA and GAM202504 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3450 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM3450 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3450 target RNA into GAM3450 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM202504 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM202504 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM202504 target RNA into GAM202504 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6467 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6467 gene: GAM3450 target protein and GAM202504 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3450 and GAM202504

GR6468 AI018257 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6468(GR6468) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6468 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6468 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6468 gene encodes GR6468 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6468 precursor RNA folds spatially, forming GR6468 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6468 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6468 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6468 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2

separate GAM precursor RNAs, GAM268370 precursor RNA and GAM275062 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM268370 RNA and GAM275062 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM268370 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM268370 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM268370 target RNA into GAM268370 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM275062 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM275062 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM275062 target RNA into GAM275062 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6468 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6468 gene: GAM268370 target protein and GAM275062 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM268370 and GAM275062

GR6469 BE787136 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6469(GR6469) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6469 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6469 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6469 gene encodes GR6469 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR6469 precursor RNA folds spatially, forming GR6469 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6469 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6469 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6469 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1799 precursor RNA, GAM30033 precursor RNA and GAM175235 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1799 RNA, GAM30033 RNA and GAM175235 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1799 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1799 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1799 target RNA into GAM1799 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM30033 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM30033 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM30033 target RNA into GAM30033 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM175235 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM175235 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM175235 target RNA into GAM175235 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6469 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6469 gene: GAM1799 target protein, GAM30033 target protein and GAM175235 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1799, GAM30033 and GAM175235

GR6470 BG236149 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6470(GR6470) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6470 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6470 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6470 gene encodes GR6470 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6470 precursor RNA folds spatially, forming GR6470 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6470 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6470 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6470 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM6758 precursor RNA, GAM8554 precursor RNA and GAM321953 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6758 RNA, GAM8554 RNA and GAM321953 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6758 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM6758 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6758 target RNA into GAM6758 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8554 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8554 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8554 target RNA into GAM8554 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM321953 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM321953 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM321953 target RNA into GAM321953 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6470 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6470 gene: GAM6758 target protein, GAM8554 target protein and GAM321953 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6758, GAM8554 and GAM321953

GR6471 BM809381 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6471 (GR6471) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6471 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6471 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6471 gene encodes GR6471 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6471 precursor RNA folds spatially, forming GR6471 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated

that GR6471 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6471 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6471 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM7944 precursor RNA, GAM8430 precursor RNA and GAM35489 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7944 RNA, GAM8430 RNA and GAM35489 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7944 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7944 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7944 target RNA into GAM7944 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8430 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8430 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8430 target RNA into GAM8430 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM35489 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM35489 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM35489 target RNA into GAM35489 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6471 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6471 gene: GAM7944 target

protein, GAM8430 target protein and GAM35489 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7944, GAM8430 and GAM35489

GR6472 AA649940 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6472(GR6472) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6472 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6472 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6472 gene encodes GR6472 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6472 precursor RNA folds spatially, forming GR6472 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6472 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6472 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6472 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM40462 precursor RNA and GAM104151 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM40462 RNA and GAM104151 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM40462 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM40462 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM40462 target RNA into GAM40462 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM104151 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM104151 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM104151 target RNA into GAM104151 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6472 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6472 gene: GAM40462 target protein and GAM104151 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM40462 and GAM104151

GR6473 AA748175 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6473(GR6473) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6473 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6473 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6473 gene encodes GR6473 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6473 precursor RNA folds spatially, forming GR6473 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6473 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6473 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6473 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM5427 precursor RNA, GAM7398 precursor RNA and GAM202235 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5427 RNA, GAM7398 RNA and GAM202235 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5427 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5427 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5427 target RNA into GAM5427 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7398 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7398 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7398 target RNA into GAM7398 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM202235 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM202235 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM202235 target RNA into GAM202235 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6473 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6473 gene: GAM5427 target protein, GAM7398 target protein and GAM202235 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5427, GAM7398 and GAM202235

GR6474 AL599303 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6474(GR6474) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6474 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR6474 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6474 gene encodes GR6474 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6474 precursor RNA folds spatially, forming GR6474 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6474 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6474 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6474 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM308 precursor RNA and GAM133629 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM308 RNA and GAM133629 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM308 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM308 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM308 target RNA into GAM308 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM133629 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM133629 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM133629 target RNA into GAM133629 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6474 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6474 gene: GAM308 target

protein and GAM133629 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM308 and GAM133629

GR6475 BM907536 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6475(GR6475) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6475 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6475 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6475 gene encodes GR6475 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6475 precursor RNA folds spatially, forming GR6475 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6475 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6475 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6475 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM277651 precursor RNA and GAM335979 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM277651 RNA and GAM335979 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM277651 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM277651 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM277651 target RNA into GAM277651 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM335979 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM335979 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM335979 target RNA into GAM335979 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6475 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6475 gene: GAM277651 target protein and GAM335979 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM277651 and GAM335979

GR6476 AI431950 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6476(GR6476) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6476 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6476 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6476 gene encodes GR6476 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6476 precursor RNA folds spatially, forming GR6476 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6476 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6476 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6476 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3816 precursor RNA and GAM162841 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3816 RNA and GAM162841 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3816 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3816 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3816 target RNA into GAM3816 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM162841 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM162841 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM162841 target RNA into GAM162841 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6476 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6476 gene: GAM3816 target protein and GAM162841 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3816 and GAM162841

GR6477 BQ002066 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6477(GR6477) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6477 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6477 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6477 gene encodes GR6477 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6477 precursor RNA folds spatially, forming GR6477 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6477 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR6477 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6477 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM129451 precursor RNA and GAM271087 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM129451 RNA and GAM271087 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM129451 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM129451 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM129451 target RNA into GAM129451 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM271087 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM271087 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM271087 target RNA into GAM271087 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6477 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6477 gene: GAM129451 target protein and GAM271087 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM129451 and GAM271087

GR6478 AW967149 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6478(GR6478) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6478 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6478 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6478 gene encodes GR6478 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6478 precursor RNA folds spatially, forming GR6478 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6478 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6478 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6478 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4642 precursor RNA, GAM27275 precursor RNA and GAM30966 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4642 RNA, GAM27275 RNA and GAM30966 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4642 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4642 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4642 target RNA into GAM4642 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM27275 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM27275 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM27275 target RNA into GAM27275 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM30966 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM30966 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM30966 target RNA into GAM30966 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6478 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6478 gene: GAM4642 target protein, GAM27275 target protein and GAM30966 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4642, GAM27275 and GAM30966

GR6479 BE671717 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6479(GR6479) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6479 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6479 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6479 gene encodes GR6479 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6479 precursor RNA folds spatially, forming GR6479 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6479 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6479 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6479 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM116094 precursor RNA and GAM258275 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM116094 RNA and GAM258275 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM116094 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM116094 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM116094 target RNA into GAM116094 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM258275 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM258275 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM258275 target RNA into GAM258275 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6479 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6479 gene: GAM116094 target protein and GAM258275 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM116094 and GAM258275

GR6480 AI288281 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6480 (GR6480) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6480 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6480 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6480 gene encodes GR6480 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6480 precursor RNA folds spatially, forming GR6480 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6480 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6480 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6480 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 5 separate GAM precursor RNAs, GAM4688 precursor RNA, GAM111245 precursor RNA, GAM119726 precursor RNA, GAM214481 precursor RNA and GAM310764 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4688 RNA, GAM111245 RNA, GAM119726 RNA, GAM214481 RNA and GAM310764 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4688 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4688 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4688 target RNA into GAM4688 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM111245 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM111245 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM111245 target RNA into GAM111245 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM119726 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM119726 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM119726 target RNA into GAM119726 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM214481 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM214481 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM214481 target RNA into GAM214481 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM310764 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM310764 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM310764 target RNA into GAM310764 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6480 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6480 gene: GAM4688 target protein, GAM111245 target protein, GAM119726 target protein, GAM214481 target protein and GAM310764 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4688, GAM111245, GAM119726, GAM214481 and GAM310764

GR6481 BE261204 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6481(GR6481) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6481 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6481 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6481 gene encodes GR6481 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6481 precursor RNA folds spatially, forming GR6481 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6481 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6481 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6481 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6304 precursor RNA and GAM136520 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6304 RNA and GAM136520 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6304 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6304 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6304 target RNA into GAM6304 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM136520 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM136520 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM136520 target RNA into GAM136520 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6481 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6481 gene: GAM6304 target protein and GAM136520 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6304 and GAM136520

GR6482 AI125244 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6482(GR6482) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6482 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6482 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6482 gene encodes GR6482 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6482 precursor RNA folds spatially, forming GR6482 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated

that GR6482 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6482 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6482 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM106789 precursor RNA and GAM260390 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM106789 RNA and GAM260390 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM106789 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM106789 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM106789 target RNA into GAM106789 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM260390 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM260390 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM260390 target RNA into GAM260390 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6482 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6482 gene: GAM106789 target protein and GAM260390 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM106789 and GAM260390

GR6483 AW078701 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6483(GR6483) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR6483 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6483 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6483 gene encodes GR6483 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6483 precursor RNA folds spatially, forming GR6483 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6483 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6483 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6483 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM121239 precursor RNA and GAM206588 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM121239 RNA and GAM206588 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM121239 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM121239 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM121239 target RNA into GAM121239 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM206588 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM206588 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM206588 target RNA into GAM206588 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6483 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6483 gene: GAM121239 target protein and GAM206588 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM121239 and GAM206588

GR6484 BG178001 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6484(GR6484) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6484 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6484 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6484 gene encodes GR6484 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6484 precursor RNA folds spatially, forming GR6484 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6484 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6484 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6484 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4676 precursor RNA and GAM6747 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4676 RNA and GAM6747 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4676 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4676 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds

to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4676 target RNA into GAM4676 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6747 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6747 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6747 target RNA into GAM6747 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6484 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6484 gene: GAM4676 target protein and GAM6747 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4676 and GAM6747

GR6485 BE327478 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6485(GR6485) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6485 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6485 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6485 gene encodes GR6485 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6485 precursor RNA folds spatially, forming GR6485 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6485 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6485 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6485 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4049 precursor RNA and GAM35690 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3

FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4049 RNA and GAM35690 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4049 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4049 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4049 target RNA into GAM4049 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM35690 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM35690 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM35690 target RNA into GAM35690 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6485 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6485 gene: GAM4049 target protein and GAM35690 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4049 and GAM35690

GR6486 BM462646 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6486(GR6486) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6486 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6486 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6486 gene encodes GR6486 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6486 precursor RNA folds spatially, forming GR6486 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6486 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6486 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6486 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3288 precursor RNA, GAM187990 precursor RNA and GAM282990 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3288 RNA, GAM187990 RNA and GAM282990 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3288 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3288 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3288 target RNA into GAM3288 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM187990 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM187990 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM187990 target RNA into GAM187990 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM282990 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM282990 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM282990 target RNA into GAM282990 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6486 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6486 gene: GAM3288 target protein, GAM187990 target protein and GAM282990 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3288, GAM187990 and GAM282990

GR6487 AI624398 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6487 (GR6487) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6487 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6487 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6487 gene encodes GR6487 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6487 precursor RNA folds spatially, forming GR6487 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6487 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6487 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6487 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1240 precursor RNA and GAM138461 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1240 RNA and GAM138461 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1240 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1240 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig. 8, thereby inhibiting translation of GAM1240 target RNA into GAM1240 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM138461 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM138461 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM138461 target RNA into GAM138461 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6487 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6487 gene: GAM1240 target protein and GAM138461 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1240 and GAM138461

GR6488 BG567765 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6488(GR6488) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6488 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6488 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6488 gene encodes GR6488 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6488 precursor RNA folds spatially, forming GR6488 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6488 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6488 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6488 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5060 precursor RNA and GAM36682 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin

shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5060 RNA and GAM36682 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5060 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5060 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5060 target RNA into GAM5060 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM36682 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM36682 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM36682 target RNA into GAM36682 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6488 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6488 gene: GAM5060 target protein and GAM36682 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5060 and GAM36682

GR6489 BF734099 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6489(GR6489) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6489 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6489 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6489 gene encodes GR6489 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6489 precursor RNA folds spatially, forming GR6489 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6489 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6489 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6489 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM143676 precursor RNA and GAM214722 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM143676 RNA and GAM214722 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM143676 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM143676 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM143676 target RNA into GAM143676 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM214722 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM214722 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM214722 target RNA into GAM214722 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6489 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6489 gene: GAM143676 target protein and GAM214722 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM143676 and GAM214722

GR6490 AI820522 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6490(GR6490) gene, which encodes an `operon-like` cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6490 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6490 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6490 gene encodes GR6490 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6490 precursor RNA folds spatially, forming GR6490 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6490 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6490 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6490 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM27109 precursor RNA and GAM325231 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM27109 RNA and GAM325231 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM27109 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM27109 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM27109 target RNA into GAM27109 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM325231 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM325231 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM325231 target RNA into GAM325231 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6490 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6490 gene: GAM27109 target protein and GAM325231 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM27109 and GAM325231

GR6491 AV735527 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6491 (GR6491) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6491 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6491 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6491 gene encodes GR6491 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6491 precursor RNA folds spatially, forming GR6491 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6491 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6491 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6491 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM6007 precursor RNA, GAM81894 precursor RNA and GAM284513 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6007 RNA, GAM81894 RNA and GAM284513 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6007 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM6007 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6007 target RNA into GAM6007 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM81894 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM81894 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM81894 target RNA into GAM81894 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM284513 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM284513 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM284513 target RNA into GAM284513 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6491 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6491 gene: GAM6007 target protein, GAM81894 target protein and GAM284513 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6007, GAM81894 and GAM284513

GR6492 BE619178 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6492(GR6492) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6492 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6492 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6492 gene encodes GR6492 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6492 precursor RNA folds spatially, forming GR6492 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated

that GR6492 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6492 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6492 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8498 precursor RNA and GAM290029 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8498 RNA and GAM290029 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8498 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8498 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8498 target RNA into GAM8498 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM290029 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM290029 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM290029 target RNA into GAM290029 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6492 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6492 gene: GAM8498 target protein and GAM290029 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8498 and GAM290029

GR6493 AW601745 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6493(GR6493) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR6493 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6493 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6493 gene encodes GR6493 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6493 precursor RNA folds spatially, forming GR6493 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6493 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6493 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6493 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM4513 precursor RNA, GAM8035 precursor RNA, GAM56196 precursor RNA and GAM155492 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4513 RNA, GAM8035 RNA, GAM56196 RNA and GAM155492 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4513 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4513 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4513 target RNA into GAM4513 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8035 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8035 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8035 target RNA into GAM8035 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM56196 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM56196 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM56196 target RNA into GAM56196 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM155492 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM155492 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM155492 target RNA into GAM155492 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6493 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6493 gene: GAM4513 target protein, GAM8035 target protein, GAM56196 target protein and GAM155492 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4513, GAM8035, GAM56196 and GAM155492

GR6494 BF983553 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6494(GR6494) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6494 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6494 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6494 gene encodes GR6494 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6494 precursor RNA folds spatially, forming GR6494 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6494 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6494 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6494 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM93600 precursor RNA and GAM143839 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM93600 RNA and GAM143839 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM93600 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM93600 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM93600 target RNA into GAM93600 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM143839 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM143839 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM143839 target RNA into GAM143839 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6494 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6494 gene: GAM93600 target protein and GAM143839 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM93600 and GAM143839

GR6495 AI452548 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6495(GR6495) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6495 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6495 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6495 gene encodes GR6495 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6495 precursor RNA folds spatially, forming GR6495 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6495 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6495 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6495 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM9339 precursor RNA, GAM254048 precursor RNA and GAM336041 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM9339 RNA, GAM254048 RNA and GAM336041 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM9339 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM9339 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM9339 target RNA into GAM9339 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM254048 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM254048 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM254048 target RNA into GAM254048 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336041 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336041 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336041

target RNA into GAM336041 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6495 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6495 gene: GAM9339 target protein, GAM254048 target protein and GAM336041 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM9339, GAM254048 and GAM336041

GR6496 BG432408 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6496(GR6496) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6496 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6496 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6496 gene encodes GR6496 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6496 precursor RNA folds spatially, forming GR6496 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6496 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6496 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6496 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM51745 precursor RNA, GAM57341 precursor RNA, GAM238849 precursor RNA and GAM289543 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM51745 RNA, GAM57341 RNA, GAM238849 RNA and GAM289543 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM51745 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM51745 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM51745 target RNA into GAM51745 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM57341 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM57341 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM57341 target RNA into GAM57341 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM238849 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM238849 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM238849 target RNA into GAM238849 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM289543 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM289543 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM289543 target RNA into GAM289543 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6496 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6496 gene: GAM51745 target protein, GAM57341 target protein, GAM238849 target protein and GAM289543 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM51745, GAM57341, GAM238849 and GAM289543

GR6497 BE386761 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6497(GR6497) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6497 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6497 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6497 gene encodes GR6497 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6497 precursor RNA folds spatially, forming GR6497 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6497 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6497 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6497 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 5 separate GAM precursor RNAs, GAM1309 precursor RNA, GAM129234 precursor RNA, GAM131901 precursor RNA, GAM270384 precursor RNA and GAM277782 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1309 RNA, GAM129234 RNA, GAM131901 RNA, GAM270384 RNA and GAM277782 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1309 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1309 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1309 target RNA into GAM1309 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM129234 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM129234 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM129234 target RNA into GAM129234 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM131901 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM131901 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM131901 target RNA into GAM131901 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM270384 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM270384 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM270384 target RNA into GAM270384 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM277782 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM277782 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM277782 target RNA into GAM277782 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6497 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6497 gene: GAM1309 target protein, GAM129234 target protein, GAM131901 target protein, GAM270384 target protein and GAM277782 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1309, GAM129234, GAM131901, GAM270384 and GAM277782

GR6498 AA996208 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6498(GR6498) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6498 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6498 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6498 gene encodes GR6498 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6498 precursor RNA folds spatially, forming GR6498 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6498 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6498 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6498 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM42990 precursor RNA and GAM64322 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM42990 RNA and GAM64322 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM42990 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM42990 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM42990 target RNA into GAM42990 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM64322 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM64322 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM64322 target RNA into GAM64322 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6498 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6498 gene: GAM42990 target protein and GAM64322 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM42990 and GAM64322

GR6499 AA297631 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6499(GR6499) gene, which encodes an `operon-like` cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6499 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6499 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6499 gene encodes GR6499 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6499 precursor RNA folds spatially, forming GR6499 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6499 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6499 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6499 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM216661 precursor RNA and GAM273133 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM216661 RNA and GAM273133 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM216661 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM216661 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM216661 target RNA into GAM216661 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM273133 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM273133 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM273133 target RNA into GAM273133 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6499 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6499 gene: GAM216661 target protein and GAM273133 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM216661 and GAM273133

GR6500 BE538423 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6500(GR6500) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6500 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6500 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6500 gene encodes GR6500 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6500 precursor RNA folds spatially, forming GR6500 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6500 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6500 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6500 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5319 precursor RNA and GAM14274 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5319 RNA and GAM14274 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5319 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5319 target RNA, herein schematically represented by

GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5319 target RNA into GAM5319 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM14274 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM14274 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM14274 target RNA into GAM14274 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6500 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6500 gene: GAM5319 target protein and GAM14274 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5319 and GAM14274

GR6501 BM741954 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6501(GR6501) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6501 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6501 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6501 gene encodes GR6501 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6501 precursor RNA folds spatially, forming GR6501 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6501 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6501 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6501 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM70642 precursor RNA and GAM235926 precursor

RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM70642 RNA and GAM235926 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM70642 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM70642 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM70642 target RNA into GAM70642 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM235926 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM235926 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM235926 target RNA into GAM235926 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6501 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6501 gene: GAM70642 target protein and GAM235926 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM70642 and GAM235926

GR6502 BE090032 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6502(GR6502) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6502 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6502 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6502 gene encodes GR6502 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6502 precursor RNA folds spatially, forming GR6502 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6502 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6502 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6502 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3018 precursor RNA and GAM236009 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3018 RNA and GAM236009 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3018 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3018 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3018 target RNA into GAM3018 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM236009 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM236009 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM236009 target RNA into GAM236009 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6502 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6502 gene: GAM3018 target protein and GAM236009 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3018 and GAM236009

bioinformatically detected regulatory gene, referred to here as Genomic Record 6503 (GR6503) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6503 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6503 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6503 gene encodes GR6503 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6503 precursor RNA folds spatially, forming GR6503 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6503 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6503 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6503 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM32986 precursor RNA and GAM227618 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM32986 RNA and GAM227618 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM32986 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM32986 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM32986 target RNA into GAM32986 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM227618 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM227618 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM227618

target RNA into GAM227618 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6503 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6503 gene: GAM32986 target protein and GAM227618 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM32986 and GAM227618

GR6504 BF674807 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6504(GR6504) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6504 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6504 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6504 gene encodes GR6504 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6504 precursor RNA folds spatially, forming GR6504 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6504 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6504 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6504 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2918 precursor RNA, GAM111959 precursor RNA and GAM255074 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2918 RNA, GAM111959 RNA and GAM255074 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2918 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2918 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2918 target RNA into GAM2918 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM111959 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM111959 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM111959 target RNA into GAM111959 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM255074 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM255074 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM255074 target RNA into GAM255074 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6504 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6504 gene: GAM2918 target protein, GAM111959 target protein and GAM255074 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2918, GAM111959 and GAM255074

GR6505 BG105131 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6505(GR6505) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6505 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6505 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6505 gene encodes GR6505 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6505 precursor RNA folds spatially, forming GR6505 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6505 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6505 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6505 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM185676 precursor RNA and GAM260211 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM185676 RNA and GAM260211 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM185676 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM185676 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM185676 target RNA into GAM185676 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM260211 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM260211 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM260211 target RNA into GAM260211 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6505 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6505 gene: GAM185676 target protein and GAM260211 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM185676 and GAM260211

6506(GR6506) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6506 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6506 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6506 gene encodes GR6506 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6506 precursor RNA folds spatially, forming GR6506 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6506 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6506 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6506 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM974 precursor RNA, GAM4998 precursor RNA, GAM7388 precursor RNA and GAM202542 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM974 RNA, GAM4998 RNA, GAM7388 RNA and GAM202542 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM974 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM974 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM974 target RNA into GAM974 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM4998 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4998 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4998 target RNA into

GAM4998 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7388 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7388 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7388 target RNA into GAM7388 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM202542 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM202542 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM202542 target RNA into GAM202542 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6506 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6506 gene: GAM974 target protein, GAM4998 target protein, GAM7388 target protein and GAM202542 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM974, GAM4998, GAM7388 and GAM202542

GR6507 BF895706 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6507(GR6507) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6507 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6507 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6507 gene encodes GR6507 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6507 precursor RNA folds spatially, forming GR6507 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6507 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6507 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6507 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5766 precursor RNA and GAM185756 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5766 RNA and GAM185756 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5766 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5766 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5766 target RNA into GAM5766 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM185756 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM185756 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM185756 target RNA into GAM185756 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6507 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6507 gene: GAM5766 target protein and GAM185756 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5766 and GAM185756

GR6508 BI767267 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6508(GR6508) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6508 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR6508 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6508 gene encodes GR6508 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6508 precursor RNA folds spatially, forming GR6508 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6508 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6508 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6508 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM85487 precursor RNA and GAM222029 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM85487 RNA and GAM222029 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM85487 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM85487 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM85487 target RNA into GAM85487 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM222029 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM222029 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM222029 target RNA into GAM222029 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6508 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6508 gene: GAM85487 target

protein and GAM222029 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM85487 and GAM222029

GR6509 AW050703 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6509(GR6509) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6509 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6509 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6509 gene encodes GR6509 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6509 precursor RNA folds spatially, forming GR6509 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6509 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6509 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6509 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM5649 precursor RNA, GAM102671 precursor RNA and GAM161749 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5649 RNA, GAM102671 RNA and GAM161749 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5649 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5649 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5649 target RNA into GAM5649 target protein, herein schematically represented by GAM1 TARGET

PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM102671 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM102671 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM102671 target RNA into GAM102671 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM161749 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM161749 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM161749 target RNA into GAM161749 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6509 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6509 gene: GAM5649 target protein, GAM102671 target protein and GAM161749 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5649, GAM102671 and GAM161749

GR6510 BQ026503 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6510(GR6510) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6510 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6510 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6510 gene encodes GR6510 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6510 precursor RNA folds spatially, forming GR6510 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6510 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6510 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR6510 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2932 precursor RNA, GAM5720 precursor RNA and GAM99741 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2932 RNA, GAM5720 RNA and GAM99741 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2932 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2932 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2932 target RNA into GAM2932 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5720 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5720 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5720 target RNA into GAM5720 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM99741 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM99741 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM99741 target RNA into GAM99741 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6510 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6510 gene: GAM2932 target protein, GAM5720 target protein and GAM99741 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2932, GAM5720 and GAM99741

GR6511 AA280162 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6511 (GR6511) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6511 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6511 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6511 gene encodes GR6511 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6511 precursor RNA folds spatially, forming GR6511 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6511 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6511 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6511 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM79167 precursor RNA and GAM210084 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM79167 RNA and GAM210084 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM79167 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM79167 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM79167 target RNA into GAM79167 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM210084 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM210084 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM210084 target RNA into GAM210084 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6511 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6511 gene: GAM79167 target protein and GAM210084 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM79167 and GAM210084

GR6512 AW959883 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6512(GR6512) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6512 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6512 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6512 gene encodes GR6512 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6512 precursor RNA folds spatially, forming GR6512 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6512 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6512 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6512 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM23027 precursor RNA, GAM282950 precursor RNA and GAM295261 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM23027 RNA, GAM282950 RNA and GAM295261 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs

corresponding to GAM RNA of Fig. 8.

GAM23027 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM23027 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM23027 target RNA into GAM23027 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM282950 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM282950 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM282950 target RNA into GAM282950 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM295261 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM295261 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM295261 target RNA into GAM295261 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6512 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6512 gene: GAM23027 target protein, GAM282950 target protein and GAM295261 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM23027, GAM282950 and GAM295261

GR6513 BM020014 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6513(GR6513) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6513 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6513 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6513 gene encodes GR6513 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR6513 precursor RNA folds spatially, forming GR6513 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6513 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6513 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6513 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM220 precursor RNA, GAM8663 precursor RNA and GAM33978 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM220 RNA, GAM8663 RNA and GAM33978 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM220 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM220 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM220 target RNA into GAM220 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8663 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8663 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8663 target RNA into GAM8663 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM33978 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM33978 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM33978 target RNA into GAM33978 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6513 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6513 gene: GAM220 target protein, GAM8663 target protein and GAM33978 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM220, GAM8663 and GAM33978

GR6514 AW239061 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6514(GR6514) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6514 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6514 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6514 gene encodes GR6514 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6514 precursor RNA folds spatially, forming GR6514 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6514 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6514 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6514 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM63821 precursor RNA, GAM103197 precursor RNA and GAM195874 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM63821 RNA, GAM103197 RNA and GAM195874 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM63821 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM63821 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM63821 target RNA into GAM63821 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM103197 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM103197 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM103197 target RNA into GAM103197 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM195874 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM195874 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM195874 target RNA into GAM195874 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6514 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6514 gene: GAM63821 target protein, GAM103197 target protein and GAM195874 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM63821, GAM103197 and GAM195874

GR6515 BM680396 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6515(GR6515) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6515 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6515 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6515 gene encodes GR6515 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6515 precursor RNA folds spatially, forming GR6515 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated

that GR6515 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6515 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6515 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM2199 precursor RNA, GAM51328 precursor RNA, GAM128200 precursor RNA and GAM265560 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2199 RNA, GAM51328 RNA, GAM128200 RNA and GAM265560 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2199 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2199 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2199 target RNA into GAM2199 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM51328 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM51328 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM51328 target RNA into GAM51328 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM128200 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM128200 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM128200 target RNA into GAM128200 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM265560 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM265560 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM265560 target RNA into GAM265560 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6515 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6515 gene: GAM2199 target protein, GAM51328 target protein, GAM128200 target protein and GAM265560 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2199, GAM51328, GAM128200 and GAM265560

GR6516 AA740800 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6516(GR6516) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6516 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6516 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6516 gene encodes GR6516 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6516 precursor RNA folds spatially, forming GR6516 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6516 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6516 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6516 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3896 precursor RNA, GAM187278 precursor RNA and GAM264674 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3896 RNA, GAM187278 RNA and GAM264674 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs

corresponding to GAM RNA of Fig. 8.

GAM3896 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3896 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3896 target RNA into GAM3896 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM187278 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM187278 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM187278 target RNA into GAM187278 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM264674 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM264674 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM264674 target RNA into GAM264674 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6516 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6516 gene: GAM3896 target protein, GAM187278 target protein and GAM264674 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3896, GAM187278 and GAM264674

GR6517 AI948902 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6517(GR6517) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6517 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6517 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6517 gene encodes GR6517 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR6517 precursor RNA folds spatially, forming GR6517 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6517 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6517 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6517 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2032 precursor RNA and GAM90861 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2032 RNA and GAM90861 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2032 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2032 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2032 target RNA into GAM2032 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM90861 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM90861 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM90861 target RNA into GAM90861 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6517 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6517 gene: GAM2032 target protein and GAM90861 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2032 and GAM90861

GR6518 BM725658 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6518(GR6518) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6518 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6518 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6518 gene encodes GR6518 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6518 precursor RNA folds spatially, forming GR6518 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6518 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6518 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6518 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8212 precursor RNA and GAM30414 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8212 RNA and GAM30414 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8212 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8212 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8212 target RNA into GAM8212 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM30414 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM30414 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM30414 target RNA into GAM30414 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6518 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6518 gene: GAM8212 target protein and GAM30414 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8212 and GAM30414

GR6519 AI735305 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6519 (GR6519) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6519 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6519 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6519 gene encodes GR6519 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6519 precursor RNA folds spatially, forming GR6519 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6519 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6519 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6519 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM8548 precursor RNA, GAM137412 precursor RNA, GAM174445 precursor RNA and GAM262773 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8548 RNA, GAM137412 RNA, GAM174445 RNA and GAM262773 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8548 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8548 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8548 target RNA into GAM8548 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM137412 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM137412 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM137412 target RNA into GAM137412 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM174445 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM174445 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM174445 target RNA into GAM174445 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM262773 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM262773 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM262773 target RNA into GAM262773 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6519 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6519 gene: GAM8548 target protein, GAM137412 target protein, GAM174445 target protein and GAM262773 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8548, GAM137412, GAM174445 and GAM262773

GR6520 BF807375 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6520(GR6520) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6520 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6520 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6520 gene encodes GR6520 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6520 precursor RNA folds spatially, forming GR6520 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6520 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6520 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6520 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3432 precursor RNA, GAM151609 precursor RNA and GAM224222 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3432 RNA, GAM151609 RNA and GAM224222 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3432 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3432 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3432 target RNA into GAM3432 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM151609 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM151609 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM151609 target RNA into GAM151609 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM224222 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM224222 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM224222 target RNA into GAM224222 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6520 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6520 gene: GAM3432 target protein, GAM151609 target protein and GAM224222 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3432, GAM151609 and GAM224222

GR6521 BG215407 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6521(GR6521) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6521 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6521 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6521 gene encodes GR6521 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6521 precursor RNA folds spatially, forming GR6521 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6521 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6521 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6521 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM113628 precursor RNA, GAM126935 precursor RNA and GAM142217 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM113628 RNA, GAM126935 RNA and GAM142217 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM113628 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM113628 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM113628 target RNA into GAM113628 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM126935 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM126935 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM126935 target RNA into GAM126935 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM142217 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM142217 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM142217 target RNA into GAM142217 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6521 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6521 gene: GAM113628 target protein, GAM126935 target protein and GAM142217 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM113628, GAM126935 and GAM142217

GR6522 BE958801 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6522(GR6522) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6522 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6522 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6522 gene encodes GR6522 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6522 precursor RNA folds spatially, forming GR6522 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6522 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6522 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6522 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM113618 precursor RNA and GAM128918 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM113618 RNA and GAM128918 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM113618 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM113618 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM113618 target RNA into GAM113618 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM128918 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM128918 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM128918 target RNA into GAM128918 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6522 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6522 gene: GAM113618 target protein and GAM128918 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes

is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM113618 and GAM128918

GR6523 H30874 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6523(GR6523) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6523 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6523 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6523 gene encodes GR6523 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6523 precursor RNA folds spatially, forming GR6523 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6523 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6523 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6523 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM918 precursor RNA, GAM74254 precursor RNA and GAM296630 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM918 RNA, GAM74254 RNA and GAM296630 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM918 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM918 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM918 target RNA into GAM918 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM74254 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM74254 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM74254 target RNA into GAM74254 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM296630 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM296630 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM296630 target RNA into GAM296630 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6523 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6523 gene: GAM918 target protein, GAM74254 target protein and GAM296630 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM918, GAM74254 and GAM296630

GR6524 AA635397 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6524(GR6524) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6524 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6524 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6524 gene encodes GR6524 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6524 precursor RNA folds spatially, forming GR6524 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6524 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6524 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6524 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM94611 precursor RNA and GAM168464 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM94611 RNA and GAM168464 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM94611 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM94611 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM94611 target RNA into GAM94611 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM168464 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM168464 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM168464 target RNA into GAM168464 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6524 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6524 gene: GAM94611 target protein and GAM168464 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM94611 and GAM168464

GR6525 BF247981 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6525(GR6525) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6525 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6525 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6525 gene encodes GR6525 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6525 precursor RNA folds spatially, forming GR6525 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6525 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6525 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6525 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM33698 precursor RNA, GAM121215 precursor RNA and GAM148119 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM33698 RNA, GAM121215 RNA and GAM148119 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM33698 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM33698 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM33698 target RNA into GAM33698 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM121215 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM121215 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM121215 target RNA into GAM121215 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM148119 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM148119 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM148119 target RNA into GAM148119 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6525 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6525 gene: GAM33698 target protein, GAM121215 target protein and GAM148119 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM33698, GAM121215 and GAM148119

GR6526 BG388333 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6526(GR6526) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6526 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6526 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6526 gene encodes GR6526 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6526 precursor RNA folds spatially, forming GR6526 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6526 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6526 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6526 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3242 precursor RNA, GAM139124 precursor RNA and GAM293103 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3242 RNA, GAM139124 RNA and GAM293103 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3242 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3242 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3242 target RNA into GAM3242 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM139124 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM139124 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM139124 target RNA into GAM139124 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM293103 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM293103 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM293103 target RNA into GAM293103 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6526 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6526 gene: GAM3242 target protein, GAM139124 target protein and GAM293103 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3242, GAM139124 and GAM293103

GR6527 BI090413 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6527(GR6527) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6527 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6527 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6527 gene encodes GR6527 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6527 precursor RNA folds spatially, forming GR6527 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6527 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6527 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6527 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM7089 precursor RNA, GAM175940 precursor RNA, GAM179627 precursor RNA and GAM268679 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7089 RNA, GAM175940 RNA, GAM179627 RNA and GAM268679 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7089 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7089 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7089 target RNA into GAM7089 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM175940 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM175940 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM175940 target RNA into GAM175940 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM179627 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM179627 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM179627 target RNA into GAM179627 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM268679 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM268679 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM268679 target RNA into GAM268679 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6527 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6527 gene: GAM7089 target protein, GAM175940 target protein, GAM179627 target protein and GAM268679 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7089, GAM175940, GAM179627 and GAM268679

GR6528 BM995241 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6528(GR6528) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6528 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6528 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6528 gene encodes GR6528 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6528 precursor RNA folds spatially, forming GR6528 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6528 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6528 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6528 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM94762 precursor RNA, GAM115814 precursor RNA and GAM243771 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM94762 RNA, GAM115814 RNA and GAM243771 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM94762 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM94762 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM94762 target RNA into GAM94762 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM115814 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM115814 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM115814 target RNA into GAM115814 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM243771 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM243771 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM243771 target RNA into GAM243771 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6528 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6528 gene: GAM94762 target protein, GAM115814 target protein and GAM243771 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM94762, GAM115814 and GAM243771

GR6529 AW833624 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6529(GR6529) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6529 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6529 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6529 gene encodes GR6529 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6529 precursor RNA folds spatially, forming GR6529 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6529 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6529 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6529 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM143906 precursor RNA and GAM279346 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM143906 RNA and GAM279346 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM143906 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM143906 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM143906 target RNA into GAM143906 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM279346 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM279346 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM279346 target RNA into GAM279346 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6529 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6529 gene: GAM143906 target protein and GAM279346 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference,

with references to GAM143906 and GAM279346

GR6530 BG502605 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6530 (GR6530) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6530 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6530 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6530 gene encodes GR6530 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6530 precursor RNA folds spatially, forming GR6530 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6530 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6530 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6530 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM4427 precursor RNA, GAM68024 precursor RNA, GAM85658 precursor RNA and GAM264054 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4427 RNA, GAM68024 RNA, GAM85658 RNA and GAM264054 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4427 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4427 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4427 target RNA into GAM4427 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM68024 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM68024 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM68024 target RNA into GAM68024 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM85658 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM85658 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM85658 target RNA into GAM85658 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM264054 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM264054 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM264054 target RNA into GAM264054 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6530 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6530 gene: GAM4427 target protein, GAM68024 target protein, GAM85658 target protein and GAM264054 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4427, GAM68024, GAM85658 and GAM264054

GR6531 AI637793 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6531 (GR6531) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6531 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6531 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6531 gene encodes GR6531 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6531 precursor RNA folds spatially, forming GR6531 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated

that GR6531 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6531 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6531 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM199237 precursor RNA and GAM325595 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM199237 RNA and GAM325595 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM199237 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM199237 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM199237 target RNA into GAM199237 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM325595 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM325595 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM325595 target RNA into GAM325595 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6531 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6531 gene: GAM199237 target protein and GAM325595 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM199237 and GAM325595

GR6532 BF110868 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6532(GR6532) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR6532 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6532 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6532 gene encodes GR6532 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6532 precursor RNA folds spatially, forming GR6532 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6532 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6532 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6532 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3286 precursor RNA and GAM8637 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3286 RNA and GAM8637 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3286 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3286 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3286 target RNA into GAM3286 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8637 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8637 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8637 target RNA into GAM8637 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6532 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6532 gene: GAM3286 target protein and GAM8637 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3286 and GAM8637

GR6533 BF350289 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6533(GR6533) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6533 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6533 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6533 gene encodes GR6533 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6533 precursor RNA folds spatially, forming GR6533 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6533 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6533 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6533 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM23789 precursor RNA and GAM328431 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM23789 RNA and GAM328431 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM23789 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM23789 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM23789 target RNA into GAM23789 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM328431 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM328431 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM328431 target RNA into GAM328431 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6533 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6533 gene: GAM23789 target protein and GAM328431 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM23789 and GAM328431

GR6534 BI860594 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6534(GR6534) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6534 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6534 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6534 gene encodes GR6534 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6534 precursor RNA folds spatially, forming GR6534 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6534 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6534 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6534 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1568 precursor RNA and GAM173043 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3

FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1568 RNA and GAM173043 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1568 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1568 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1568 target RNA into GAM1568 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM173043 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM173043 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM173043 target RNA into GAM173043 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6534 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6534 gene: GAM1568 target protein and GAM173043 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1568 and GAM173043

GR6535 AI829555 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6535(GR6535) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6535 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6535 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6535 gene encodes GR6535 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6535 precursor RNA folds spatially, forming GR6535 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6535 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6535 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6535 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM165657 precursor RNA and GAM275047 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM165657 RNA and GAM275047 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM165657 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM165657 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM165657 target RNA into GAM165657 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM275047 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM275047 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM275047 target RNA into GAM275047 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6535 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6535 gene: GAM165657 target protein and GAM275047 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM165657 and GAM275047

6536(GR6536) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6536 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6536 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6536 gene encodes GR6536 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6536 precursor RNA folds spatially, forming GR6536 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6536 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6536 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6536 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM233195 precursor RNA, GAM266174 precursor RNA and GAM295532 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM233195 RNA, GAM266174 RNA and GAM295532 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM233195 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM233195 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM233195 target RNA into GAM233195 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM266174 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM266174 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM266174

target RNA into GAM266174 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM295532 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM295532 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM295532 target RNA into GAM295532 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6536 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6536 gene: GAM233195 target protein, GAM266174 target protein and GAM295532 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM233195, GAM266174 and GAM295532

GR6537 H09583 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6537(GR6537) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6537 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6537 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6537 gene encodes GR6537 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6537 precursor RNA folds spatially, forming GR6537 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6537 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6537 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6537 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM283390 precursor RNA and GAM305764 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin

shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM283390 RNA and GAM305764 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM283390 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM283390 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM283390 target RNA into GAM283390 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM305764 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM305764 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM305764 target RNA into GAM305764 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6537 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6537 gene: GAM283390 target protein and GAM305764 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM283390 and GAM305764

GR6538 BF698921 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6538(GR6538) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6538 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6538 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6538 gene encodes GR6538 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6538 precursor RNA folds spatially, forming GR6538 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6538 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6538 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6538 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM23722 precursor RNA, GAM257637 precursor RNA and GAM259782 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM23722 RNA, GAM257637 RNA and GAM259782 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM23722 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM23722 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM23722 target RNA into GAM23722 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM257637 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM257637 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM257637 target RNA into GAM257637 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM259782 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM259782 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM259782 target RNA into GAM259782 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6538 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR6538 gene: GAM23722 target protein, GAM257637 target protein and GAM259782 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM23722, GAM257637 and GAM259782

GR6539 BG946502 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6539 (GR6539) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6539 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6539 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6539 gene encodes GR6539 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6539 precursor RNA folds spatially, forming GR6539 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6539 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6539 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6539 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM117742 precursor RNA and GAM197186 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM117742 RNA and GAM197186 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM117742 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM117742 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM117742

target RNA into GAM117742 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM197186 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM197186 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM197186 target RNA into GAM197186 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6539 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6539 gene: GAM117742 target protein and GAM197186 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM117742 and GAM197186

GR6540 BM972068 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6540(GR6540) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6540 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6540 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6540 gene encodes GR6540 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6540 precursor RNA folds spatially, forming GR6540 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6540 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6540 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6540 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4353 precursor RNA, GAM93496 precursor RNA and GAM214337 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED

PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4353 RNA, GAM93496 RNA and GAM214337 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4353 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4353 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4353 target RNA into GAM4353 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM93496 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM93496 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM93496 target RNA into GAM93496 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM214337 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM214337 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM214337 target RNA into GAM214337 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6540 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6540 gene: GAM4353 target protein, GAM93496 target protein and GAM214337 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4353, GAM93496 and GAM214337

GR6541 AI762416 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6541(GR6541) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6541 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6541 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6541 gene encodes GR6541 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6541 precursor RNA folds spatially, forming GR6541 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6541 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6541 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6541 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM5927 precursor RNA, GAM77470 precursor RNA and GAM252902 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5927 RNA, GAM77470 RNA and GAM252902 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5927 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5927 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5927 target RNA into GAM5927 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM77470 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM77470 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM77470 target RNA into GAM77470 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM252902 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM252902 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM252902 target RNA into GAM252902 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6541 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6541 gene: GAM5927 target protein, GAM77470 target protein and GAM252902 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5927, GAM77470 and GAM252902

GR6542 AV706608 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6542(GR6542) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6542 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6542 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6542 gene encodes GR6542 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6542 precursor RNA folds spatially, forming GR6542 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6542 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6542 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6542 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM127184 precursor RNA and GAM261609 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM127184 RNA and GAM261609 RNA, herein schematically

represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM127184 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM127184 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM127184 target RNA into GAM127184 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM261609 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM261609 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM261609 target RNA into GAM261609 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6542 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6542 gene: GAM127184 target protein and GAM261609 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM127184 and GAM261609

GR6543 AI198700 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6543(GR6543) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6543 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6543 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6543 gene encodes GR6543 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6543 precursor RNA folds spatially, forming GR6543 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6543 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6543 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6543 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6560 precursor RNA and GAM34146 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6560 RNA and GAM34146 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6560 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6560 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6560 target RNA into GAM6560 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM34146 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM34146 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM34146 target RNA into GAM34146 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6543 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6543 gene: GAM6560 target protein and GAM34146 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6560 and GAM34146

GR6544 W53009 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6544(GR6544) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6544 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR6544 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6544 gene encodes GR6544 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6544 precursor RNA folds spatially, forming GR6544 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6544 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6544 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6544 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2917 precursor RNA, GAM8533 precursor RNA and GAM279310 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2917 RNA, GAM8533 RNA and GAM279310 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2917 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2917 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2917 target RNA into GAM2917 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8533 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8533 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8533 target RNA into GAM8533 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM279310 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM279310 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM279310 target RNA into GAM279310 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6544 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6544 gene: GAM2917 target protein, GAM8533 target protein and GAM279310 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2917, GAM8533 and GAM279310

GR6545 BF057866 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6545(GR6545) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6545 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6545 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6545 gene encodes GR6545 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6545 precursor RNA folds spatially, forming GR6545 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6545 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6545 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6545 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3294 precursor RNA, GAM40540 precursor RNA and GAM328558 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3294 RNA, GAM40540 RNA and GAM328558 RNA, herein

schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3294 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3294 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3294 target RNA into GAM3294 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM40540 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM40540 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM40540 target RNA into GAM40540 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM328558 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM328558 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM328558 target RNA into GAM328558 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6545 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6545 gene: GAM3294 target protein, GAM40540 target protein and GAM328558 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3294, GAM40540 and GAM328558

GR6546 F06363 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6546(GR6546) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6546 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6546 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6546 gene encodes GR6546 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6546 precursor RNA folds spatially, forming GR6546 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6546 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6546 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6546 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2179 precursor RNA and GAM3667 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2179 RNA and GAM3667 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2179 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2179 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2179 target RNA into GAM2179 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM3667 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3667 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3667 target RNA into GAM3667 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6546 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6546 gene: GAM2179 target protein and GAM3667 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2179 and GAM3667

GR6547 AL043604 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6547(GR6547) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6547 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6547 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6547 gene encodes GR6547 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6547 precursor RNA folds spatially, forming GR6547 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6547 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6547 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6547 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM224240 precursor RNA and GAM307332 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM224240 RNA and GAM307332 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM224240 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM224240 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM224240 target RNA into GAM224240 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM307332 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM307332 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM307332 target RNA into GAM307332 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6547 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6547 gene: GAM224240 target protein and GAM307332 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM224240 and GAM307332

GR6548 BF791133 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6548(GR6548) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6548 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6548 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6548 gene encodes GR6548 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6548 precursor RNA folds spatially, forming GR6548 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6548 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6548 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6548 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM42964 precursor RNA and GAM47874 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM42964 RNA and GAM47874 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM42964 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM42964 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM42964 target RNA into GAM42964 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM47874 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM47874 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM47874 target RNA into GAM47874 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6548 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6548 gene: GAM42964 target protein and GAM47874 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM42964 and GAM47874

GR6549 AA968695 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6549(GR6549) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6549 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6549 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6549 gene encodes GR6549 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6549 precursor RNA folds spatially, forming GR6549 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6549 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6549 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6549 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM10326 precursor RNA and GAM93073 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM10326 RNA and GAM93073 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM10326 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM10326 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM10326 target RNA into GAM10326 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM93073 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM93073 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM93073 target RNA into GAM93073 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6549 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6549 gene: GAM10326 target protein and GAM93073 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM10326 and GAM93073

GR6550 R40668 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6550(GR6550) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6550 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6550 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6550 gene encodes GR6550 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6550 precursor RNA folds spatially, forming GR6550 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6550 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6550 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6550 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2082 precursor RNA and GAM219643 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2082 RNA and GAM219643 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2082 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2082 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2082 target RNA into GAM2082 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM219643 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM219643 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM219643 target RNA into GAM219643 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6550 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6550 gene: GAM2082 target protein and GAM219643 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes

is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2082 and GAM219643

GR6551 BG327831 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6551 (GR6551) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6551 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6551 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6551 gene encodes GR6551 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6551 precursor RNA folds spatially, forming GR6551 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6551 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6551 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6551 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4852 precursor RNA and GAM260155 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4852 RNA and GAM260155 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4852 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4852 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4852 target RNA into GAM4852 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM260155 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM260155 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM260155 target RNA into GAM260155 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6551 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6551 gene: GAM4852 target protein and GAM260155 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4852 and GAM260155

GR6552 BG476910 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6552(GR6552) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6552 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6552 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6552 gene encodes GR6552 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6552 precursor RNA folds spatially, forming GR6552 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6552 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6552 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6552 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM22517 precursor RNA, GAM34205 precursor RNA and GAM138866 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM22517 RNA, GAM34205 RNA and GAM138866 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM22517 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM22517 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM22517 target RNA into GAM22517 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM34205 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM34205 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM34205 target RNA into GAM34205 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM138866 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM138866 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM138866 target RNA into GAM138866 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6552 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6552 gene: GAM22517 target protein, GAM34205 target protein and GAM138866 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM22517, GAM34205 and GAM138866

GR6553 BF797041 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6553(GR6553) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6553 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6553 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6553 gene encodes GR6553 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6553 precursor RNA folds spatially, forming GR6553 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6553 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6553 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6553 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM201934 precursor RNA and GAM254535 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM201934 RNA and GAM254535 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM201934 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM201934 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM201934 target RNA into GAM201934 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM254535 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM254535 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM254535 target RNA into GAM254535 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6553 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6553 gene: GAM201934 target protein and GAM254535 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference,

with references to GAM201934 and GAM254535

GR6554 BM669031 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6554 (GR6554) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6554 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6554 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6554 gene encodes GR6554 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6554 precursor RNA folds spatially, forming GR6554 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6554 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6554 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6554 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM15952 precursor RNA, GAM18264 precursor RNA and GAM225988 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM15952 RNA, GAM18264 RNA and GAM225988 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM15952 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM15952 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM15952 target RNA into GAM15952 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM18264 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM18264 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM18264 target RNA into GAM18264 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM225988 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM225988 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM225988 target RNA into GAM225988 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6554 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6554 gene: GAM15952 target protein, GAM18264 target protein and GAM225988 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM15952, GAM18264 and GAM225988

GR6555 BG682105 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6555(GR6555) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6555 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6555 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6555 gene encodes GR6555 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6555 precursor RNA folds spatially, forming GR6555 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6555 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6555 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6555 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM126702 precursor RNA and GAM269987 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM126702 RNA and GAM269987 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM126702 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM126702 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM126702 target RNA into GAM126702 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM269987 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM269987 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM269987 target RNA into GAM269987 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6555 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6555 gene: GAM126702 target protein and GAM269987 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM126702 and GAM269987

GR6556 BF977891 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6556(GR6556) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6556 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6556 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6556 gene encodes GR6556 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6556 precursor RNA folds spatially, forming GR6556 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6556 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6556 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6556 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2002 precursor RNA, GAM18748 precursor RNA and GAM49671 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2002 RNA, GAM18748 RNA and GAM49671 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2002 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2002 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2002 target RNA into GAM2002 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM18748 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM18748 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM18748 target RNA into GAM18748 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM49671 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM49671 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM49671 target RNA into GAM49671 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6556 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6556 gene: GAM2002 target protein, GAM18748 target protein and GAM49671 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2002, GAM18748 and GAM49671

GR6557 BE736612 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6557(GR6557) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6557 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6557 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6557 gene encodes GR6557 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6557 precursor RNA folds spatially, forming GR6557 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6557 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6557 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6557 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM58606 precursor RNA and GAM93175 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM58606 RNA and GAM93175 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM58606 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM58606 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM58606 target RNA into GAM58606 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM93175 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM93175 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM93175 target RNA into GAM93175 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6557 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6557 gene: GAM58606 target protein and GAM93175 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM58606 and GAM93175

GR6558 AA483867 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6558(GR6558) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6558 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6558 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6558 gene encodes GR6558 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6558 precursor RNA folds spatially, forming GR6558 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6558 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6558 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6558 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3

separate GAM precursor RNAs, GAM7203 precursor RNA, GAM171691 precursor RNA and GAM217185 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7203 RNA, GAM171691 RNA and GAM217185 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7203 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7203 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7203 target RNA into GAM7203 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM171691 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM171691 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM171691 target RNA into GAM171691 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM217185 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM217185 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM217185 target RNA into GAM217185 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6558 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6558 gene: GAM7203 target protein, GAM171691 target protein and GAM217185 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7203, GAM171691 and GAM217185

GR6559 AV721649 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6559 (GR6559) gene, which encodes an `operon-like` cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6559 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6559 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6559 gene encodes GR6559 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6559 precursor RNA folds spatially, forming GR6559 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6559 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6559 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6559 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7536 precursor RNA and GAM16214 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7536 RNA and GAM16214 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7536 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7536 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7536 target RNA into GAM7536 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM16214 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM16214 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM16214 target RNA into GAM16214 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6559 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6559 gene: GAM7536 target protein and GAM16214 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7536 and GAM16214

GR6560 BM562932 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6560(GR6560) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6560 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6560 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6560 gene encodes GR6560 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6560 precursor RNA folds spatially, forming GR6560 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6560 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6560 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6560 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1462 precursor RNA and GAM254498 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1462 RNA and GAM254498 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1462 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1462 target RNA, herein schematically represented by

GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1462 target RNA into GAM1462 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM254498 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM254498 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM254498 target RNA into GAM254498 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6560 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6560 gene: GAM1462 target protein and GAM254498 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1462 and GAM254498

GR6561 BG483147 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6561 (GR6561) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6561 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6561 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6561 gene encodes GR6561 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6561 precursor RNA folds spatially, forming GR6561 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6561 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6561 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6561 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6016 precursor RNA and GAM7532 precursor

RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6016 RNA and GAM7532 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6016 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6016 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6016 target RNA into GAM6016 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7532 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7532 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7532 target RNA into GAM7532 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6561 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6561 gene: GAM6016 target protein and GAM7532 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6016 and GAM7532

GR6562 BF087463 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6562(GR6562) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6562 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6562 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6562 gene encodes GR6562 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6562 precursor RNA folds spatially, forming GR6562 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6562 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6562 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6562 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1130 precursor RNA and GAM207420 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1130 RNA and GAM207420 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1130 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1130 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1130 target RNA into GAM1130 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM207420 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM207420 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM207420 target RNA into GAM207420 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6562 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6562 gene: GAM1130 target protein and GAM207420 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1130 and GAM207420

bioinformatically detected regulatory gene, referred to here as Genomic Record 6563(GR6563) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6563 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6563 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6563 gene encodes GR6563 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6563 precursor RNA folds spatially, forming GR6563 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6563 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6563 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6563 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3347 precursor RNA and GAM6412 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3347 RNA and GAM6412 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3347 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3347 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3347 target RNA into GAM3347 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6412 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6412 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6412 target RNA into

GAM6412 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6563 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6563 gene: GAM3347 target protein and GAM6412 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3347 and GAM6412

GR6564 AI239787 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6564(GR6564) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6564 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6564 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6564 gene encodes GR6564 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6564 precursor RNA folds spatially, forming GR6564 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6564 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6564 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6564 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM110048 precursor RNA and GAM130133 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM110048 RNA and GAM130133 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM110048 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM110048 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM110048 target RNA into GAM110048 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM130133 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM130133 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM130133 target RNA into GAM130133 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6564 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6564 gene: GAM110048 target protein and GAM130133 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM110048 and GAM130133

GR6565 BG339422 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6565(GR6565) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6565 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6565 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6565 gene encodes GR6565 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6565 precursor RNA folds spatially, forming GR6565 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6565 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6565 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6565 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM309976 precursor RNA and GAM333513 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM309976 RNA and GAM333513 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM309976 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM309976 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM309976 target RNA into GAM309976 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM333513 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM333513 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM333513 target RNA into GAM333513 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6565 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6565 gene: GAM309976 target protein and GAM333513 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM309976 and GAM333513

GR6566 BG742518 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6566(GR6566) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6566 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6566 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6566 gene encodes GR6566 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6566 precursor RNA folds spatially, forming GR6566 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6566 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6566 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6566 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM112756 precursor RNA and GAM187348 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM112756 RNA and GAM187348 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM112756 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM112756 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM112756 target RNA into GAM112756 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM187348 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM187348 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM187348 target RNA into GAM187348 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6566 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6566 gene: GAM112756 target protein and GAM187348 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM112756 and GAM187348

GR6567 BM798106 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6567 (GR6567) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6567 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6567 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6567 gene encodes GR6567 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6567 precursor RNA folds spatially, forming GR6567 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6567 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6567 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6567 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM99391 precursor RNA and GAM219673 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM99391 RNA and GAM219673 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM99391 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM99391 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM99391 target RNA into GAM99391 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM219673 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM219673 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM219673 target RNA into GAM219673 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6567 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6567 gene: GAM99391 target protein and GAM219673 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM99391 and GAM219673

GR6568 AA926806 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6568(GR6568) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6568 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6568 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6568 gene encodes GR6568 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6568 precursor RNA folds spatially, forming GR6568 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6568 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6568 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6568 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM85 precursor RNA and GAM242247 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM85 RNA and GAM242247 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM85 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM85 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM85 target RNA into GAM85 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM242247 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM242247 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM242247 target RNA into GAM242247 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6568 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6568 gene: GAM85 target protein and GAM242247 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM85 and GAM242247

GR6569 BG619502 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6569(GR6569) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6569 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6569 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6569 gene encodes GR6569 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6569 precursor RNA folds spatially, forming GR6569 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6569 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6569 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6569 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3923 precursor RNA, GAM6318 precursor RNA and GAM279010 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3923 RNA, GAM6318 RNA and GAM279010 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3923 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3923 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3923 target RNA into GAM3923 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6318 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6318 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6318 target RNA into GAM6318 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM279010 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM279010 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM279010 target RNA into GAM279010 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6569 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6569 gene: GAM3923 target protein, GAM6318 target protein and GAM279010 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3923, GAM6318 and GAM279010

GR6570 W25549 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6570 (GR6570) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6570 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6570 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6570 gene encodes GR6570 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6570 precursor RNA folds spatially, forming GR6570 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6570 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6570 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6570 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM219487 precursor RNA and GAM316899 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM219487 RNA and GAM316899 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM219487 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM219487 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM219487 target RNA into GAM219487 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM316899 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM316899 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM316899 target RNA into GAM316899 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6570 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6570 gene: GAM219487 target protein and GAM316899 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM219487 and GAM316899

GR6571 BE156381 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6571 (GR6571) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6571 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6571 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6571 gene encodes GR6571 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6571 precursor RNA folds spatially, forming GR6571 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6571 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6571 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6571 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM181677 precursor RNA and GAM298991 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM181677 RNA and GAM298991 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM181677 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM181677 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM181677 target RNA into GAM181677 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM298991 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM298991 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM298991 target RNA into GAM298991 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6571 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6571 gene: GAM181677 target protein and GAM298991 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM181677 and GAM298991

GR6572 AI160834 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6572(GR6572) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6572 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6572 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6572 gene encodes GR6572 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6572 precursor RNA folds spatially, forming GR6572 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6572 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6572 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6572 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM314480 precursor RNA and GAM327384 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM314480 RNA and GAM327384 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM314480 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM314480 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM314480 target RNA into GAM314480 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM327384 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM327384 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM327384 target RNA into GAM327384 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6572 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6572 gene: GAM314480 target protein and GAM327384 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM314480 and GAM327384

GR6573 BF366619 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6573(GR6573) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6573 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6573 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6573 gene encodes GR6573 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6573 precursor RNA folds spatially, forming GR6573 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6573 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6573 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6573 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM266 precursor RNA and GAM203883 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM266 RNA and GAM203883 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM266 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM266 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM266 target RNA into GAM266 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM203883 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM203883 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM203883 target RNA into GAM203883 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6573 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6573 gene: GAM266 target protein and GAM203883 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference,

with references to GAM266 and GAM203883

GR6574 BF028879 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6574(GR6574) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6574 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6574 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6574 gene encodes GR6574 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6574 precursor RNA folds spatially, forming GR6574 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6574 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6574 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6574 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM103909 precursor RNA and GAM176841 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM103909 RNA and GAM176841 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM103909 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM103909 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM103909 target RNA into GAM103909 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM176841 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM176841 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM176841 target RNA into GAM176841 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6574 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6574 gene: GAM103909 target protein and GAM176841 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM103909 and GAM176841

GR6575 BG142152 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6575(GR6575) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6575 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6575 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6575 gene encodes GR6575 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6575 precursor RNA folds spatially, forming GR6575 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6575 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6575 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6575 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM7238 precursor RNA, GAM97820 precursor RNA and GAM119110 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7238 RNA, GAM97820 RNA and GAM119110 RNA, herein

schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7238 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7238 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7238 target RNA into GAM7238 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM97820 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM97820 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM97820 target RNA into GAM97820 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM119110 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM119110 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM119110 target RNA into GAM119110 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6575 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6575 gene: GAM7238 target protein, GAM97820 target protein and GAM119110 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7238, GAM97820 and GAM119110

GR6576 BI002049 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6576(GR6576) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6576 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6576 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6576 gene encodes GR6576 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6576 precursor RNA folds spatially, forming GR6576 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6576 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6576 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6576 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM9098 precursor RNA and GAM91750 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM9098 RNA and GAM91750 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM9098 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM9098 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM9098 target RNA into GAM9098 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM91750 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM91750 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM91750 target RNA into GAM91750 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6576 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6576 gene: GAM9098 target protein and GAM91750 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM9098 and GAM91750

GR6577 BF103304 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6577(GR6577) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6577 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6577 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6577 gene encodes GR6577 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6577 precursor RNA folds spatially, forming GR6577 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6577 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6577 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6577 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM26679 precursor RNA, GAM59048 precursor RNA and GAM132574 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM26679 RNA, GAM59048 RNA and GAM132574 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM26679 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM26679 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM26679 target RNA into GAM26679 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM59048 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM59048 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM59048 target RNA into GAM59048 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM132574 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM132574 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM132574 target RNA into GAM132574 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6577 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6577 gene: GAM26679 target protein, GAM59048 target protein and GAM132574 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM26679, GAM59048 and GAM132574

GR6578 BG108085 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6578(GR6578) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6578 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6578 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6578 gene encodes GR6578 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6578 precursor RNA folds spatially, forming GR6578 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6578 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6578 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6578 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2

separate GAM precursor RNAs, GAM5455 precursor RNA and GAM14123 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5455 RNA and GAM14123 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5455 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5455 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5455 target RNA into GAM5455 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM14123 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM14123 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM14123 target RNA into GAM14123 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6578 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6578 gene: GAM5455 target protein and GAM14123 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5455 and GAM14123

GR6579 AI810441 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6579 (GR6579) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6579 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6579 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6579 gene encodes GR6579 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR6579 precursor RNA folds spatially, forming GR6579 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6579 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6579 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6579 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4339 precursor RNA and GAM96997 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4339 RNA and GAM96997 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4339 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4339 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4339 target RNA into GAM4339 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM96997 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM96997 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM96997 target RNA into GAM96997 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6579 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6579 gene: GAM4339 target protein and GAM96997 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4339 and GAM96997

GR6580 BI602923 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6580 (GR6580) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6580 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6580 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6580 gene encodes GR6580 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6580 precursor RNA folds spatially, forming GR6580 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6580 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6580 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6580 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM5104 precursor RNA, GAM6410 precursor RNA and GAM20385 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5104 RNA, GAM6410 RNA and GAM20385 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5104 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5104 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5104 target RNA into GAM5104 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6410 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6410 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds

to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6410 target RNA into GAM6410 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM20385 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM20385 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM20385 target RNA into GAM20385 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6580 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6580 gene: GAM5104 target protein, GAM6410 target protein and GAM20385 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5104, GAM6410 and GAM20385

GR6581 BG747296 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6581 (GR6581) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6581 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6581 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6581 gene encodes GR6581 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6581 precursor RNA folds spatially, forming GR6581 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6581 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6581 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6581 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM2948 precursor RNA, GAM3969 precursor RNA,

GAM124612 precursor RNA and GAM289835 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2948 RNA, GAM3969 RNA, GAM124612 RNA and GAM289835 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2948 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2948 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2948 target RNA into GAM2948 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM3969 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3969 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3969 target RNA into GAM3969 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM124612 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM124612 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM124612 target RNA into GAM124612 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM289835 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM289835 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM289835 target RNA into GAM289835 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6581 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6581 gene: GAM2948 target protein, GAM3969 target protein, GAM124612 target protein and GAM289835 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3

TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2948, GAM3969, GAM124612 and GAM289835

GR6582 BI258503 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6582(GR6582) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6582 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6582 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6582 gene encodes GR6582 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6582 precursor RNA folds spatially, forming GR6582 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6582 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6582 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6582 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6760 precursor RNA and GAM275972 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6760 RNA and GAM275972 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6760 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6760 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6760 target RNA into GAM6760 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM275972 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM275972 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM275972 target RNA into GAM275972 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6582 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6582 gene: GAM6760 target protein and GAM275972 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6760 and GAM275972

GR6583 BF667852 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6583(GR6583) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6583 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6583 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6583 gene encodes GR6583 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6583 precursor RNA folds spatially, forming GR6583 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6583 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6583 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6583 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM25746 precursor RNA, GAM79976 precursor RNA and GAM168779 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM25746 RNA, GAM79976 RNA and GAM168779 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM25746 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM25746 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM25746 target RNA into GAM25746 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM79976 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM79976 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM79976 target RNA into GAM79976 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM168779 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM168779 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM168779 target RNA into GAM168779 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6583 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6583 gene: GAM25746 target protein, GAM79976 target protein and GAM168779 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM25746, GAM79976 and GAM168779

GR6584 AW951531 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6584(GR6584) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6584 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6584 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6584 gene encodes GR6584 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6584 precursor RNA folds spatially, forming GR6584 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6584 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6584 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6584 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM93861 precursor RNA, GAM99056 precursor RNA and GAM219018 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM93861 RNA, GAM99056 RNA and GAM219018 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM93861 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM93861 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM93861 target RNA into GAM93861 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM99056 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM99056 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM99056 target RNA into GAM99056 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM219018 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM219018 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM219018

target RNA into GAM219018 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6584 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6584 gene: GAM93861 target protein, GAM99056 target protein and GAM219018 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM93861, GAM99056 and GAM219018

GR6585 BG928852 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6585(GR6585) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6585 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6585 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6585 gene encodes GR6585 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6585 precursor RNA folds spatially, forming GR6585 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6585 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6585 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6585 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8660 precursor RNA and GAM121299 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8660 RNA and GAM121299 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8660 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8660 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8660 target RNA into GAM8660 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM121299 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM121299 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM121299 target RNA into GAM121299 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6585 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6585 gene: GAM8660 target protein and GAM121299 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8660 and GAM121299

GR6586 W79122 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6586(GR6586) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6586 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6586 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6586 gene encodes GR6586 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6586 precursor RNA folds spatially, forming GR6586 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6586 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6586 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6586 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM32052 precursor RNA and GAM208244 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM32052 RNA and GAM208244 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM32052 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM32052 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM32052 target RNA into GAM32052 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM208244 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM208244 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM208244 target RNA into GAM208244 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6586 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6586 gene: GAM32052 target protein and GAM208244 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM32052 and GAM208244

GR6587 BG472089 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6587(GR6587) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6587 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6587 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6587 gene encodes GR6587 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6587 precursor RNA folds spatially, forming GR6587 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6587 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6587 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6587 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM20514 precursor RNA and GAM193841 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM20514 RNA and GAM193841 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM20514 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM20514 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM20514 target RNA into GAM20514 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM193841 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM193841 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM193841 target RNA into GAM193841 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6587 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6587 gene: GAM20514 target protein and GAM193841 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference,

with references to GAM20514 and GAM193841

GR6588 AA453258 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6588(GR6588) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6588 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6588 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6588 gene encodes GR6588 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6588 precursor RNA folds spatially, forming GR6588 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6588 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6588 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6588 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1083 precursor RNA and GAM26667 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1083 RNA and GAM26667 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1083 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1083 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1083 target RNA into GAM1083 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM26667 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM26667 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM26667 target RNA into GAM26667 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6588 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6588 gene: GAM1083 target protein and GAM26667 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1083 and GAM26667

GR6589 BF675577 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6589(GR6589) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6589 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6589 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6589 gene encodes GR6589 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6589 precursor RNA folds spatially, forming GR6589 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6589 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6589 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6589 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5538 precursor RNA and GAM65247 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5538 RNA and GAM65247 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding

to GAM RNA of Fig. 8.

GAM5538 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5538 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5538 target RNA into GAM5538 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM65247 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM65247 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM65247 target RNA into GAM65247 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6589 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6589 gene: GAM5538 target protein and GAM65247 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5538 and GAM65247

GR6590 BM010859 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6590(GR6590) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6590 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6590 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6590 gene encodes GR6590 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6590 precursor RNA folds spatially, forming GR6590 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6590 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6590 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR6590 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM98866 precursor RNA, GAM113586 precursor RNA and GAM149132 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM98866 RNA, GAM113586 RNA and GAM149132 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM98866 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM98866 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM98866 target RNA into GAM98866 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM113586 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM113586 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM113586 target RNA into GAM113586 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM149132 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM149132 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM149132 target RNA into GAM149132 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6590 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6590 gene: GAM98866 target protein, GAM113586 target protein and GAM149132 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM98866, GAM113586 and GAM149132

GR6591 BM687511 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6591 (GR6591) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6591 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6591 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6591 gene encodes GR6591 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6591 precursor RNA folds spatially, forming GR6591 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6591 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6591 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6591 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7528 precursor RNA and GAM334176 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7528 RNA and GAM334176 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7528 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7528 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7528 target RNA into GAM7528 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM334176 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM334176 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM334176 target RNA into GAM334176 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6591 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6591 gene: GAM7528 target protein and GAM334176 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7528 and GAM334176

GR6592 BI459594 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6592(GR6592) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6592 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6592 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6592 gene encodes GR6592 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6592 precursor RNA folds spatially, forming GR6592 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6592 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6592 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6592 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1444 precursor RNA and GAM265366 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1444 RNA and GAM265366 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1444 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1444 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1444 target RNA into GAM1444 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM265366 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM265366 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM265366 target RNA into GAM265366 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6592 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6592 gene: GAM1444 target protein and GAM265366 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1444 and GAM265366

GR6593 R30691 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6593(GR6593) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6593 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6593 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6593 gene encodes GR6593 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6593 precursor RNA folds spatially, forming GR6593 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6593 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6593 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6593 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4576 precursor RNA and GAM251141 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4576 RNA and GAM251141 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4576 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4576 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4576 target RNA into GAM4576 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM251141 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM251141 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM251141 target RNA into GAM251141 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6593 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6593 gene: GAM4576 target protein and GAM251141 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4576 and GAM251141

GR6594 BI560891 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6594(GR6594) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6594 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6594 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6594 gene encodes GR6594 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6594 precursor RNA folds spatially, forming GR6594 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6594 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6594 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6594 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM114997 precursor RNA and GAM218871 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM114997 RNA and GAM218871 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM114997 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM114997 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM114997 target RNA into GAM114997 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM218871 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM218871 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM218871 target RNA into GAM218871 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6594 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6594 gene: GAM114997 target protein and GAM218871 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes

is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM114997 and GAM218871

GR6595 AU124912 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6595(GR6595) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6595 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6595 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6595 gene encodes GR6595 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6595 precursor RNA folds spatially, forming GR6595 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6595 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6595 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6595 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6573 precursor RNA and GAM111873 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6573 RNA and GAM111873 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6573 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6573 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6573 target RNA into GAM6573 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM111873 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM111873 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM111873 target RNA into GAM111873 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6595 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6595 gene: GAM6573 target protein and GAM111873 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6573 and GAM111873

GR6596 BF312550 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6596 (GR6596) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6596 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6596 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6596 gene encodes GR6596 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6596 precursor RNA folds spatially, forming GR6596 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6596 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6596 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6596 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3671 precursor RNA and GAM7770 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3671 RNA and GAM7770 RNA, herein schematically

represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3671 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3671 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3671 target RNA into GAM3671 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7770 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7770 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7770 target RNA into GAM7770 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6596 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6596 gene: GAM3671 target protein and GAM7770 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3671 and GAM7770

GR6597 BI914327 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6597(GR6597) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6597 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6597 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6597 gene encodes GR6597 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6597 precursor RNA folds spatially, forming GR6597 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6597 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6597 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6597 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1987 precursor RNA and GAM120165 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1987 RNA and GAM120165 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1987 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1987 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1987 target RNA into GAM1987 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM120165 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM120165 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM120165 target RNA into GAM120165 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6597 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6597 gene: GAM1987 target protein and GAM120165 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1987 and GAM120165

GR6598 BF839468 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6598(GR6598) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6598 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR6598 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6598 gene encodes GR6598 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6598 precursor RNA folds spatially, forming GR6598 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6598 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6598 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6598 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2459 precursor RNA and GAM48887 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2459 RNA and GAM48887 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2459 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2459 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2459 target RNA into GAM2459 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM48887 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM48887 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM48887 target RNA into GAM48887 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6598 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6598 gene: GAM2459 target

protein and GAM48887 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2459 and GAM48887

GR6599 H89180 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6599(GR6599) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6599 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6599 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6599 gene encodes GR6599 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6599 precursor RNA folds spatially, forming GR6599 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6599 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6599 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6599 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM294794 precursor RNA and GAM300401 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM294794 RNA and GAM300401 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM294794 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM294794 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM294794 target RNA into GAM294794 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM300401 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM300401 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM300401 target RNA into GAM300401 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6599 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6599 gene: GAM294794 target protein and GAM300401 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM294794 and GAM300401

GR6600 BF575763 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6600(GR6600) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6600 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6600 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6600 gene encodes GR6600 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6600 precursor RNA folds spatially, forming GR6600 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6600 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6600 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6600 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM4923 precursor RNA, GAM141402 precursor RNA, GAM212242 precursor RNA and GAM325234 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4923 RNA, GAM141402 RNA, GAM212242 RNA and GAM325234 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4923 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4923 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4923 target RNA into GAM4923 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM141402 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM141402 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM141402 target RNA into GAM141402 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM212242 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM212242 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM212242 target RNA into GAM212242 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM325234 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM325234 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM325234 target RNA into GAM325234 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6600 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6600 gene: GAM4923 target protein, GAM141402 target protein, GAM212242 target protein and GAM325234 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4923, GAM141402, GAM212242 and GAM325234

bioinformatically detected regulatory gene, referred to here as Genomic Record 6601 (GR6601) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6601 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6601 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6601 gene encodes GR6601 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6601 precursor RNA folds spatially, forming GR6601 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6601 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6601 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6601 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM7341 precursor RNA, GAM90589 precursor RNA and GAM257674 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7341 RNA, GAM90589 RNA and GAM257674 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7341 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7341 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7341 target RNA into GAM7341 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM90589 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM90589 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM90589 target RNA into GAM90589 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM257674 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM257674 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM257674 target RNA into GAM257674 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6601 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6601 gene: GAM7341 target protein, GAM90589 target protein and GAM257674 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7341, GAM90589 and GAM257674

GR6602 BI464418 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6602(GR6602) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6602 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6602 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6602 gene encodes GR6602 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6602 precursor RNA folds spatially, forming GR6602 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6602 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6602 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6602 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4335 precursor RNA, GAM5309 precursor RNA and GAM95289 precursor RNA, herein schematically represented by GAM1 FOLDED

PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4335 RNA, GAM5309 RNA and GAM95289 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4335 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4335 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4335 target RNA into GAM4335 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5309 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5309 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5309 target RNA into GAM5309 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM95289 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM95289 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM95289 target RNA into GAM95289 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6602 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6602 gene: GAM4335 target protein, GAM5309 target protein and GAM95289 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4335, GAM5309 and GAM95289

GR6603 BF381611 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6603(GR6603) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR6603 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6603 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6603 gene encodes GR6603 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6603 precursor RNA folds spatially, forming GR6603 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6603 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6603 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6603 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM53305 precursor RNA, GAM100566 precursor RNA and GAM305205 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM53305 RNA, GAM100566 RNA and GAM305205 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM53305 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM53305 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM53305 target RNA into GAM53305 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM100566 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM100566 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM100566 target RNA into GAM100566 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM305205 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM305205 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM305205 target RNA into GAM305205 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6603 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6603 gene: GAM53305 target protein, GAM100566 target protein and GAM305205 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM53305, GAM100566 and GAM305205

GR6604 R22491 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6604(GR6604) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6604 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6604 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6604 gene encodes GR6604 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6604 precursor RNA folds spatially, forming GR6604 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6604 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6604 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6604 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM55424 precursor RNA and GAM60186 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM55424 RNA and GAM60186 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM55424 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM55424 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM55424 target RNA into GAM55424 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM60186 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM60186 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM60186 target RNA into GAM60186 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6604 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6604 gene: GAM55424 target protein and GAM60186 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM55424 and GAM60186

GR6605 T82151 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6605(GR6605) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6605 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6605 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6605 gene encodes GR6605 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6605 precursor RNA folds spatially, forming GR6605 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6605 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR6605 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6605 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6671 precursor RNA and GAM226692 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6671 RNA and GAM226692 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6671 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6671 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6671 target RNA into GAM6671 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM226692 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM226692 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM226692 target RNA into GAM226692 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6605 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6605 gene: GAM6671 target protein and GAM226692 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6671 and GAM226692

GR6606 AV752691 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6606(GR6606) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6606 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6606 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6606 gene encodes GR6606 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6606 precursor RNA folds spatially, forming GR6606 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6606 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6606 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6606 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM641 precursor RNA and GAM115399 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM641 RNA and GAM115399 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM641 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM641 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM641 target RNA into GAM641 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM115399 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM115399 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM115399 target RNA into GAM115399 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6606 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6606 gene: GAM641 target protein and GAM115399 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM641 and GAM115399

GR6607 BI200149 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6607(GR6607) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6607 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6607 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6607 gene encodes GR6607 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6607 precursor RNA folds spatially, forming GR6607 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6607 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6607 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6607 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM189050 precursor RNA and GAM269219 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM189050 RNA and GAM269219 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM189050 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM189050 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM189050

target RNA into GAM189050 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM269219 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM269219 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM269219 target RNA into GAM269219 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6607 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6607 gene: GAM189050 target protein and GAM269219 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM189050 and GAM269219

GR6608 BI012769 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6608(GR6608) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6608 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6608 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6608 gene encodes GR6608 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6608 precursor RNA folds spatially, forming GR6608 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6608 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6608 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6608 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3899 precursor RNA and GAM94044 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3899 RNA and GAM94044 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3899 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3899 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3899 target RNA into GAM3899 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM94044 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM94044 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM94044 target RNA into GAM94044 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6608 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6608 gene: GAM3899 target protein and GAM94044 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3899 and GAM94044

GR6609 AW134796 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6609(GR6609) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6609 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6609 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6609 gene encodes GR6609 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6609 precursor RNA folds spatially, forming GR6609 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated

that GR6609 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6609 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6609 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM9865 precursor RNA, GAM103291 precursor RNA and GAM244133 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM9865 RNA, GAM103291 RNA and GAM244133 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM9865 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM9865 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM9865 target RNA into GAM9865 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM103291 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM103291 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM103291 target RNA into GAM103291 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM244133 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM244133 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM244133 target RNA into GAM244133 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6609 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6609 gene: GAM9865 target

protein, GAM103291 target protein and GAM244133 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM9865, GAM103291 and GAM244133

GR6610 BM759615 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6610(GR6610) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6610 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6610 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6610 gene encodes GR6610 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6610 precursor RNA folds spatially, forming GR6610 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6610 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6610 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6610 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM20324 precursor RNA and GAM96216 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM20324 RNA and GAM96216 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM20324 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM20324 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM20324 target RNA into GAM20324 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM96216 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM96216 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM96216 target RNA into GAM96216 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6610 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6610 gene: GAM20324 target protein and GAM96216 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM20324 and GAM96216

GR6611 AW440916 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6611 (GR6611) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6611 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6611 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6611 gene encodes GR6611 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6611 precursor RNA folds spatially, forming GR6611 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6611 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6611 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6611 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM2507 precursor RNA, GAM185838 precursor RNA, GAM291229 precursor RNA and GAM330006 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2507 RNA, GAM185838 RNA, GAM291229 RNA and GAM330006 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2507 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2507 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2507 target RNA into GAM2507 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM185838 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM185838 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM185838 target RNA into GAM185838 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM291229 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM291229 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM291229 target RNA into GAM291229 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM330006 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM330006 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM330006 target RNA into GAM330006 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6611 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6611 gene: GAM2507 target protein, GAM185838 target protein, GAM291229 target protein and GAM330006 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2507, GAM185838, GAM291229 and GAM330006

GR6612 BF749980 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6612(GR6612) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6612 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6612 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6612 gene encodes GR6612 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6612 precursor RNA folds spatially, forming GR6612 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6612 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6612 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6612 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM61825 precursor RNA, GAM107614 precursor RNA and GAM223643 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM61825 RNA, GAM107614 RNA and GAM223643 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM61825 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM61825 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM61825 target RNA into GAM61825 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM107614 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM107614 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM107614 target RNA into GAM107614 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM223643 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM223643 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM223643 target RNA into GAM223643 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6612 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6612 gene: GAM61825 target protein, GAM107614 target protein and GAM223643 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM61825, GAM107614 and GAM223643

GR6613 BG258808 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6613(GR6613) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6613 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6613 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6613 gene encodes GR6613 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6613 precursor RNA folds spatially, forming GR6613 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6613 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6613 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6613 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM74 precursor RNA, GAM250709 precursor RNA and

GAM322918 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM74 RNA, GAM250709 RNA and GAM322918 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM74 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM74 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM74 target RNA into GAM74 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM250709 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM250709 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM250709 target RNA into GAM250709 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM322918 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM322918 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM322918 target RNA into GAM322918 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6613 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6613 gene: GAM74 target protein, GAM250709 target protein and GAM322918 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM74, GAM250709 and GAM322918

GR6614 R16860 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6614(GR6614) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR6614 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6614 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6614 gene encodes GR6614 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6614 precursor RNA folds spatially, forming GR6614 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6614 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6614 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6614 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM21449 precursor RNA and GAM46170 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM21449 RNA and GAM46170 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM21449 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM21449 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM21449 target RNA into GAM21449 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM46170 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM46170 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM46170 target RNA into GAM46170 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6614 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6614 gene: GAM21449 target protein and GAM46170 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM21449 and GAM46170

GR6615 AW891118 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6615 (GR6615) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6615 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6615 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6615 gene encodes GR6615 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6615 precursor RNA folds spatially, forming GR6615 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6615 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6615 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6615 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM228560 precursor RNA and GAM274165 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM228560 RNA and GAM274165 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM228560 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM228560 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM228560 target RNA into GAM228560 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM274165 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM274165 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM274165 target RNA into GAM274165 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6615 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6615 gene: GAM228560 target protein and GAM274165 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM228560 and GAM274165

GR6616 BG898149 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6616(GR6616) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6616 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6616 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6616 gene encodes GR6616 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6616 precursor RNA folds spatially, forming GR6616 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6616 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6616 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6616 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM152970 precursor RNA and GAM327305 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3

FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM152970 RNA and GAM327305 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM152970 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM152970 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM152970 target RNA into GAM152970 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM327305 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM327305 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM327305 target RNA into GAM327305 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6616 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6616 gene: GAM152970 target protein and GAM327305 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM152970 and GAM327305

GR6617 BG767360 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6617(GR6617) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6617 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6617 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6617 gene encodes GR6617 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6617 precursor RNA folds spatially, forming GR6617 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6617 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6617 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6617 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3188 precursor RNA and GAM101811 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3188 RNA and GAM101811 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3188 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3188 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3188 target RNA into GAM3188 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM101811 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM101811 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM101811 target RNA into GAM101811 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6617 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6617 gene: GAM3188 target protein and GAM101811 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3188 and GAM101811

6618(GR6618) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6618 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6618 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6618 gene encodes GR6618 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6618 precursor RNA folds spatially, forming GR6618 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6618 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6618 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6618 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM300902 precursor RNA and GAM326207 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM300902 RNA and GAM326207 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM300902 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM300902 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM300902 target RNA into GAM300902 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM326207 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM326207 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM326207 target RNA into GAM326207 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6618 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6618 gene: GAM300902 target protein and GAM326207 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM300902 and GAM326207

GR6619 BF994353 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6619(GR6619) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6619 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6619 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6619 gene encodes GR6619 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6619 precursor RNA folds spatially, forming GR6619 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6619 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6619 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6619 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM265078 precursor RNA and GAM275400 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM265078 RNA and GAM275400 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM265078 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM265078 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM265078 target RNA into GAM265078 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM275400 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM275400 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM275400 target RNA into GAM275400 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6619 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6619 gene: GAM265078 target protein and GAM275400 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM265078 and GAM275400

GR6620 BI226811 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6620(GR6620) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6620 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6620 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6620 gene encodes GR6620 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6620 precursor RNA folds spatially, forming GR6620 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6620 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6620 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6620 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2

separate GAM precursor RNAs, GAM6704 precursor RNA and GAM88300 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6704 RNA and GAM88300 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6704 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6704 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6704 target RNA into GAM6704 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM88300 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM88300 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM88300 target RNA into GAM88300 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6620 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6620 gene: GAM6704 target protein and GAM88300 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6704 and GAM88300

GR6621 AA174034 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6621 (GR6621) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6621 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6621 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6621 gene encodes GR6621 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR6621 precursor RNA folds spatially, forming GR6621 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6621 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6621 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6621 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM156 precursor RNA, GAM52477 precursor RNA and GAM96748 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM156 RNA, GAM52477 RNA and GAM96748 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM156 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM156 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM156 target RNA into GAM156 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM52477 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM52477 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM52477 target RNA into GAM52477 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM96748 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM96748 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM96748 target RNA into GAM96748 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6621 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6621 gene: GAM156 target protein, GAM52477 target protein and GAM96748 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM156, GAM52477 and GAM96748

GR6622 BM046741 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6622(GR6622) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6622 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6622 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6622 gene encodes GR6622 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6622 precursor RNA folds spatially, forming GR6622 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6622 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6622 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6622 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1010 precursor RNA and GAM161725 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1010 RNA and GAM161725 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1010 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1010 target RNA, herein schematically represented by

GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1010 target RNA into GAM1010 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM161725 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM161725 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM161725 target RNA into GAM161725 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6622 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6622 gene: GAM1010 target protein and GAM161725 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1010 and GAM161725

GR6623 BQ007048 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6623(GR6623) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6623 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6623 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6623 gene encodes GR6623 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6623 precursor RNA folds spatially, forming GR6623 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6623 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6623 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6623 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3354 precursor RNA, GAM6425 precursor RNA and

GAM296192 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3354 RNA, GAM6425 RNA and GAM296192 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3354 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3354 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3354 target RNA into GAM3354 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6425 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6425 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6425 target RNA into GAM6425 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM296192 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM296192 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM296192 target RNA into GAM296192 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6623 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6623 gene: GAM3354 target protein, GAM6425 target protein and GAM296192 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3354, GAM6425 and GAM296192

GR6624 AA034457 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6624(GR6624) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR6624 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6624 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6624 gene encodes GR6624 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6624 precursor RNA folds spatially, forming GR6624 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6624 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6624 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6624 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM7046 precursor RNA, GAM7293 precursor RNA and GAM42708 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7046 RNA, GAM7293 RNA and GAM42708 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7046 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7046 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7046 target RNA into GAM7046 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7293 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7293 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7293 target RNA into GAM7293 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM42708 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM42708 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM42708 target RNA into GAM42708 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6624 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6624 gene: GAM7046 target protein, GAM7293 target protein and GAM42708 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7046, GAM7293 and GAM42708

GR6625 AW674573 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6625(GR6625) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6625 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6625 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6625 gene encodes GR6625 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6625 precursor RNA folds spatially, forming GR6625 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6625 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6625 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6625 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5214 precursor RNA and GAM99138 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5214 RNA and GAM99138 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5214 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5214 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5214 target RNA into GAM5214 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM99138 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM99138 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM99138 target RNA into GAM99138 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6625 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6625 gene: GAM5214 target protein and GAM99138 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5214 and GAM99138

GR6626 BF763408 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6626(GR6626) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6626 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6626 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6626 gene encodes GR6626 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6626 precursor RNA folds spatially, forming GR6626 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6626 folded precursor RNA comprises a plurality of what is known in the

art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6626 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6626 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM4323 precursor RNA, GAM62647 precursor RNA, GAM128813 precursor RNA and GAM138929 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4323 RNA, GAM62647 RNA, GAM128813 RNA and GAM138929 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4323 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4323 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4323 target RNA into GAM4323 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM62647 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM62647 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM62647 target RNA into GAM62647 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM128813 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM128813 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM128813 target RNA into GAM128813 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM138929 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM138929 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM138929

target RNA into GAM138929 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6626 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6626 gene: GAM4323 target protein, GAM62647 target protein, GAM128813 target protein and GAM138929 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4323, GAM62647, GAM128813 and GAM138929

GR6627 BF663681 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6627(GR6627) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6627 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6627 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6627 gene encodes GR6627 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6627 precursor RNA folds spatially, forming GR6627 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6627 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6627 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6627 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2441 precursor RNA and GAM216166 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2441 RNA and GAM216166 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2441 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2441 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2441 target RNA into GAM2441 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM216166 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM216166 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM216166 target RNA into GAM216166 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6627 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6627 gene: GAM2441 target protein and GAM216166 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2441 and GAM216166

GR6628 BM551428 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6628(GR6628) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6628 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6628 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6628 gene encodes GR6628 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6628 precursor RNA folds spatially, forming GR6628 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6628 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6628 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6628 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM83733 precursor RNA, GAM263819 precursor RNA, GAM270421 precursor RNA and GAM302662 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM83733 RNA, GAM263819 RNA, GAM270421 RNA and GAM302662 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM83733 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM83733 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM83733 target RNA into GAM83733 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM263819 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM263819 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM263819 target RNA into GAM263819 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM270421 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM270421 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM270421 target RNA into GAM270421 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM302662 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM302662 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM302662 target RNA into GAM302662 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6628 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR6628 gene: GAM83733 target protein, GAM263819 target protein, GAM270421 target protein and GAM302662 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM83733, GAM263819, GAM270421 and GAM302662

GR6629 AI799306 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6629(GR6629) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6629 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6629 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6629 gene encodes GR6629 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6629 precursor RNA folds spatially, forming GR6629 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6629 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6629 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6629 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM280197 precursor RNA and GAM302555 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM280197 RNA and GAM302555 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM280197 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM280197 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM280197

target RNA into GAM280197 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM302555 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM302555 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM302555 target RNA into GAM302555 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6629 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6629 gene: GAM280197 target protein and GAM302555 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM280197 and GAM302555

GR6630 AW291666 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6630(GR6630) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6630 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6630 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6630 gene encodes GR6630 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6630 precursor RNA folds spatially, forming GR6630 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6630 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6630 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6630 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6406 precursor RNA and GAM44918 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6406 RNA and GAM44918 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6406 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6406 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6406 target RNA into GAM6406 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM44918 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM44918 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM44918 target RNA into GAM44918 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6630 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6630 gene: GAM6406 target protein and GAM44918 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6406 and GAM44918

GR6631 BI496400 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6631 (GR6631) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6631 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6631 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6631 gene encodes GR6631 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6631 precursor RNA folds spatially, forming GR6631 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated

that GR6631 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6631 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6631 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM209 precursor RNA, GAM57950 precursor RNA and GAM139831 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM209 RNA, GAM57950 RNA and GAM139831 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM209 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM209 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM209 target RNA into GAM209 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM57950 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM57950 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM57950 target RNA into GAM57950 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM139831 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM139831 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM139831 target RNA into GAM139831 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6631 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6631 gene: GAM209 target

protein, GAM57950 target protein and GAM139831 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM209, GAM57950 and GAM139831

GR6632 AU121369 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6632(GR6632) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6632 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6632 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6632 gene encodes GR6632 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6632 precursor RNA folds spatially, forming GR6632 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6632 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6632 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6632 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM151571 precursor RNA and GAM315619 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM151571 RNA and GAM315619 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM151571 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM151571 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM151571 target RNA into GAM151571 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM315619 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM315619 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM315619 target RNA into GAM315619 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6632 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6632 gene: GAM151571 target protein and GAM315619 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM151571 and GAM315619

GR6633 AA463845 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6633(GR6633) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6633 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6633 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6633 gene encodes GR6633 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6633 precursor RNA folds spatially, forming GR6633 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6633 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6633 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6633 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM307749 precursor RNA and GAM312596 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM307749 RNA and GAM312596 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM307749 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM307749 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM307749 target RNA into GAM307749 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM312596 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM312596 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM312596 target RNA into GAM312596 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6633 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6633 gene: GAM307749 target protein and GAM312596 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM307749 and GAM312596

GR6634 BM090883 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6634(GR6634) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6634 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6634 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6634 gene encodes GR6634 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6634 precursor RNA folds spatially, forming GR6634 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6634 folded precursor RNA comprises a plurality of what is known in the

art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6634 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6634 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM43344 precursor RNA and GAM335755 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM43344 RNA and GAM335755 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM43344 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM43344 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM43344 target RNA into GAM43344 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM335755 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM335755 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM335755 target RNA into GAM335755 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6634 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6634 gene: GAM43344 target protein and GAM335755 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM43344 and GAM335755

GR6635 AV694951 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6635(GR6635) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR6635 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6635 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6635 gene encodes GR6635 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6635 precursor RNA folds spatially, forming GR6635 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6635 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6635 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6635 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4728 precursor RNA, GAM25859 precursor RNA and GAM230767 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4728 RNA, GAM25859 RNA and GAM230767 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4728 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4728 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4728 target RNA into GAM4728 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM25859 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM25859 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM25859 target RNA into GAM25859 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM230767 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM230767 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM230767 target RNA into GAM230767 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6635 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6635 gene: GAM4728 target protein, GAM25859 target protein and GAM230767 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4728, GAM25859 and GAM230767

GR6636 BI919074 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6636(GR6636) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6636 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6636 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6636 gene encodes GR6636 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6636 precursor RNA folds spatially, forming GR6636 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6636 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6636 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6636 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2113 precursor RNA, GAM29099 precursor RNA and GAM257825 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2113 RNA, GAM29099 RNA and GAM257825 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2113 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2113 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2113 target RNA into GAM2113 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM29099 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM29099 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM29099 target RNA into GAM29099 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM257825 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM257825 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM257825 target RNA into GAM257825 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6636 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6636 gene: GAM2113 target protein, GAM29099 target protein and GAM257825 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2113, GAM29099 and GAM257825

GR6637 BF954755 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6637(GR6637) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6637 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6637

gene was detected is described hereinabove with reference to Figs. 8-18.

GR6637 gene encodes GR6637 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6637 precursor RNA folds spatially, forming GR6637 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6637 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6637 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6637 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2388 precursor RNA and GAM7092 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2388 RNA and GAM7092 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2388 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2388 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2388 target RNA into GAM2388 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7092 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7092 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7092 target RNA into GAM7092 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6637 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6637 gene: GAM2388 target protein and GAM7092 target protein, herein schematically represented by GAM1

TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2388 and GAM7092

GR6638 BM929290 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6638(GR6638) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6638 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6638 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6638 gene encodes GR6638 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6638 precursor RNA folds spatially, forming GR6638 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6638 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6638 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6638 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7624 precursor RNA and GAM271329 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7624 RNA and GAM271329 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7624 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7624 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7624 target RNA into GAM7624 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM271329 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM271329 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM271329 target RNA into GAM271329 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6638 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6638 gene: GAM7624 target protein and GAM271329 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7624 and GAM271329

GR6639 BM826732 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6639(GR6639) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6639 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6639 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6639 gene encodes GR6639 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6639 precursor RNA folds spatially, forming GR6639 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6639 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6639 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6639 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3721 precursor RNA and GAM8176 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM3721 RNA and GAM8176 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3721 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3721 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3721 target RNA into GAM3721 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8176 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8176 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8176 target RNA into GAM8176 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6639 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6639 gene: GAM3721 target protein and GAM8176 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3721 and GAM8176

GR6640 BG285871 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6640 (GR6640) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6640 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6640 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6640 gene encodes GR6640 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6640 precursor RNA folds spatially, forming GR6640 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6640 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6640 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6640 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM42086 precursor RNA and GAM59267 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM42086 RNA and GAM59267 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM42086 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM42086 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM42086 target RNA into GAM42086 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM59267 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM59267 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM59267 target RNA into GAM59267 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6640 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6640 gene: GAM42086 target protein and GAM59267 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM42086 and GAM59267

GR6641 BF210820 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6641 (GR6641) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6641 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6641 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6641 gene encodes GR6641 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6641 precursor RNA folds spatially, forming GR6641 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6641 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6641 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6641 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5471 precursor RNA and GAM153652 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5471 RNA and GAM153652 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5471 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5471 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5471 target RNA into GAM5471 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM153652 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM153652 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM153652 target RNA into GAM153652 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6641 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR6641 gene: GAM5471 target protein and GAM153652 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5471 and GAM153652

GR6642 BG661345 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6642(GR6642) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6642 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6642 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6642 gene encodes GR6642 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6642 precursor RNA folds spatially, forming GR6642 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6642 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6642 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6642 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4898 precursor RNA and GAM5776 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4898 RNA and GAM5776 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4898 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4898 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4898 target RNA into GAM4898 target protein, herein schematically represented by GAM1 TARGET

PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5776 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5776 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5776 target RNA into GAM5776 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6642 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6642 gene: GAM4898 target protein and GAM5776 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4898 and GAM5776

GR6643 BG003932 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6643(GR6643) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6643 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6643 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6643 gene encodes GR6643 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6643 precursor RNA folds spatially, forming GR6643 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6643 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6643 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6643 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2321 precursor RNA and GAM8105 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2321 RNA and GAM8105 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2321 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2321 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2321 target RNA into GAM2321 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8105 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8105 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8105 target RNA into GAM8105 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6643 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6643 gene: GAM2321 target protein and GAM8105 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2321 and GAM8105

GR6644 AI906902 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6644(GR6644) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6644 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6644 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6644 gene encodes GR6644 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6644 precursor RNA folds spatially, forming GR6644 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6644 folded precursor RNA comprises a plurality of what is known in the

art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6644 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6644 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5429 precursor RNA and GAM142425 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5429 RNA and GAM142425 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5429 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5429 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5429 target RNA into GAM5429 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM142425 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM142425 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM142425 target RNA into GAM142425 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6644 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6644 gene: GAM5429 target protein and GAM142425 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5429 and GAM142425

GR6645 BI825175 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6645(GR6645) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR6645 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6645 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6645 gene encodes GR6645 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6645 precursor RNA folds spatially, forming GR6645 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6645 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6645 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6645 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM6268 precursor RNA, GAM81182 precursor RNA and GAM124391 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6268 RNA, GAM81182 RNA and GAM124391 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6268 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6268 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6268 target RNA into GAM6268 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM81182 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM81182 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM81182 target RNA into GAM81182 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM124391 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM124391 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM124391 target RNA into GAM124391 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6645 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6645 gene: GAM6268 target protein, GAM81182 target protein and GAM124391 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6268, GAM81182 and GAM124391

GR6646 BE464344 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6646(GR6646) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6646 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6646 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6646 gene encodes GR6646 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6646 precursor RNA folds spatially, forming GR6646 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6646 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6646 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6646 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM18053 precursor RNA and GAM29372 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM18053 RNA and GAM29372 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM18053 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM18053 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM18053 target RNA into GAM18053 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM29372 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM29372 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM29372 target RNA into GAM29372 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6646 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6646 gene: GAM18053 target protein and GAM29372 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM18053 and GAM29372

GR6647 BI032355 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6647(GR6647) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6647 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6647 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6647 gene encodes GR6647 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6647 precursor RNA folds spatially, forming GR6647 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6647 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR6647 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6647 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM73935 precursor RNA, GAM96288 precursor RNA and GAM140379 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM73935 RNA, GAM96288 RNA and GAM140379 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM73935 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM73935 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM73935 target RNA into GAM73935 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM96288 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM96288 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM96288 target RNA into GAM96288 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM140379 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM140379 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM140379 target RNA into GAM140379 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6647 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6647 gene: GAM73935 target protein, GAM96288 target protein and GAM140379 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN.

The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM73935, GAM96288 and GAM140379

GR6648 BQ083208 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6648 (GR6648) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6648 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6648 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6648 gene encodes GR6648 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6648 precursor RNA folds spatially, forming GR6648 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6648 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6648 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6648 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM5855 precursor RNA, GAM109883 precursor RNA and GAM157422 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5855 RNA, GAM109883 RNA and GAM157422 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5855 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5855 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5855 target RNA into GAM5855 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM109883 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM109883 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM109883 target RNA into GAM109883 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM157422 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM157422 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM157422 target RNA into GAM157422 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6648 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6648 gene: GAM5855 target protein, GAM109883 target protein and GAM157422 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5855, GAM109883 and GAM157422

GR6649 AV760927 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6649(GR6649) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6649 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6649 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6649 gene encodes GR6649 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6649 precursor RNA folds spatially, forming GR6649 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6649 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6649 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6649 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 5 separate GAM precursor RNAs, GAM7631 precursor RNA, GAM47252 precursor RNA, GAM131967 precursor RNA, GAM184500 precursor RNA and GAM313615 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7631 RNA, GAM47252 RNA, GAM131967 RNA, GAM184500 RNA and GAM313615 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7631 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7631 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7631 target RNA into GAM7631 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM47252 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM47252 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM47252 target RNA into GAM47252 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM131967 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM131967 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM131967 target RNA into GAM131967 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM184500 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM184500 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM184500 target RNA into GAM184500 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM313615 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM313615 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM313615 target RNA into GAM313615 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6649 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6649 gene: GAM7631 target protein, GAM47252 target protein, GAM131967 target protein, GAM184500 target protein and GAM313615 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7631, GAM47252, GAM131967, GAM184500 and GAM313615

GR6650 AI559495 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6650(GR6650) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6650 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6650 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6650 gene encodes GR6650 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6650 precursor RNA folds spatially, forming GR6650 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6650 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6650 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6650 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1556 precursor RNA, GAM272885 precursor RNA and GAM297786 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1556 RNA, GAM272885 RNA and GAM297786 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1556 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1556 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1556 target RNA into GAM1556 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM272885 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM272885 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM272885 target RNA into GAM272885 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM297786 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM297786 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM297786 target RNA into GAM297786 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6650 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6650 gene: GAM1556 target protein, GAM272885 target protein and GAM297786 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1556, GAM272885 and GAM297786

GR6651 BG400861 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6651(GR6651) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6651 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6651 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6651 gene encodes GR6651 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6651 precursor RNA folds spatially, forming GR6651 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6651 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6651 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6651 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM262559 precursor RNA and GAM266336 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM262559 RNA and GAM266336 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM262559 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM262559 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM262559 target RNA into GAM262559 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM266336 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM266336 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM266336 target RNA into GAM266336 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6651 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6651 gene: GAM262559 target protein and GAM266336 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes

is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM262559 and GAM266336

GR6652 AA694110 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6652(GR6652) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6652 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6652 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6652 gene encodes GR6652 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6652 precursor RNA folds spatially, forming GR6652 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6652 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6652 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6652 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM7976 precursor RNA, GAM154567 precursor RNA and GAM225527 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7976 RNA, GAM154567 RNA and GAM225527 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7976 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7976 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7976 target RNA into GAM7976 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM154567 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM154567 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM154567 target RNA into GAM154567 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM225527 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM225527 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM225527 target RNA into GAM225527 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6652 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6652 gene: GAM7976 target protein, GAM154567 target protein and GAM225527 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7976, GAM154567 and GAM225527

GR6653 BF445189 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6653(GR6653) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6653 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6653 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6653 gene encodes GR6653 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6653 precursor RNA folds spatially, forming GR6653 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6653 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6653 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6653 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5593 precursor RNA and GAM324562 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5593 RNA and GAM324562 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5593 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5593 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5593 target RNA into GAM5593 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM324562 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM324562 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM324562 target RNA into GAM324562 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6653 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6653 gene: GAM5593 target protein and GAM324562 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5593 and GAM324562

GR6654 BE276110 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6654(GR6654) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6654 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6654 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6654 gene encodes GR6654 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6654 precursor RNA folds spatially, forming GR6654 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6654 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6654 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6654 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 6 separate GAM precursor RNAs, GAM1774 precursor RNA, GAM113909 precursor RNA, GAM115227 precursor RNA, GAM155464 precursor RNA, GAM161207 precursor RNA and GAM223196 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1774 RNA, GAM113909 RNA, GAM115227 RNA, GAM155464 RNA, GAM161207 RNA and GAM223196 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1774 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1774 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1774 target RNA into GAM1774 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM113909 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM113909 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM113909 target RNA into GAM113909 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM115227 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM115227 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM115227 target RNA into GAM115227 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM155464 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM155464 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM155464 target RNA into GAM155464 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM161207 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM161207 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM161207 target RNA into GAM161207 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM223196 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM223196 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM223196 target RNA into GAM223196 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6654 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6654 gene: GAM1774 target protein, GAM113909 target protein, GAM115227 target protein, GAM155464 target protein, GAM161207 target protein and GAM223196 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1774, GAM113909, GAM115227, GAM155464, GAM161207 and GAM223196

GR6655 BM149096 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6655(GR6655) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6655 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6655 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6655 gene encodes GR6655 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6655 precursor RNA folds spatially, forming GR6655 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6655 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6655 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6655 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2437 precursor RNA and GAM26629 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2437 RNA and GAM26629 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2437 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2437 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2437 target RNA into GAM2437 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM26629 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM26629 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM26629 target RNA into GAM26629 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6655 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6655 gene: GAM2437 target protein and GAM26629 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference,

with references to GAM2437 and GAM26629

GR6656 AU099633 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6656(GR6656) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6656 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6656 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6656 gene encodes GR6656 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6656 precursor RNA folds spatially, forming GR6656 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6656 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6656 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6656 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM103468 precursor RNA and GAM276459 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM103468 RNA and GAM276459 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM103468 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM103468 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM103468 target RNA into GAM103468 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM276459 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM276459 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM276459 target RNA into GAM276459 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6656 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6656 gene: GAM103468 target protein and GAM276459 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM103468 and GAM276459

GR6657 N58504 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6657(GR6657) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6657 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6657 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6657 gene encodes GR6657 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6657 precursor RNA folds spatially, forming GR6657 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6657 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6657 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6657 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM435 precursor RNA, GAM5882 precursor RNA, GAM192959 precursor RNA and GAM203296 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM435 RNA, GAM5882 RNA, GAM192959 RNA and GAM203296

RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM435 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM435 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM435 target RNA into GAM435 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5882 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5882 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5882 target RNA into GAM5882 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM192959 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM192959 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM192959 target RNA into GAM192959 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM203296 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM203296 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM203296 target RNA into GAM203296 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6657 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6657 gene: GAM435 target protein, GAM5882 target protein, GAM192959 target protein and GAM203296 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM435, GAM5882, GAM192959 and GAM203296

GR6658 AA621276 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6658(GR6658) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR6658 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6658 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6658 gene encodes GR6658 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6658 precursor RNA folds spatially, forming GR6658 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6658 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6658 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6658 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7537 precursor RNA and GAM118384 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7537 RNA and GAM118384 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7537 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7537 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7537 target RNA into GAM7537 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM118384 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM118384 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM118384 target RNA into GAM118384 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6658 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6658 gene: GAM7537 target protein and GAM118384 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7537 and GAM118384

GR6659 AW996431 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6659 (GR6659) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6659 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6659 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6659 gene encodes GR6659 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6659 precursor RNA folds spatially, forming GR6659 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6659 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6659 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6659 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3045 precursor RNA and GAM250557 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3045 RNA and GAM250557 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3045 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3045 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds

to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3045 target RNA into GAM3045 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM250557 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM250557 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM250557 target RNA into GAM250557 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6659 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6659 gene: GAM3045 target protein and GAM250557 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3045 and GAM250557

GR6660 BF510054 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6660 (GR6660) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6660 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6660 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6660 gene encodes GR6660 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6660 precursor RNA folds spatially, forming GR6660 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6660 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6660 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6660 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2079 precursor RNA, GAM45213 precursor RNA and GAM55261 precursor RNA, herein schematically represented by GAM1 FOLDED

PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2079 RNA, GAM45213 RNA and GAM55261 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2079 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2079 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2079 target RNA into GAM2079 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM45213 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM45213 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM45213 target RNA into GAM45213 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM55261 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM55261 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM55261 target RNA into GAM55261 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6660 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6660 gene: GAM2079 target protein, GAM45213 target protein and GAM55261 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2079, GAM45213 and GAM55261

GR6661 AW369260 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6661 (GR6661) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR6661 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6661 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6661 gene encodes GR6661 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6661 precursor RNA folds spatially, forming GR6661 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6661 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6661 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6661 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM5226 precursor RNA, GAM185328 precursor RNA, GAM194917 precursor RNA and GAM277961 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5226 RNA, GAM185328 RNA, GAM194917 RNA and GAM277961 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5226 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5226 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5226 target RNA into GAM5226 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM185328 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM185328 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM185328 target RNA into GAM185328 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM194917 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM194917 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM194917 target RNA into GAM194917 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM277961 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM277961 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM277961 target RNA into GAM277961 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6661 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6661 gene: GAM5226 target protein, GAM185328 target protein, GAM194917 target protein and GAM277961 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5226, GAM185328, GAM194917 and GAM277961

GR6662 BF238322 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6662(GR6662) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6662 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6662 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6662 gene encodes GR6662 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6662 precursor RNA folds spatially, forming GR6662 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6662 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6662 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6662 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM278606 precursor RNA and GAM303690 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM278606 RNA and GAM303690 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM278606 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM278606 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM278606 target RNA into GAM278606 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM303690 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM303690 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM303690 target RNA into GAM303690 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6662 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6662 gene: GAM278606 target protein and GAM303690 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM278606 and GAM303690

GR6663 AA828456 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6663(GR6663) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6663 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6663 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6663 gene encodes GR6663 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6663 precursor RNA folds spatially, forming GR6663 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6663 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6663 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6663 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM46983 precursor RNA, GAM220823 precursor RNA and GAM281100 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM46983 RNA, GAM220823 RNA and GAM281100 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM46983 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM46983 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM46983 target RNA into GAM46983 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM220823 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM220823 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM220823 target RNA into GAM220823 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM281100 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM281100 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM281100 target RNA into GAM281100 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6663 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6663 gene: GAM46983 target protein, GAM220823 target protein and GAM281100 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM46983, GAM220823 and GAM281100

GR6664 BG204457 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6664(GR6664) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6664 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6664 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6664 gene encodes GR6664 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6664 precursor RNA folds spatially, forming GR6664 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6664 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6664 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6664 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM248025 precursor RNA and GAM315906 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM248025 RNA and GAM315906 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM248025 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM248025 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM248025 target RNA into GAM248025 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM315906 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM315906 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM315906 target RNA into GAM315906 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6664 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6664 gene: GAM248025 target protein and GAM315906 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM248025 and GAM315906

GR6665 BM856347 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6665(GR6665) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6665 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6665 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6665 gene encodes GR6665 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6665 precursor RNA folds spatially, forming GR6665 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6665 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6665 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6665 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2143 precursor RNA and GAM5394 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2143 RNA and GAM5394 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2143 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2143 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2143 target RNA into GAM2143 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5394 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5394 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5394 target RNA into GAM5394 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6665 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6665 gene: GAM2143 target protein and GAM5394 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2143 and GAM5394

GR6666 AW798994 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6666(GR6666) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6666 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6666 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6666 gene encodes GR6666 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6666 precursor RNA folds spatially, forming GR6666 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6666 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6666 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6666 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM58493 precursor RNA and GAM160811 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM58493 RNA and GAM160811 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM58493 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM58493 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM58493 target RNA into GAM58493 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM160811 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM160811 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM160811 target RNA into GAM160811 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6666 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6666 gene: GAM58493 target protein and GAM160811 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM58493 and GAM160811

GR6667 BG772860 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6667(GR6667) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6667 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6667 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6667 gene encodes GR6667 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6667 precursor RNA folds spatially, forming GR6667 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6667 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6667 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6667 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM60227 precursor RNA, GAM103063 precursor RNA and GAM147786 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM60227 RNA, GAM103063 RNA and GAM147786 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM60227 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM60227 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM60227 target RNA into GAM60227 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM103063 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM103063 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM103063 target RNA into GAM103063 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM147786 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM147786 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM147786 target RNA into GAM147786 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6667 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6667 gene: GAM60227 target protein, GAM103063 target protein and GAM147786 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM60227, GAM103063 and GAM147786

GR6668 BM842564 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6668 (GR6668) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6668 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6668 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6668 gene encodes GR6668 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6668 precursor RNA folds spatially, forming GR6668 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6668 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6668 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6668 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3

separate GAM precursor RNAs, GAM3831 precursor RNA, GAM42759 precursor RNA and GAM61226 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3831 RNA, GAM42759 RNA and GAM61226 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3831 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3831 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3831 target RNA into GAM3831 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM42759 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM42759 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM42759 target RNA into GAM42759 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM61226 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM61226 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM61226 target RNA into GAM61226 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6668 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6668 gene: GAM3831 target protein, GAM42759 target protein and GAM61226 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3831, GAM42759 and GAM61226

GR6669 AW819413 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6669 (GR6669) gene, which encodes an `operon-like` cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6669 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6669 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6669 gene encodes GR6669 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6669 precursor RNA folds spatially, forming GR6669 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6669 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6669 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6669 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM139981 precursor RNA and GAM287606 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM139981 RNA and GAM287606 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM139981 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM139981 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM139981 target RNA into GAM139981 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM287606 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM287606 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM287606 target RNA into GAM287606 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6669 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6669 gene: GAM139981 target protein and GAM287606 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM139981 and GAM287606

GR6670 BE870085 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6670(GR6670) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6670 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6670 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6670 gene encodes GR6670 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6670 precursor RNA folds spatially, forming GR6670 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6670 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6670 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6670 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM3732 precursor RNA, GAM5434 precursor RNA, GAM5949 precursor RNA and GAM118171 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3732 RNA, GAM5434 RNA, GAM5949 RNA and GAM118171 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3732 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM3732 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3732 target RNA into GAM3732 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5434 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5434 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5434 target RNA into GAM5434 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5949 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5949 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5949 target RNA into GAM5949 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM118171 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM118171 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM118171 target RNA into GAM118171 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6670 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6670 gene: GAM3732 target protein, GAM5434 target protein, GAM5949 target protein and GAM118171 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3732, GAM5434, GAM5949 and GAM118171

GR6671 BI550366 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6671(GR6671) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6671 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6671

gene was detected is described hereinabove with reference to Figs. 8-18.

GR6671 gene encodes GR6671 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6671 precursor RNA folds spatially, forming GR6671 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6671 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6671 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6671 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM43665 precursor RNA and GAM85296 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM43665 RNA and GAM85296 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM43665 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM43665 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM43665 target RNA into GAM43665 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM85296 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM85296 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM85296 target RNA into GAM85296 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6671 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6671 gene: GAM43665 target protein and GAM85296 target protein, herein schematically represented by GAM1

TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM43665 and GAM85296

GR6672 AI336269 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6672(GR6672) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6672 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6672 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6672 gene encodes GR6672 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6672 precursor RNA folds spatially, forming GR6672 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6672 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6672 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6672 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5447 precursor RNA and GAM151739 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5447 RNA and GAM151739 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5447 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5447 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5447 target RNA into GAM5447 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM151739 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM151739 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM151739 target RNA into GAM151739 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6672 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6672 gene: GAM5447 target protein and GAM151739 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5447 and GAM151739

GR6673 BG724018 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6673(GR6673) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6673 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6673 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6673 gene encodes GR6673 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6673 precursor RNA folds spatially, forming GR6673 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6673 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6673 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6673 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM99429 precursor RNA and GAM118885 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM99429 RNA and GAM118885 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM99429 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM99429 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM99429 target RNA into GAM99429 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM118885 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM118885 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM118885 target RNA into GAM118885 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6673 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6673 gene: GAM99429 target protein and GAM118885 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM99429 and GAM118885

GR6674 BF184216 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6674(GR6674) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6674 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6674 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6674 gene encodes GR6674 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6674 precursor RNA folds spatially, forming GR6674 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6674 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6674 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6674 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2324 precursor RNA and GAM37490 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2324 RNA and GAM37490 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2324 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2324 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2324 target RNA into GAM2324 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM37490 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM37490 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM37490 target RNA into GAM37490 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6674 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6674 gene: GAM2324 target protein and GAM37490 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2324 and GAM37490

GR6675 AI916543 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6675(GR6675) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6675 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6675 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6675 gene encodes GR6675 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6675 precursor RNA folds spatially, forming GR6675 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6675 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6675 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6675 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM162594 precursor RNA and GAM269580 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM162594 RNA and GAM269580 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM162594 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM162594 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM162594 target RNA into GAM162594 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM269580 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM269580 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM269580 target RNA into GAM269580 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6675 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR6675 gene: GAM162594 target protein and GAM269580 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM162594 and GAM269580

GR6676 AA069288 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6676(GR6676) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6676 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6676 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6676 gene encodes GR6676 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6676 precursor RNA folds spatially, forming GR6676 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6676 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6676 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6676 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3708 precursor RNA and GAM315043 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3708 RNA and GAM315043 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3708 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3708 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3708 target RNA into GAM3708 target protein, herein schematically represented by GAM1 TARGET

PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM315043 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM315043 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM315043 target RNA into GAM315043 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6676 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6676 gene: GAM3708 target protein and GAM315043 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3708 and GAM315043

GR6677 BF894780 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6677(GR6677) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6677 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6677 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6677 gene encodes GR6677 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6677 precursor RNA folds spatially, forming GR6677 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6677 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6677 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6677 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3024 precursor RNA, GAM64655 precursor RNA and GAM251051 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3024 RNA, GAM64655 RNA and GAM251051 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3024 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3024 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3024 target RNA into GAM3024 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM64655 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM64655 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM64655 target RNA into GAM64655 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM251051 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM251051 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM251051 target RNA into GAM251051 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6677 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6677 gene: GAM3024 target protein, GAM64655 target protein and GAM251051 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3024, GAM64655 and GAM251051

GR6678 BQ018648 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6678(GR6678) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6678 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR6678 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6678 gene encodes GR6678 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6678 precursor RNA folds spatially, forming GR6678 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6678 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6678 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6678 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7584 precursor RNA and GAM112162 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7584 RNA and GAM112162 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7584 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7584 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7584 target RNA into GAM7584 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM112162 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM112162 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM112162 target RNA into GAM112162 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6678 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6678 gene: GAM7584 target

protein and GAM112162 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7584 and GAM112162

GR6679 BF697400 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6679(GR6679) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6679 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6679 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6679 gene encodes GR6679 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6679 precursor RNA folds spatially, forming GR6679 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6679 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6679 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6679 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM92624 precursor RNA and GAM272846 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM92624 RNA and GAM272846 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM92624 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM92624 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM92624 target RNA into GAM92624 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM272846 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM272846 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM272846 target RNA into GAM272846 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6679 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6679 gene: GAM92624 target protein and GAM272846 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM92624 and GAM272846

GR6680 BG425699 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6680(GR6680) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6680 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6680 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6680 gene encodes GR6680 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6680 precursor RNA folds spatially, forming GR6680 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6680 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6680 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6680 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2679 precursor RNA, GAM41878 precursor RNA and GAM132145 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2679 RNA, GAM41878 RNA and GAM132145 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2679 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2679 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2679 target RNA into GAM2679 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM41878 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM41878 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM41878 target RNA into GAM41878 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM132145 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM132145 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM132145 target RNA into GAM132145 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6680 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6680 gene: GAM2679 target protein, GAM41878 target protein and GAM132145 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2679, GAM41878 and GAM132145

GR6681 AU140098 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6681(GR6681) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6681 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6681

gene was detected is described hereinabove with reference to Figs. 8-18.

GR6681 gene encodes GR6681 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6681 precursor RNA folds spatially, forming GR6681 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6681 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6681 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6681 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM202441 precursor RNA and GAM300856 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM202441 RNA and GAM300856 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM202441 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM202441 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM202441 target RNA into GAM202441 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM300856 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM300856 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM300856 target RNA into GAM300856 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6681 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6681 gene: GAM202441 target protein and GAM300856 target protein, herein schematically represented by GAM1

TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM202441 and GAM300856

GR6682 BE614490 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6682(GR6682) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6682 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6682 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6682 gene encodes GR6682 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6682 precursor RNA folds spatially, forming GR6682 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6682 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6682 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6682 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5248 precursor RNA and GAM14936 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5248 RNA and GAM14936 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5248 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5248 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5248 target RNA into GAM5248 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM14936 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM14936 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM14936 target RNA into GAM14936 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6682 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6682 gene: GAM5248 target protein and GAM14936 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5248 and GAM14936

GR6683 BI859402 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6683(GR6683) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6683 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6683 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6683 gene encodes GR6683 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6683 precursor RNA folds spatially, forming GR6683 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6683 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6683 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6683 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM479 precursor RNA and GAM101490 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM479 RNA and GAM101490 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM479 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM479 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM479 target RNA into GAM479 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM101490 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM101490 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM101490 target RNA into GAM101490 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6683 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6683 gene: GAM479 target protein and GAM101490 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM479 and GAM101490

GR6684 BM720599 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6684(GR6684) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6684 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6684 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6684 gene encodes GR6684 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6684 precursor RNA folds spatially, forming GR6684 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6684 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6684 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6684 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM4791 precursor RNA, GAM98358 precursor RNA, GAM213695 precursor RNA and GAM266886 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4791 RNA, GAM98358 RNA, GAM213695 RNA and GAM266886 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4791 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4791 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4791 target RNA into GAM4791 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM98358 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM98358 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM98358 target RNA into GAM98358 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM213695 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM213695 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM213695 target RNA into GAM213695 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM266886 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM266886 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM266886 target RNA into GAM266886 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6684 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6684 gene: GAM4791 target protein, GAM98358 target protein, GAM213695 target protein and GAM266886 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4791, GAM98358, GAM213695 and GAM266886

GR6685 BE902861 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6685(GR6685) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6685 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6685 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6685 gene encodes GR6685 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6685 precursor RNA folds spatially, forming GR6685 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6685 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6685 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6685 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM213170 precursor RNA and GAM331315 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM213170 RNA and GAM331315 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM213170 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM213170 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM213170 target RNA into GAM213170 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM331315 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM331315 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM331315 target RNA into GAM331315 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6685 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6685 gene: GAM213170 target protein and GAM331315 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM213170 and GAM331315

GR6686 AA838356 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6686(GR6686) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6686 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6686 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6686 gene encodes GR6686 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6686 precursor RNA folds spatially, forming GR6686 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6686 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6686 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6686 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3

separate GAM precursor RNAs, GAM31957 precursor RNA, GAM107633 precursor RNA and GAM222809 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM31957 RNA, GAM107633 RNA and GAM222809 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM31957 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM31957 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM31957 target RNA into GAM31957 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM107633 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM107633 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM107633 target RNA into GAM107633 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM222809 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM222809 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM222809 target RNA into GAM222809 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6686 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6686 gene: GAM31957 target protein, GAM107633 target protein and GAM222809 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM31957, GAM107633 and GAM222809

GR6687 BI524091 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6687 (GR6687) gene, which encodes an `operon-like` cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6687 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6687 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6687 gene encodes GR6687 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6687 precursor RNA folds spatially, forming GR6687 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6687 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6687 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6687 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM11285 precursor RNA and GAM188722 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM11285 RNA and GAM188722 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM11285 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM11285 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM11285 target RNA into GAM11285 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM188722 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM188722 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM188722 target RNA into GAM188722 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6687 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6687 gene: GAM11285 target protein and GAM188722 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM11285 and GAM188722

GR6688 BG188781 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6688(GR6688) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6688 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6688 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6688 gene encodes GR6688 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6688 precursor RNA folds spatially, forming GR6688 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6688 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6688 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6688 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM8552 precursor RNA, GAM12501 precursor RNA and GAM51800 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8552 RNA, GAM12501 RNA and GAM51800 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8552 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM8552 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8552 target RNA into GAM8552 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM12501 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM12501 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM12501 target RNA into GAM12501 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM51800 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM51800 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM51800 target RNA into GAM51800 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6688 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6688 gene: GAM8552 target protein, GAM12501 target protein and GAM51800 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8552, GAM12501 and GAM51800

GR6689 BG824217 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6689(GR6689) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6689 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6689 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6689 gene encodes GR6689 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6689 precursor RNA folds spatially, forming GR6689 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated

that GR6689 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6689 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6689 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM6707 precursor RNA, GAM72583 precursor RNA and GAM194992 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6707 RNA, GAM72583 RNA and GAM194992 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6707 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6707 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6707 target RNA into GAM6707 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM72583 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM72583 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM72583 target RNA into GAM72583 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM194992 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM194992 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM194992 target RNA into GAM194992 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6689 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6689 gene: GAM6707 target

protein, GAM72583 target protein and GAM194992 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6707, GAM72583 and GAM194992

GR6690 N46436 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6690(GR6690) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6690 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6690 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6690 gene encodes GR6690 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6690 precursor RNA folds spatially, forming GR6690 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6690 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6690 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6690 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6126 precursor RNA and GAM7506 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6126 RNA and GAM7506 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6126 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6126 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6126 target RNA into GAM6126 target protein, herein schematically represented by GAM1 TARGET

PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7506 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7506 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7506 target RNA into GAM7506 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6690 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6690 gene: GAM6126 target protein and GAM7506 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6126 and GAM7506

GR6691 AI699313 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6691 (GR6691) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6691 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6691 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6691 gene encodes GR6691 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6691 precursor RNA folds spatially, forming GR6691 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6691 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6691 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6691 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM91871 precursor RNA, GAM94027 precursor RNA and GAM113813 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM91871 RNA, GAM94027 RNA and GAM113813 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM91871 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM91871 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM91871 target RNA into GAM91871 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM94027 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM94027 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM94027 target RNA into GAM94027 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM113813 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM113813 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM113813 target RNA into GAM113813 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6691 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6691 gene: GAM91871 target protein, GAM94027 target protein and GAM113813 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM91871, GAM94027 and GAM113813

GR6692 N79307 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6692(GR6692) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6692 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR6692 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6692 gene encodes GR6692 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6692 precursor RNA folds spatially, forming GR6692 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6692 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6692 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6692 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM69780 precursor RNA and GAM224152 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM69780 RNA and GAM224152 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM69780 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM69780 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM69780 target RNA into GAM69780 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM224152 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM224152 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM224152 target RNA into GAM224152 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6692 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6692 gene: GAM69780 target

protein and GAM224152 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM69780 and GAM224152

GR6693 AA778138 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6693(GR6693) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6693 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6693 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6693 gene encodes GR6693 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6693 precursor RNA folds spatially, forming GR6693 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6693 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6693 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6693 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM190392 precursor RNA and GAM227002 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM190392 RNA and GAM227002 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM190392 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM190392 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM190392 target RNA into GAM190392 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM227002 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM227002 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM227002 target RNA into GAM227002 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6693 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6693 gene: GAM190392 target protein and GAM227002 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM190392 and GAM227002

GR6694 BI835840 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6694(GR6694) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6694 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6694 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6694 gene encodes GR6694 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6694 precursor RNA folds spatially, forming GR6694 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6694 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6694 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6694 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3353 precursor RNA, GAM257310 precursor RNA and GAM277428 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3353 RNA, GAM257310 RNA and GAM277428 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3353 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3353 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3353 target RNA into GAM3353 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM257310 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM257310 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM257310 target RNA into GAM257310 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM277428 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM277428 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM277428 target RNA into GAM277428 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6694 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6694 gene: GAM3353 target protein, GAM257310 target protein and GAM277428 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3353, GAM257310 and GAM277428

GR6695 R96039 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6695(GR6695) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6695 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6695

gene was detected is described hereinabove with reference to Figs. 8-18.

GR6695 gene encodes GR6695 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6695 precursor RNA folds spatially, forming GR6695 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6695 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6695 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6695 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM31261 precursor RNA and GAM42286 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM31261 RNA and GAM42286 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM31261 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM31261 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM31261 target RNA into GAM31261 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM42286 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM42286 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM42286 target RNA into GAM42286 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6695 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6695 gene: GAM31261 target protein and GAM42286 target protein, herein schematically represented by GAM1

TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM31261 and GAM42286

GR6696 BE546945 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6696(GR6696) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6696 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6696 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6696 gene encodes GR6696 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6696 precursor RNA folds spatially, forming GR6696 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6696 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6696 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6696 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2843 precursor RNA and GAM201086 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2843 RNA and GAM201086 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2843 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2843 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2843 target RNA into GAM2843 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM201086 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM201086 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM201086 target RNA into GAM201086 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6696 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6696 gene: GAM2843 target protein and GAM201086 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2843 and GAM201086

GR6697 BG431331 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6697(GR6697) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6697 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6697 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6697 gene encodes GR6697 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6697 precursor RNA folds spatially, forming GR6697 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6697 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6697 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6697 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM901 precursor RNA, GAM38878 precursor RNA and GAM170325 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM901 RNA, GAM38878 RNA and GAM170325 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM901 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM901 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM901 target RNA into GAM901 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM38878 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM38878 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM38878 target RNA into GAM38878 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM170325 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM170325 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM170325 target RNA into GAM170325 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6697 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6697 gene: GAM901 target protein, GAM38878 target protein and GAM170325 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM901, GAM38878 and GAM170325

GR6698 AI051860 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6698(GR6698) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6698 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6698 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6698 gene encodes GR6698 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6698 precursor RNA folds spatially, forming GR6698 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6698 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6698 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6698 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8223 precursor RNA and GAM251913 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8223 RNA and GAM251913 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8223 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8223 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8223 target RNA into GAM8223 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM251913 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM251913 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM251913 target RNA into GAM251913 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6698 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6698 gene: GAM8223 target protein and GAM251913 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes

is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8223 and GAM251913

GR6699 AA548373 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6699(GR6699) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6699 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6699 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6699 gene encodes GR6699 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6699 precursor RNA folds spatially, forming GR6699 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6699 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6699 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6699 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM263200 precursor RNA and GAM285557 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM263200 RNA and GAM285557 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM263200 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM263200 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM263200 target RNA into GAM263200 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM285557 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM285557 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM285557 target RNA into GAM285557 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6699 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6699 gene: GAM263200 target protein and GAM285557 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM263200 and GAM285557

GR6700 BG531012 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6700(GR6700) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6700 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6700 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6700 gene encodes GR6700 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6700 precursor RNA folds spatially, forming GR6700 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6700 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6700 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6700 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4232 precursor RNA and GAM72290 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4232 RNA and GAM72290 RNA, herein schematically

represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4232 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4232 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4232 target RNA into GAM4232 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM72290 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM72290 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM72290 target RNA into GAM72290 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6700 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6700 gene: GAM4232 target protein and GAM72290 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4232 and GAM72290

GR6701 BF887110 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6701(GR6701) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6701 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6701 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6701 gene encodes GR6701 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6701 precursor RNA folds spatially, forming GR6701 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6701 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6701 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6701 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM95333 precursor RNA and GAM306159 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM95333 RNA and GAM306159 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM95333 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM95333 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM95333 target RNA into GAM95333 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM306159 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM306159 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM306159 target RNA into GAM306159 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6701 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6701 gene: GAM95333 target protein and GAM306159 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM95333 and GAM306159

GR6702 BG024623 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6702(GR6702) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6702 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR6702 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6702 gene encodes GR6702 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6702 precursor RNA folds spatially, forming GR6702 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6702 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6702 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6702 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5204 precursor RNA and GAM54922 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5204 RNA and GAM54922 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5204 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5204 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5204 target RNA into GAM5204 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM54922 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM54922 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM54922 target RNA into GAM54922 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6702 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6702 gene: GAM5204 target

protein and GAM54922 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5204 and GAM54922

GR6703 BG566321 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6703(GR6703) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6703 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6703 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6703 gene encodes GR6703 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6703 precursor RNA folds spatially, forming GR6703 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6703 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6703 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6703 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 5 separate GAM precursor RNAs, GAM47862 precursor RNA, GAM133428 precursor RNA, GAM154934 precursor RNA, GAM219389 precursor RNA and GAM286140 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM47862 RNA, GAM133428 RNA, GAM154934 RNA, GAM219389 RNA and GAM286140 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM47862 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM47862 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM47862 target RNA into GAM47862 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM133428 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM133428 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM133428 target RNA into GAM133428 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM154934 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM154934 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM154934 target RNA into GAM154934 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM219389 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM219389 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM219389 target RNA into GAM219389 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM286140 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM286140 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM286140 target RNA into GAM286140 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6703 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6703 gene: GAM47862 target protein, GAM133428 target protein, GAM154934 target protein, GAM219389 target protein and GAM286140 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM47862, GAM133428, GAM154934, GAM219389 and GAM286140

GR6704 BF922141 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6704(GR6704) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR6704 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6704 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6704 gene encodes GR6704 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6704 precursor RNA folds spatially, forming GR6704 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6704 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6704 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6704 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM6476 precursor RNA, GAM265310 precursor RNA and GAM280707 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6476 RNA, GAM265310 RNA and GAM280707 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6476 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6476 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6476 target RNA into GAM6476 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM265310 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM265310 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM265310 target RNA into GAM265310 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM280707 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM280707 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM280707 target RNA into GAM280707 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6704 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6704 gene: GAM6476 target protein, GAM265310 target protein and GAM280707 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6476, GAM265310 and GAM280707

GR6705 AW003121 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6705(GR6705) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6705 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6705 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6705 gene encodes GR6705 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6705 precursor RNA folds spatially, forming GR6705 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6705 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6705 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6705 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM199644 precursor RNA and GAM252264 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM199644 RNA and GAM252264 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM199644 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM199644 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM199644 target RNA into GAM199644 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM252264 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM252264 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM252264 target RNA into GAM252264 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6705 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6705 gene: GAM199644 target protein and GAM252264 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM199644 and GAM252264

GR6706 AW269306 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6706(GR6706) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6706 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6706 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6706 gene encodes GR6706 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6706 precursor RNA folds spatially, forming GR6706 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6706 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR6706 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6706 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM25267 precursor RNA, GAM53649 precursor RNA and GAM242783 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM25267 RNA, GAM53649 RNA and GAM242783 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM25267 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM25267 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM25267 target RNA into GAM25267 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM53649 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM53649 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM53649 target RNA into GAM53649 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM242783 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM242783 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM242783 target RNA into GAM242783 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6706 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6706 gene: GAM25267 target protein, GAM53649 target protein and GAM242783 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN.

The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM25267, GAM53649 and GAM242783

GR6707 AI872644 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6707(GR6707) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6707 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6707 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6707 gene encodes GR6707 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6707 precursor RNA folds spatially, forming GR6707 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6707 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6707 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6707 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM188051 precursor RNA and GAM296752 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM188051 RNA and GAM296752 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM188051 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM188051 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM188051 target RNA into GAM188051 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM296752 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM296752 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM296752 target RNA into GAM296752 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6707 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6707 gene: GAM188051 target protein and GAM296752 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM188051 and GAM296752

GR6708 BF746355 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6708(GR6708) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6708 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6708 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6708 gene encodes GR6708 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6708 precursor RNA folds spatially, forming GR6708 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6708 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6708 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6708 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM56345 precursor RNA and GAM141179 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM56345 RNA and GAM141179 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM56345 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM56345 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM56345 target RNA into GAM56345 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM141179 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM141179 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM141179 target RNA into GAM141179 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6708 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6708 gene: GAM56345 target protein and GAM141179 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM56345 and GAM141179

GR6709 BG718082 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6709(GR6709) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6709 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6709 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6709 gene encodes GR6709 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6709 precursor RNA folds spatially, forming GR6709 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6709 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6709 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6709 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4681 precursor RNA and GAM6110 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4681 RNA and GAM6110 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4681 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4681 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4681 target RNA into GAM4681 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6110 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6110 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6110 target RNA into GAM6110 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6709 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6709 gene: GAM4681 target protein and GAM6110 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4681 and GAM6110

GR6710 BE834730 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6710(GR6710) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6710 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6710 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6710 gene encodes GR6710 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6710 precursor RNA folds spatially, forming GR6710 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6710 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6710 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6710 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1654 precursor RNA, GAM266113 precursor RNA and GAM297900 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1654 RNA, GAM266113 RNA and GAM297900 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1654 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1654 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1654 target RNA into GAM1654 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM266113 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM266113 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM266113 target RNA into GAM266113 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM297900 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM297900 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM297900 target RNA into GAM297900 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6710 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6710 gene: GAM1654 target protein, GAM266113 target protein and GAM297900 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1654, GAM266113 and GAM297900

GR6711 BI559579 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6711 (GR6711) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6711 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6711 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6711 gene encodes GR6711 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6711 precursor RNA folds spatially, forming GR6711 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6711 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6711 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6711 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5470 precursor RNA and GAM200723 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5470 RNA and GAM200723 RNA, herein schematically

represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5470 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5470 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5470 target RNA into GAM5470 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM200723 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM200723 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM200723 target RNA into GAM200723 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6711 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6711 gene: GAM5470 target protein and GAM200723 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5470 and GAM200723

GR6712 AW862899 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6712(GR6712) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6712 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6712 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6712 gene encodes GR6712 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6712 precursor RNA folds spatially, forming GR6712 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6712 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6712 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6712 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM17479 precursor RNA and GAM153081 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM17479 RNA and GAM153081 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM17479 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM17479 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM17479 target RNA into GAM17479 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM153081 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM153081 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM153081 target RNA into GAM153081 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6712 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6712 gene: GAM17479 target protein and GAM153081 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM17479 and GAM153081

GR6713 AA432005 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6713(GR6713) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6713 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR6713 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6713 gene encodes GR6713 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6713 precursor RNA folds spatially, forming GR6713 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6713 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6713 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6713 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM285871 precursor RNA and GAM293386 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM285871 RNA and GAM293386 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM285871 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM285871 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM285871 target RNA into GAM285871 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM293386 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM293386 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM293386 target RNA into GAM293386 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6713 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6713 gene: GAM285871 target

protein and GAM293386 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM285871 and GAM293386

GR6714 AI028487 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6714(GR6714) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6714 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6714 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6714 gene encodes GR6714 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6714 precursor RNA folds spatially, forming GR6714 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6714 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6714 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6714 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5614 precursor RNA and GAM297980 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5614 RNA and GAM297980 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5614 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5614 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5614 target RNA into GAM5614 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM297980 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM297980 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM297980 target RNA into GAM297980 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6714 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6714 gene: GAM5614 target protein and GAM297980 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5614 and GAM297980

GR6715 AW439122 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6715(GR6715) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6715 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6715 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6715 gene encodes GR6715 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6715 precursor RNA folds spatially, forming GR6715 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6715 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6715 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6715 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM286533 precursor RNA and GAM329180 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM286533 RNA and GAM329180 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM286533 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM286533 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM286533 target RNA into GAM286533 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM329180 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM329180 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM329180 target RNA into GAM329180 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6715 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6715 gene: GAM286533 target protein and GAM329180 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM286533 and GAM329180

GR6716 AI279011 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6716(GR6716) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6716 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6716 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6716 gene encodes GR6716 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6716 precursor RNA folds spatially, forming GR6716 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6716 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR6716 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6716 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5040 precursor RNA and GAM280617 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5040 RNA and GAM280617 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5040 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5040 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5040 target RNA into GAM5040 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM280617 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM280617 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM280617 target RNA into GAM280617 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6716 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6716 gene: GAM5040 target protein and GAM280617 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5040 and GAM280617

GR6717 BG216626 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6717(GR6717) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6717 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6717 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6717 gene encodes GR6717 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6717 precursor RNA folds spatially, forming GR6717 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6717 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6717 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6717 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8198 precursor RNA and GAM177583 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8198 RNA and GAM177583 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8198 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8198 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8198 target RNA into GAM8198 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM177583 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM177583 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM177583 target RNA into GAM177583 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6717 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6717 gene: GAM8198 target protein and GAM177583 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8198 and GAM177583

GR6718 AA767679 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6718(GR6718) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6718 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6718 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6718 gene encodes GR6718 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6718 precursor RNA folds spatially, forming GR6718 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6718 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6718 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6718 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5148 precursor RNA and GAM7301 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5148 RNA and GAM7301 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5148 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5148 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5148 target RNA into

GAM5148 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7301 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7301 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7301 target RNA into GAM7301 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6718 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6718 gene: GAM5148 target protein and GAM7301 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5148 and GAM7301

GR6719 BE538964 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6719(GR6719) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6719 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6719 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6719 gene encodes GR6719 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6719 precursor RNA folds spatially, forming GR6719 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6719 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6719 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6719 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3136 precursor RNA and GAM108005 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3136 RNA and GAM108005 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3136 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3136 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3136 target RNA into GAM3136 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM108005 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM108005 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM108005 target RNA into GAM108005 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6719 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6719 gene: GAM3136 target protein and GAM108005 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3136 and GAM108005

GR6720 BE937524 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6720(GR6720) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6720 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6720 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6720 gene encodes GR6720 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6720 precursor RNA folds spatially, forming GR6720 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated

that GR6720 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6720 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6720 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8618 precursor RNA and GAM30392 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8618 RNA and GAM30392 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8618 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8618 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8618 target RNA into GAM8618 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM30392 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM30392 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM30392 target RNA into GAM30392 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6720 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6720 gene: GAM8618 target protein and GAM30392 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8618 and GAM30392

GR6721 BG506436 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6721(GR6721) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR6721 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6721 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6721 gene encodes GR6721 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6721 precursor RNA folds spatially, forming GR6721 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6721 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6721 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6721 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM324012 precursor RNA and GAM330794 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM324012 RNA and GAM330794 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM324012 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM324012 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM324012 target RNA into GAM324012 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM330794 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM330794 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM330794 target RNA into GAM330794 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6721 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6721 gene: GAM324012 target protein and GAM330794 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM324012 and GAM330794

GR6722 BG178977 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6722(GR6722) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6722 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6722 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6722 gene encodes GR6722 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6722 precursor RNA folds spatially, forming GR6722 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6722 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6722 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6722 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5933 precursor RNA and GAM186669 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5933 RNA and GAM186669 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5933 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5933 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds

to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5933 target RNA into GAM5933 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM186669 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM186669 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM186669 target RNA into GAM186669 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6722 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6722 gene: GAM5933 target protein and GAM186669 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5933 and GAM186669

GR6723 BE076300 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6723(GR6723) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6723 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6723 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6723 gene encodes GR6723 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6723 precursor RNA folds spatially, forming GR6723 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6723 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6723 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6723 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6787 precursor RNA and GAM226433 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3

FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6787 RNA and GAM226433 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6787 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6787 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6787 target RNA into GAM6787 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM226433 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM226433 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM226433 target RNA into GAM226433 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6723 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6723 gene: GAM6787 target protein and GAM226433 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6787 and GAM226433

GR6724 H15367 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6724(GR6724) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6724 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6724 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6724 gene encodes GR6724 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6724 precursor RNA folds spatially, forming GR6724 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6724 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6724 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6724 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8686 precursor RNA and GAM134558 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8686 RNA and GAM134558 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8686 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8686 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8686 target RNA into GAM8686 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM134558 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM134558 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM134558 target RNA into GAM134558 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6724 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6724 gene: GAM8686 target protein and GAM134558 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8686 and GAM134558

6725(GR6725) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6725 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6725 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6725 gene encodes GR6725 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6725 precursor RNA folds spatially, forming GR6725 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6725 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6725 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6725 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3373 precursor RNA and GAM68944 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3373 RNA and GAM68944 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3373 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3373 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3373 target RNA into GAM3373 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM68944 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM68944 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM68944 target RNA into GAM68944 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6725 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6725 gene: GAM3373 target protein and GAM68944 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3373 and GAM68944

GR6726 BG035730 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6726(GR6726) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6726 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6726 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6726 gene encodes GR6726 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6726 precursor RNA folds spatially, forming GR6726 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6726 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6726 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6726 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM85739 precursor RNA and GAM217285 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM85739 RNA and GAM217285 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM85739 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM85739 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM85739 target RNA into GAM85739 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM217285 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM217285 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM217285 target RNA into GAM217285 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6726 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6726 gene: GAM85739 target protein and GAM217285 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM85739 and GAM217285

GR6727 BG709530 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6727(GR6727) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6727 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6727 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6727 gene encodes GR6727 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6727 precursor RNA folds spatially, forming GR6727 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6727 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6727 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6727 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2

separate GAM precursor RNAs, GAM124998 precursor RNA and GAM227240 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM124998 RNA and GAM227240 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM124998 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM124998 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM124998 target RNA into GAM124998 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM227240 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM227240 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM227240 target RNA into GAM227240 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6727 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6727 gene: GAM124998 target protein and GAM227240 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM124998 and GAM227240

GR6728 BE964425 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6728(GR6728) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6728 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6728 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6728 gene encodes GR6728 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR6728 precursor RNA folds spatially, forming GR6728 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6728 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6728 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6728 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM5367 precursor RNA, GAM25035 precursor RNA and GAM101595 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5367 RNA, GAM25035 RNA and GAM101595 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5367 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5367 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5367 target RNA into GAM5367 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM25035 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM25035 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM25035 target RNA into GAM25035 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM101595 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM101595 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM101595 target RNA into GAM101595 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6728 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6728 gene: GAM5367 target protein, GAM25035 target protein and GAM101595 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5367, GAM25035 and GAM101595

GR6729 BF108881 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6729(GR6729) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6729 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6729 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6729 gene encodes GR6729 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6729 precursor RNA folds spatially, forming GR6729 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6729 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6729 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6729 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM21142 precursor RNA and GAM257009 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM21142 RNA and GAM257009 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM21142 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM21142 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM21142 target RNA into GAM21142 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM257009 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM257009 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM257009 target RNA into GAM257009 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6729 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6729 gene: GAM21142 target protein and GAM257009 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM21142 and GAM257009

GR6730 BE262127 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6730(GR6730) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6730 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6730 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6730 gene encodes GR6730 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6730 precursor RNA folds spatially, forming GR6730 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6730 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6730 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6730 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM6033 precursor RNA, GAM118688 precursor RNA

and GAM227749 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6033 RNA, GAM118688 RNA and GAM227749 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6033 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6033 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6033 target RNA into GAM6033 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM118688 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM118688 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM118688 target RNA into GAM118688 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM227749 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM227749 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM227749 target RNA into GAM227749 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6730 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6730 gene: GAM6033 target protein, GAM118688 target protein and GAM227749 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6033, GAM118688 and GAM227749

GR6731 BE312799 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6731(GR6731) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR6731 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6731 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6731 gene encodes GR6731 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6731 precursor RNA folds spatially, forming GR6731 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6731 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6731 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6731 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM946 precursor RNA and GAM2313 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM946 RNA and GAM2313 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM946 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM946 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM946 target RNA into GAM946 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM2313 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2313 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2313 target RNA into GAM2313 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6731 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6731 gene: GAM946 target protein and GAM2313 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM946 and GAM2313

GR6732 AV648172 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6732(GR6732) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6732 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6732 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6732 gene encodes GR6732 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6732 precursor RNA folds spatially, forming GR6732 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6732 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6732 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6732 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3734 precursor RNA and GAM64798 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3734 RNA and GAM64798 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3734 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3734 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds

to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3734 target RNA into GAM3734 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM64798 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM64798 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM64798 target RNA into GAM64798 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6732 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6732 gene: GAM3734 target protein and GAM64798 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3734 and GAM64798

GR6733 AW611811 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6733(GR6733) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6733 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6733 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6733 gene encodes GR6733 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6733 precursor RNA folds spatially, forming GR6733 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6733 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6733 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6733 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM63191 precursor RNA and GAM89501 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3

FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM63191 RNA and GAM89501 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM63191 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM63191 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM63191 target RNA into GAM63191 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM89501 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM89501 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM89501 target RNA into GAM89501 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6733 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6733 gene: GAM63191 target protein and GAM89501 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM63191 and GAM89501

GR6734 BE695411 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6734(GR6734) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6734 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6734 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6734 gene encodes GR6734 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6734 precursor RNA folds spatially, forming GR6734 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6734 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6734 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6734 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4062 precursor RNA and GAM88567 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4062 RNA and GAM88567 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4062 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4062 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4062 target RNA into GAM4062 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM88567 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM88567 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM88567 target RNA into GAM88567 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6734 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6734 gene: GAM4062 target protein and GAM88567 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4062 and GAM88567

6735(GR6735) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6735 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6735 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6735 gene encodes GR6735 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6735 precursor RNA folds spatially, forming GR6735 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6735 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6735 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6735 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM58619 precursor RNA and GAM265527 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM58619 RNA and GAM265527 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM58619 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM58619 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM58619 target RNA into GAM58619 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM265527 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM265527 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM265527 target RNA into GAM265527 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6735 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6735 gene: GAM58619 target protein and GAM265527 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM58619 and GAM265527

GR6736 AI828975 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6736(GR6736) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6736 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6736 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6736 gene encodes GR6736 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6736 precursor RNA folds spatially, forming GR6736 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6736 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6736 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6736 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM103635 precursor RNA and GAM208955 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM103635 RNA and GAM208955 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM103635 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM103635 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM103635 target RNA into GAM103635 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM208955 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM208955 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM208955 target RNA into GAM208955 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6736 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6736 gene: GAM103635 target protein and GAM208955 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM103635 and GAM208955

GR6737 BF987921 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6737(GR6737) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6737 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6737 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6737 gene encodes GR6737 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6737 precursor RNA folds spatially, forming GR6737 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6737 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6737 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6737 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2

separate GAM precursor RNAs, GAM84023 precursor RNA and GAM113971 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM84023 RNA and GAM113971 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM84023 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM84023 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM84023 target RNA into GAM84023 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM113971 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM113971 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM113971 target RNA into GAM113971 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6737 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6737 gene: GAM84023 target protein and GAM113971 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM84023 and GAM113971

GR6738 AI745163 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6738(GR6738) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6738 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6738 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6738 gene encodes GR6738 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR6738 precursor RNA folds spatially, forming GR6738 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6738 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6738 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6738 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM176524 precursor RNA and GAM300484 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM176524 RNA and GAM300484 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM176524 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM176524 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM176524 target RNA into GAM176524 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM300484 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM300484 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM300484 target RNA into GAM300484 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6738 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6738 gene: GAM176524 target protein and GAM300484 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM176524 and GAM300484

GR6739 AI961256 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6739(GR6739) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6739 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6739 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6739 gene encodes GR6739 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6739 precursor RNA folds spatially, forming GR6739 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6739 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6739 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6739 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1211 precursor RNA and GAM298040 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1211 RNA and GAM298040 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1211 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1211 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1211 target RNA into GAM1211 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM298040 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM298040 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM298040 target RNA into GAM298040 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6739 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6739 gene: GAM1211 target protein and GAM298040 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1211 and GAM298040

GR6740 BE542596 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6740(GR6740) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6740 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6740 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6740 gene encodes GR6740 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6740 precursor RNA folds spatially, forming GR6740 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6740 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6740 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6740 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM42320 precursor RNA, GAM74041 precursor RNA and GAM219817 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM42320 RNA, GAM74041 RNA and GAM219817 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM42320 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM42320 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM42320 target RNA into GAM42320 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM74041 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM74041 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM74041 target RNA into GAM74041 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM219817 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM219817 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM219817 target RNA into GAM219817 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6740 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6740 gene: GAM42320 target protein, GAM74041 target protein and GAM219817 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM42320, GAM74041 and GAM219817

GR6741 BI092786 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6741 (GR6741) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6741 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6741 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6741 gene encodes GR6741 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6741 precursor RNA folds spatially, forming GR6741 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6741 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6741 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6741 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM19081 precursor RNA, GAM79333 precursor RNA, GAM119293 precursor RNA and GAM306824 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM19081 RNA, GAM79333 RNA, GAM119293 RNA and GAM306824 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM19081 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM19081 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM19081 target RNA into GAM19081 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM79333 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM79333 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM79333 target RNA into GAM79333 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM119293 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM119293 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM119293 target RNA into GAM119293 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM306824 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM306824 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM306824 target RNA into GAM306824 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6741 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6741 gene: GAM19081 target protein, GAM79333 target protein, GAM119293 target protein and GAM306824 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM19081, GAM79333, GAM119293 and GAM306824

GR6742 BQ059342 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6742(GR6742) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6742 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6742 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6742 gene encodes GR6742 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6742 precursor RNA folds spatially, forming GR6742 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6742 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6742 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6742 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM3984 precursor RNA, GAM5301 precursor RNA, GAM219561 precursor RNA and GAM315040 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3984 RNA, GAM5301 RNA, GAM219561 RNA and GAM315040 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3984 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3984 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3984 target RNA into GAM3984 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5301 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5301 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5301 target RNA into GAM5301 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM219561 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM219561 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM219561 target RNA into GAM219561 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM315040 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM315040 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM315040 target RNA into GAM315040 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6742 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6742 gene: GAM3984 target protein, GAM5301 target protein, GAM219561 target protein and GAM315040 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3984, GAM5301, GAM219561 and GAM315040

6743(GR6743) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6743 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6743 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6743 gene encodes GR6743 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6743 precursor RNA folds spatially, forming GR6743 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6743 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6743 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6743 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM43717 precursor RNA and GAM88269 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM43717 RNA and GAM88269 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM43717 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM43717 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM43717 target RNA into GAM43717 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM88269 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM88269 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM88269 target RNA into GAM88269 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6743 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6743 gene: GAM43717 target protein and GAM88269 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM43717 and GAM88269

GR6744 BF527470 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6744(GR6744) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6744 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6744 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6744 gene encodes GR6744 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6744 precursor RNA folds spatially, forming GR6744 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6744 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6744 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6744 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM209633 precursor RNA and GAM227688 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM209633 RNA and GAM227688 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM209633 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM209633 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM209633 target RNA into GAM209633 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM227688 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM227688 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM227688 target RNA into GAM227688 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6744 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6744 gene: GAM209633 target protein and GAM227688 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM209633 and GAM227688

GR6745 AL693309 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6745(GR6745) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6745 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6745 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6745 gene encodes GR6745 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6745 precursor RNA folds spatially, forming GR6745 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6745 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6745 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6745 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3

separate GAM precursor RNAs, GAM148346 precursor RNA, GAM321018 precursor RNA and GAM331914 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM148346 RNA, GAM321018 RNA and GAM331914 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM148346 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM148346 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM148346 target RNA into GAM148346 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM321018 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM321018 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM321018 target RNA into GAM321018 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM331914 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM331914 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM331914 target RNA into GAM331914 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6745 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6745 gene: GAM148346 target protein, GAM321018 target protein and GAM331914 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM148346, GAM321018 and GAM331914

GR6746 BF907589 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6746(GR6746) gene, which encodes an `operon-like` cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6746 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6746 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6746 gene encodes GR6746 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6746 precursor RNA folds spatially, forming GR6746 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6746 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6746 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6746 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1977 precursor RNA and GAM136645 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1977 RNA and GAM136645 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1977 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1977 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1977 target RNA into GAM1977 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM136645 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM136645 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM136645 target RNA into GAM136645 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6746 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6746 gene: GAM1977 target protein and GAM136645 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1977 and GAM136645

GR6747 BF353187 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6747(GR6747) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6747 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6747 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6747 gene encodes GR6747 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6747 precursor RNA folds spatially, forming GR6747 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6747 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6747 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6747 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM142788 precursor RNA, GAM144573 precursor RNA, GAM261847 precursor RNA and GAM300183 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM142788 RNA, GAM144573 RNA, GAM261847 RNA and GAM300183 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM142788 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM142788 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM142788 target RNA into GAM142788 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM144573 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM144573 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM144573 target RNA into GAM144573 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM261847 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM261847 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM261847 target RNA into GAM261847 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM300183 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM300183 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM300183 target RNA into GAM300183 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6747 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6747 gene: GAM142788 target protein, GAM144573 target protein, GAM261847 target protein and GAM300183 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM142788, GAM144573, GAM261847 and GAM300183

GR6748 AU152276 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6748(GR6748) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6748 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6748

gene was detected is described hereinabove with reference to Figs. 8-18.

GR6748 gene encodes GR6748 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6748 precursor RNA folds spatially, forming GR6748 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6748 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6748 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6748 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM606 precursor RNA and GAM180149 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM606 RNA and GAM180149 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM606 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM606 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM606 target RNA into GAM606 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM180149 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM180149 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM180149 target RNA into GAM180149 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6748 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6748 gene: GAM606 target protein and GAM180149 target protein, herein schematically represented by GAM1

TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM606 and GAM180149

GR6749 AV729616 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6749(GR6749) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6749 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6749 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6749 gene encodes GR6749 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6749 precursor RNA folds spatially, forming GR6749 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6749 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6749 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6749 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2447 precursor RNA, GAM298973 precursor RNA and GAM332822 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2447 RNA, GAM298973 RNA and GAM332822 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2447 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2447 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2447 target RNA into GAM2447 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM298973 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM298973 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM298973 target RNA into GAM298973 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM332822 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM332822 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM332822 target RNA into GAM332822 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6749 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6749 gene: GAM2447 target protein, GAM298973 target protein and GAM332822 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2447, GAM298973 and GAM332822

GR6750 BF726840 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6750(GR6750) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6750 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6750 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6750 gene encodes GR6750 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6750 precursor RNA folds spatially, forming GR6750 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6750 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6750 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6750 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM17342 precursor RNA and GAM323903 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM17342 RNA and GAM323903 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM17342 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM17342 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM17342 target RNA into GAM17342 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM323903 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM323903 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM323903 target RNA into GAM323903 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6750 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6750 gene: GAM17342 target protein and GAM323903 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM17342 and GAM323903

GR6751 BI457085 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6751(GR6751) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6751 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6751 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6751 gene encodes GR6751 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6751 precursor RNA folds spatially, forming GR6751 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6751 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6751 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6751 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM61328 precursor RNA and GAM314509 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM61328 RNA and GAM314509 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM61328 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM61328 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM61328 target RNA into GAM61328 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM314509 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM314509 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM314509 target RNA into GAM314509 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6751 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6751 gene: GAM61328 target protein and GAM314509 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes

is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM61328 and GAM314509

GR6752 AW401686 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6752(GR6752) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6752 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6752 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6752 gene encodes GR6752 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6752 precursor RNA folds spatially, forming GR6752 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6752 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6752 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6752 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1450 precursor RNA and GAM316126 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1450 RNA and GAM316126 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1450 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1450 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1450 target RNA into GAM1450 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM316126 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM316126 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM316126 target RNA into GAM316126 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6752 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6752 gene: GAM1450 target protein and GAM316126 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1450 and GAM316126

GR6753 BF672063 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6753(GR6753) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6753 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6753 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6753 gene encodes GR6753 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6753 precursor RNA folds spatially, forming GR6753 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6753 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6753 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6753 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM5487 precursor RNA, GAM8041 precursor RNA and GAM190826 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM5487 RNA, GAM8041 RNA and GAM190826 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5487 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5487 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5487 target RNA into GAM5487 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8041 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8041 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8041 target RNA into GAM8041 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM190826 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM190826 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM190826 target RNA into GAM190826 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6753 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6753 gene: GAM5487 target protein, GAM8041 target protein and GAM190826 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5487, GAM8041 and GAM190826

GR6754 AL704516 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6754(GR6754) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6754 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6754 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6754 gene encodes GR6754 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6754 precursor RNA folds spatially, forming GR6754 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6754 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6754 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6754 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM4891 precursor RNA, GAM63093 precursor RNA, GAM189165 precursor RNA and GAM312691 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4891 RNA, GAM63093 RNA, GAM189165 RNA and GAM312691 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4891 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4891 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4891 target RNA into GAM4891 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM63093 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM63093 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM63093 target RNA into GAM63093 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM189165 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM189165 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM189165 target RNA into GAM189165 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM312691 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM312691 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM312691 target RNA into GAM312691 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6754 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6754 gene: GAM4891 target protein, GAM63093 target protein, GAM189165 target protein and GAM312691 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4891, GAM63093, GAM189165 and GAM312691

GR6755 BG169510 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6755(GR6755) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6755 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6755 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6755 gene encodes GR6755 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6755 precursor RNA folds spatially, forming GR6755 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6755 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6755 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6755 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7901 precursor RNA and GAM113620 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7901 RNA and GAM113620 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7901 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7901 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7901 target RNA into GAM7901 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM113620 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM113620 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM113620 target RNA into GAM113620 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6755 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6755 gene: GAM7901 target protein and GAM113620 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7901 and GAM113620

GR6756 AI434958 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6756(GR6756) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6756 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6756 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6756 gene encodes GR6756 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6756 precursor RNA folds spatially, forming GR6756 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated

that GR6756 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6756 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6756 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM39115 precursor RNA and GAM217998 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM39115 RNA and GAM217998 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM39115 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM39115 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM39115 target RNA into GAM39115 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM217998 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM217998 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM217998 target RNA into GAM217998 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6756 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6756 gene: GAM39115 target protein and GAM217998 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM39115 and GAM217998

GR6757 AI125994 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6757(GR6757) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR6757 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6757 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6757 gene encodes GR6757 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6757 precursor RNA folds spatially, forming GR6757 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6757 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6757 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6757 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM188004 precursor RNA, GAM281651 precursor RNA and GAM305478 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM188004 RNA, GAM281651 RNA and GAM305478 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM188004 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM188004 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM188004 target RNA into GAM188004 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM281651 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM281651 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM281651 target RNA into GAM281651 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM305478 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM305478 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM305478 target RNA into GAM305478 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6757 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6757 gene: GAM188004 target protein, GAM281651 target protein and GAM305478 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM188004, GAM281651 and GAM305478

GR6758 BM017992 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6758(GR6758) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6758 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6758 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6758 gene encodes GR6758 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6758 precursor RNA folds spatially, forming GR6758 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6758 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6758 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6758 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1766 precursor RNA and GAM169090 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1766 RNA and GAM169090 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1766 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1766 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1766 target RNA into GAM1766 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM169090 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM169090 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM169090 target RNA into GAM169090 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6758 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6758 gene: GAM1766 target protein and GAM169090 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1766 and GAM169090

GR6759 AA872389 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6759(GR6759) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6759 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6759 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6759 gene encodes GR6759 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6759 precursor RNA folds spatially, forming GR6759 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6759 folded precursor RNA comprises a plurality of what is known in the

art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6759 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6759 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM54954 precursor RNA and GAM305241 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM54954 RNA and GAM305241 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM54954 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM54954 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM54954 target RNA into GAM54954 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM305241 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM305241 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM305241 target RNA into GAM305241 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6759 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6759 gene: GAM54954 target protein and GAM305241 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM54954 and GAM305241

GR6760 BF243772 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6760(GR6760) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR6760 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6760 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6760 gene encodes GR6760 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6760 precursor RNA folds spatially, forming GR6760 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6760 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6760 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6760 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2938 precursor RNA and GAM3297 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2938 RNA and GAM3297 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2938 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2938 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2938 target RNA into GAM2938 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM3297 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3297 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3297 target RNA into GAM3297 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly

utilities, of GR6760 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6760 gene: GAM2938 target protein and GAM3297 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2938 and GAM3297

GR6761 BG340258 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6761 (GR6761) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6761 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6761 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6761 gene encodes GR6761 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6761 precursor RNA folds spatially, forming GR6761 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6761 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6761 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6761 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3104 precursor RNA and GAM96253 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3104 RNA and GAM96253 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3104 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3104 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig. 8, thereby inhibiting translation of GAM3104 target RNA into GAM3104 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM96253 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM96253 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM96253 target RNA into GAM96253 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6761 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6761 gene: GAM3104 target protein and GAM96253 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3104 and GAM96253

GR6762 BG435038 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6762(GR6762) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6762 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6762 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6762 gene encodes GR6762 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6762 precursor RNA folds spatially, forming GR6762 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6762 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6762 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6762 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM161173 precursor RNA, GAM264989 precursor RNA and GAM292027 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded

precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM161173 RNA, GAM264989 RNA and GAM292027 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM161173 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM161173 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM161173 target RNA into GAM161173 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM264989 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM264989 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM264989 target RNA into GAM264989 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM292027 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM292027 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM292027 target RNA into GAM292027 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6762 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6762 gene: GAM161173 target protein, GAM264989 target protein and GAM292027 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM161173, GAM264989 and GAM292027

GR6763 AI017367 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6763(GR6763) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6763 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6763 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6763 gene encodes GR6763 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6763 precursor RNA folds spatially, forming GR6763 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6763 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6763 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6763 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM220708 precursor RNA and GAM331383 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM220708 RNA and GAM331383 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM220708 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM220708 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM220708 target RNA into GAM220708 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM331383 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM331383 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM331383 target RNA into GAM331383 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6763 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6763 gene: GAM220708 target protein and GAM331383 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM220708 and GAM331383

GR6764 BE670123 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6764(GR6764) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6764 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6764 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6764 gene encodes GR6764 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6764 precursor RNA folds spatially, forming GR6764 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6764 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6764 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6764 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM541 precursor RNA and GAM305963 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM541 RNA and GAM305963 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM541 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM541 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM541 target RNA into

GAM541 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM305963 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM305963 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM305963 target RNA into GAM305963 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6764 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6764 gene: GAM541 target protein and GAM305963 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM541 and GAM305963

GR6765 BI765891 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6765(GR6765) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6765 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6765 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6765 gene encodes GR6765 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6765 precursor RNA folds spatially, forming GR6765 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6765 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6765 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6765 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM8266 precursor RNA, GAM119455 precursor RNA and GAM123661 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED

PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8266 RNA, GAM119455 RNA and GAM123661 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8266 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8266 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8266 target RNA into GAM8266 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM119455 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM119455 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM119455 target RNA into GAM119455 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM123661 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM123661 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM123661 target RNA into GAM123661 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6765 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6765 gene: GAM8266 target protein, GAM119455 target protein and GAM123661 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8266, GAM119455 and GAM123661

GR6766 AA745479 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6766(GR6766) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6766 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6766 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6766 gene encodes GR6766 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6766 precursor RNA folds spatially, forming GR6766 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6766 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6766 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6766 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM163727 precursor RNA and GAM177577 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM163727 RNA and GAM177577 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM163727 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM163727 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM163727 target RNA into GAM163727 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM177577 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM177577 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM177577 target RNA into GAM177577 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6766 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR6766 gene: GAM163727 target protein and GAM177577 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM163727 and GAM177577

GR6767 BG778757 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6767(GR6767) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6767 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6767 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6767 gene encodes GR6767 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6767 precursor RNA folds spatially, forming GR6767 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6767 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6767 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6767 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM86 precursor RNA, GAM43983 precursor RNA and GAM331212 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM86 RNA, GAM43983 RNA and GAM331212 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM86 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM86 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM86 target RNA into GAM86 target

protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM43983 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM43983 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM43983 target RNA into GAM43983 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM331212 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM331212 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM331212 target RNA into GAM331212 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6767 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6767 gene: GAM86 target protein, GAM43983 target protein and GAM331212 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM86, GAM43983 and GAM331212

GR6768 BM676377 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6768(GR6768) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6768 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6768 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6768 gene encodes GR6768 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6768 precursor RNA folds spatially, forming GR6768 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6768 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6768 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6768 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM73738 precursor RNA and GAM82062 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM73738 RNA and GAM82062 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM73738 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM73738 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM73738 target RNA into GAM73738 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM82062 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM82062 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM82062 target RNA into GAM82062 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6768 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6768 gene: GAM73738 target protein and GAM82062 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM73738 and GAM82062

GR6769 BG115237 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6769(GR6769) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6769 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR6769 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6769 gene encodes GR6769 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6769 precursor RNA folds spatially, forming GR6769 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6769 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6769 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6769 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM6125 precursor RNA, GAM88320 precursor RNA and GAM312720 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6125 RNA, GAM88320 RNA and GAM312720 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6125 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6125 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6125 target RNA into GAM6125 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM88320 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM88320 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM88320 target RNA into GAM88320 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM312720 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM312720 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM312720 target RNA into GAM312720 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6769 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6769 gene: GAM6125 target protein, GAM88320 target protein and GAM312720 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6125, GAM88320 and GAM312720

GR6770 AI174969 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6770(GR6770) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6770 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6770 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6770 gene encodes GR6770 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6770 precursor RNA folds spatially, forming GR6770 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6770 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6770 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6770 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6447 precursor RNA and GAM257093 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6447 RNA and GAM257093 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding

to GAM RNA of Fig. 8.

GAM6447 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6447 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6447 target RNA into GAM6447 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM257093 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM257093 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM257093 target RNA into GAM257093 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6770 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6770 gene: GAM6447 target protein and GAM257093 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6447 and GAM257093

GR6771 AV698000 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6771(GR6771) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6771 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6771 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6771 gene encodes GR6771 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6771 precursor RNA folds spatially, forming GR6771 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6771 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6771 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR6771 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM27602 precursor RNA, GAM45946 precursor RNA, GAM224845 precursor RNA and GAM318863 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM27602 RNA, GAM45946 RNA, GAM224845 RNA and GAM318863 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM27602 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM27602 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM27602 target RNA into GAM27602 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM45946 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM45946 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM45946 target RNA into GAM45946 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM224845 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM224845 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM224845 target RNA into GAM224845 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM318863 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM318863 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM318863 target RNA into GAM318863 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly

utilities, of GR6771 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6771 gene: GAM27602 target protein, GAM45946 target protein, GAM224845 target protein and GAM318863 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM27602, GAM45946, GAM224845 and GAM318863

GR6772 BI260542 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6772(GR6772) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6772 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6772 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6772 gene encodes GR6772 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6772 precursor RNA folds spatially, forming GR6772 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6772 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6772 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6772 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5377 precursor RNA and GAM257436 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5377 RNA and GAM257436 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5377 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5377 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds

to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5377 target RNA into GAM5377 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM257436 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM257436 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM257436 target RNA into GAM257436 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6772 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6772 gene: GAM5377 target protein and GAM257436 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5377 and GAM257436

GR6773 BI759484 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6773(GR6773) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6773 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6773 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6773 gene encodes GR6773 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6773 precursor RNA folds spatially, forming GR6773 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6773 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6773 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6773 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4788 precursor RNA and GAM5012 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3

FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4788 RNA and GAM5012 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4788 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4788 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4788 target RNA into GAM4788 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5012 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5012 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5012 target RNA into GAM5012 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6773 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6773 gene: GAM4788 target protein and GAM5012 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4788 and GAM5012

GR6774 AA707908 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6774(GR6774) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6774 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6774 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6774 gene encodes GR6774 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6774 precursor RNA folds spatially, forming GR6774 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6774 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6774 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6774 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2775 precursor RNA, GAM59592 precursor RNA and GAM194603 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2775 RNA, GAM59592 RNA and GAM194603 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2775 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2775 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2775 target RNA into GAM2775 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM59592 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM59592 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM59592 target RNA into GAM59592 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM194603 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM194603 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM194603 target RNA into GAM194603 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6774 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6774 gene: GAM2775 target protein, GAM59592 target protein and GAM194603 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2775, GAM59592 and GAM194603

GR6775 BG680327 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6775(GR6775) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6775 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6775 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6775 gene encodes GR6775 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6775 precursor RNA folds spatially, forming GR6775 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6775 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6775 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6775 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3047 precursor RNA and GAM281189 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3047 RNA and GAM281189 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3047 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3047 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig. 8, thereby inhibiting translation of GAM3047 target RNA into GAM3047 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM281189 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM281189 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM281189 target RNA into GAM281189 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6775 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6775 gene: GAM3047 target protein and GAM281189 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3047 and GAM281189

GR6776 BE207213 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6776(GR6776) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6776 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6776 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6776 gene encodes GR6776 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6776 precursor RNA folds spatially, forming GR6776 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6776 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6776 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6776 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM72033 precursor RNA and GAM113352 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin

shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM72033 RNA and GAM113352 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM72033 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM72033 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM72033 target RNA into GAM72033 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM113352 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM113352 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM113352 target RNA into GAM113352 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6776 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6776 gene: GAM72033 target protein and GAM113352 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM72033 and GAM113352

GR6777 AA485309 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6777(GR6777) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6777 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6777 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6777 gene encodes GR6777 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6777 precursor RNA folds spatially, forming GR6777 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6777 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6777 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6777 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7156 precursor RNA and GAM55511 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7156 RNA and GAM55511 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7156 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7156 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7156 target RNA into GAM7156 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM55511 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM55511 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM55511 target RNA into GAM55511 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6777 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6777 gene: GAM7156 target protein and GAM55511 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7156 and GAM55511

GR6778 BG491255 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6778(GR6778) gene, which encodes an `operon-like` cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6778 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6778 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6778 gene encodes GR6778 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6778 precursor RNA folds spatially, forming GR6778 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6778 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6778 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6778 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM78697 precursor RNA, GAM138782 precursor RNA, GAM230203 precursor RNA and GAM305814 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM78697 RNA, GAM138782 RNA, GAM230203 RNA and GAM305814 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM78697 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM78697 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM78697 target RNA into GAM78697 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM138782 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM138782 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM138782 target RNA into GAM138782 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM230203 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM230203 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM230203 target RNA into GAM230203 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM305814 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM305814 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM305814 target RNA into GAM305814 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6778 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6778 gene: GAM78697 target protein, GAM138782 target protein, GAM230203 target protein and GAM305814 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM78697, GAM138782, GAM230203 and GAM305814

GR6779 AI523944 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6779(GR6779) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6779 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6779 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6779 gene encodes GR6779 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6779 precursor RNA folds spatially, forming GR6779 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6779 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6779 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR6779 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM123203 precursor RNA and GAM260807 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM123203 RNA and GAM260807 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM123203 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM123203 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM123203 target RNA into GAM123203 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM260807 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM260807 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM260807 target RNA into GAM260807 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6779 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6779 gene: GAM123203 target protein and GAM260807 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM123203 and GAM260807

GR6780 W74561 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6780(GR6780) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6780 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6780

gene was detected is described hereinabove with reference to Figs. 8-18.

GR6780 gene encodes GR6780 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6780 precursor RNA folds spatially, forming GR6780 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6780 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6780 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6780 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM147210 precursor RNA and GAM216785 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM147210 RNA and GAM216785 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM147210 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM147210 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM147210 target RNA into GAM147210 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM216785 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM216785 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM216785 target RNA into GAM216785 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6780 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6780 gene: GAM147210 target protein and GAM216785 target protein, herein schematically represented by GAM1

TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM147210 and GAM216785

GR6781 BE745860 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6781 (GR6781) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6781 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6781 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6781 gene encodes GR6781 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6781 precursor RNA folds spatially, forming GR6781 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6781 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6781 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6781 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM39396 precursor RNA, GAM189712 precursor RNA and GAM267882 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM39396 RNA, GAM189712 RNA and GAM267882 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM39396 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM39396 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM39396 target RNA into GAM39396 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM189712 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM189712 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM189712 target RNA into GAM189712 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM267882 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM267882 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM267882 target RNA into GAM267882 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6781 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6781 gene: GAM39396 target protein, GAM189712 target protein and GAM267882 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM39396, GAM189712 and GAM267882

GR6782 R52603 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6782(GR6782) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6782 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6782 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6782 gene encodes GR6782 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6782 precursor RNA folds spatially, forming GR6782 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6782 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6782 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6782 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2183 precursor RNA and GAM100839 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2183 RNA and GAM100839 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2183 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2183 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2183 target RNA into GAM2183 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM100839 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM100839 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM100839 target RNA into GAM100839 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6782 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6782 gene: GAM2183 target protein and GAM100839 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2183 and GAM100839

GR6783 BE158768 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6783(GR6783) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6783 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6783 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6783 gene encodes GR6783 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6783 precursor RNA folds spatially, forming GR6783 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6783 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6783 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6783 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM6036 precursor RNA, GAM139194 precursor RNA and GAM262474 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6036 RNA, GAM139194 RNA and GAM262474 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6036 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6036 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6036 target RNA into GAM6036 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM139194 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM139194 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM139194 target RNA into GAM139194 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM262474 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM262474 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM262474

target RNA into GAM262474 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6783 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6783 gene: GAM6036 target protein, GAM139194 target protein and GAM262474 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6036, GAM139194 and GAM262474

GR6784 BM560331 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6784(GR6784) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6784 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6784 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6784 gene encodes GR6784 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6784 precursor RNA folds spatially, forming GR6784 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6784 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6784 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6784 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM105877 precursor RNA, GAM179148 precursor RNA, GAM212253 precursor RNA and GAM275842 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM105877 RNA, GAM179148 RNA, GAM212253 RNA and GAM275842 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM105877 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM105877 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM105877 target RNA into GAM105877 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM179148 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM179148 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM179148 target RNA into GAM179148 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM212253 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM212253 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM212253 target RNA into GAM212253 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM275842 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM275842 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM275842 target RNA into GAM275842 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6784 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6784 gene: GAM105877 target protein, GAM179148 target protein, GAM212253 target protein and GAM275842 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM105877, GAM179148, GAM212253 and GAM275842

GR6785 BG981180 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6785(GR6785) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6785 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6785 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6785 gene encodes GR6785 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6785 precursor RNA folds spatially, forming GR6785 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6785 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6785 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6785 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 5 separate GAM precursor RNAs, GAM237 precursor RNA, GAM178739 precursor RNA, GAM178740 precursor RNA, GAM336638 precursor RNA and GAM336639 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM237 RNA, GAM178739 RNA, GAM178740 RNA, GAM336638 RNA and GAM336639 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM237 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM237 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM237 target RNA into GAM237 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM178739 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM178739 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM178739 target RNA into GAM178739 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM178740 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM178740 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM178740 target RNA into GAM178740 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336638 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336638 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336638 target RNA into GAM336638 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336639 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336639 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336639 target RNA into GAM336639 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6785 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6785 gene: GAM237 target protein, GAM178739 target protein, GAM178740 target protein, GAM336638 target protein and GAM336639 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM237, GAM178739, GAM178740, GAM336638 and GAM336639

GR6786 AI564799 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6786(GR6786) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6786 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6786 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6786 gene encodes GR6786 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6786 precursor RNA folds spatially, forming GR6786 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6786 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6786 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6786 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM5290 precursor RNA, GAM52808 precursor RNA and GAM250660 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5290 RNA, GAM52808 RNA and GAM250660 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5290 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5290 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5290 target RNA into GAM5290 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM52808 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM52808 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM52808 target RNA into GAM52808 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM250660 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM250660 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM250660 target RNA into GAM250660 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6786 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR6786 gene: GAM5290 target protein, GAM52808 target protein and GAM250660 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5290, GAM52808 and GAM250660

GR6787 BF968174 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6787(GR6787) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6787 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6787 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6787 gene encodes GR6787 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6787 precursor RNA folds spatially, forming GR6787 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6787 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6787 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6787 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM137 precursor RNA and GAM193664 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM137 RNA and GAM193664 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM137 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM137 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM137 target RNA into

GAM137 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM193664 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM193664 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM193664 target RNA into GAM193664 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6787 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6787 gene: GAM137 target protein and GAM193664 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM137 and GAM193664

GR6788 BM988227 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6788(GR6788) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6788 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6788 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6788 gene encodes GR6788 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6788 precursor RNA folds spatially, forming GR6788 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6788 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6788 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6788 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM937 precursor RNA, GAM40510 precursor RNA and GAM270469 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED

PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM937 RNA, GAM40510 RNA and GAM270469 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM937 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM937 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM937 target RNA into GAM937 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM40510 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM40510 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM40510 target RNA into GAM40510 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM270469 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM270469 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM270469 target RNA into GAM270469 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6788 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6788 gene: GAM937 target protein, GAM40510 target protein and GAM270469 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM937, GAM40510 and GAM270469

GR6789 BM770677 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6789(GR6789) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6789 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6789 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6789 gene encodes GR6789 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6789 precursor RNA folds spatially, forming GR6789 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6789 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6789 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6789 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM275771 precursor RNA and GAM323379 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM275771 RNA and GAM323379 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM275771 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM275771 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM275771 target RNA into GAM275771 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM323379 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM323379 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM323379 target RNA into GAM323379 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6789 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR6789 gene: GAM275771 target protein and GAM323379 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM275771 and GAM323379

GR6790 R31939 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6790(GR6790) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6790 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6790 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6790 gene encodes GR6790 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6790 precursor RNA folds spatially, forming GR6790 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6790 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6790 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6790 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM130344 precursor RNA, GAM151699 precursor RNA and GAM312884 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM130344 RNA, GAM151699 RNA and GAM312884 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM130344 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM130344 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM130344

target RNA into GAM130344 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM151699 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM151699 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM151699 target RNA into GAM151699 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM312884 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM312884 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM312884 target RNA into GAM312884 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6790 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6790 gene: GAM130344 target protein, GAM151699 target protein and GAM312884 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM130344, GAM151699 and GAM312884

GR6791 AA975231 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6791(GR6791) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6791 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6791 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6791 gene encodes GR6791 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6791 precursor RNA folds spatially, forming GR6791 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6791 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6791 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6791 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM260951 precursor RNA and GAM276950 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM260951 RNA and GAM276950 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM260951 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM260951 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM260951 target RNA into GAM260951 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM276950 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM276950 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM276950 target RNA into GAM276950 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6791 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6791 gene: GAM260951 target protein and GAM276950 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM260951 and GAM276950

GR6792 AW949059 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6792(GR6792) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6792 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR6792 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6792 gene encodes GR6792 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6792 precursor RNA folds spatially, forming GR6792 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6792 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6792 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6792 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3983 precursor RNA and GAM27232 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3983 RNA and GAM27232 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3983 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3983 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3983 target RNA into GAM3983 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM27232 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM27232 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM27232 target RNA into GAM27232 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6792 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6792 gene: GAM3983 target

protein and GAM27232 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3983 and GAM27232

GR6793 BI789212 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6793(GR6793) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6793 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6793 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6793 gene encodes GR6793 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6793 precursor RNA folds spatially, forming GR6793 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6793 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6793 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6793 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM46715 precursor RNA, GAM136839 precursor RNA and GAM140642 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM46715 RNA, GAM136839 RNA and GAM140642 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM46715 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM46715 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM46715 target RNA into GAM46715 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM136839 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM136839 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM136839 target RNA into GAM136839 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM140642 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM140642 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM140642 target RNA into GAM140642 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6793 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6793 gene: GAM46715 target protein, GAM136839 target protein and GAM140642 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM46715, GAM136839 and GAM140642

GR6794 H51541 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6794(GR6794) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6794 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6794 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6794 gene encodes GR6794 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6794 precursor RNA folds spatially, forming GR6794 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6794 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6794 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR6794 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM295554 precursor RNA and GAM309527 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM295554 RNA and GAM309527 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM295554 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM295554 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM295554 target RNA into GAM295554 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM309527 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM309527 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM309527 target RNA into GAM309527 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6794 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6794 gene: GAM295554 target protein and GAM309527 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM295554 and GAM309527

GR6795 BG654473 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6795(GR6795) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6795 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6795

gene was detected is described hereinabove with reference to Figs. 8-18.

GR6795 gene encodes GR6795 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6795 precursor RNA folds spatially, forming GR6795 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6795 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6795 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6795 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6064 precursor RNA and GAM111777 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6064 RNA and GAM111777 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6064 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6064 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6064 target RNA into GAM6064 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM111777 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM111777 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM111777 target RNA into GAM111777 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6795 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6795 gene: GAM6064 target protein and GAM111777 target protein, herein schematically represented by GAM1

TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6064 and GAM111777

GR6796 BE393333 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6796(GR6796) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6796 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6796 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6796 gene encodes GR6796 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6796 precursor RNA folds spatially, forming GR6796 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6796 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6796 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6796 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4226 precursor RNA and GAM216129 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4226 RNA and GAM216129 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4226 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4226 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4226 target RNA into GAM4226 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM216129 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM216129 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM216129 target RNA into GAM216129 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6796 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6796 gene: GAM4226 target protein and GAM216129 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4226 and GAM216129

GR6797 BM009590 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6797(GR6797) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6797 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6797 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6797 gene encodes GR6797 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6797 precursor RNA folds spatially, forming GR6797 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6797 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6797 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6797 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM16344 precursor RNA and GAM262168 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM16344 RNA and GAM262168 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM16344 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM16344 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM16344 target RNA into GAM16344 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM262168 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM262168 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM262168 target RNA into GAM262168 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6797 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6797 gene: GAM16344 target protein and GAM262168 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM16344 and GAM262168

GR6798 AL598277 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6798(GR6798) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6798 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6798 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6798 gene encodes GR6798 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6798 precursor RNA folds spatially, forming GR6798 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6798 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6798 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6798 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM285745 precursor RNA, GAM291930 precursor RNA and GAM313231 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM285745 RNA, GAM291930 RNA and GAM313231 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM285745 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM285745 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM285745 target RNA into GAM285745 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM291930 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM291930 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM291930 target RNA into GAM291930 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM313231 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM313231 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM313231 target RNA into GAM313231 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6798 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6798 gene: GAM285745 target protein, GAM291930 target protein and GAM313231 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6,

hereby incorporated by reference, with references to GAM285745, GAM291930 and GAM313231

GR6799 R61492 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6799(GR6799) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6799 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6799 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6799 gene encodes GR6799 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6799 precursor RNA folds spatially, forming GR6799 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6799 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6799 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6799 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM67992 precursor RNA and GAM136572 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM67992 RNA and GAM136572 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM67992 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM67992 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM67992 target RNA into GAM67992 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM136572 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM136572 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM136572 target RNA into GAM136572 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6799 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6799 gene: GAM67992 target protein and GAM136572 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM67992 and GAM136572

GR6800 AI809301 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6800(GR6800) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6800 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6800 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6800 gene encodes GR6800 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6800 precursor RNA folds spatially, forming GR6800 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6800 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6800 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6800 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM98420 precursor RNA, GAM149101 precursor RNA and GAM270460 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM98420 RNA, GAM149101 RNA and GAM270460 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM98420 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM98420 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM98420 target RNA into GAM98420 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM149101 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM149101 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM149101 target RNA into GAM149101 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM270460 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM270460 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM270460 target RNA into GAM270460 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6800 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6800 gene: GAM98420 target protein, GAM149101 target protein and GAM270460 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM98420, GAM149101 and GAM270460

GR6801 BF093691 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6801 (GR6801) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6801 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6801 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6801 gene encodes GR6801 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6801 precursor RNA folds spatially, forming GR6801 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6801 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6801 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6801 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5451 precursor RNA and GAM5920 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5451 RNA and GAM5920 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5451 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5451 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5451 target RNA into GAM5451 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5920 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5920 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5920 target RNA into GAM5920 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6801 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6801 gene: GAM5451 target protein and GAM5920 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference,

with references to GAM5451 and GAM5920

GR6802 W94432 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6802 (GR6802) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6802 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6802 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6802 gene encodes GR6802 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6802 precursor RNA folds spatially, forming GR6802 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6802 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6802 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6802 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM105705 precursor RNA, GAM122434 precursor RNA and GAM172510 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM105705 RNA, GAM122434 RNA and GAM172510 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM105705 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM105705 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM105705 target RNA into GAM105705 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM122434 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM122434 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM122434 target RNA into GAM122434 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM172510 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM172510 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM172510 target RNA into GAM172510 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6802 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6802 gene: GAM105705 target protein, GAM122434 target protein and GAM172510 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM105705, GAM122434 and GAM172510

GR6803 BG475969 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6803(GR6803) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6803 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6803 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6803 gene encodes GR6803 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6803 precursor RNA folds spatially, forming GR6803 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6803 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6803 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6803 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM172367 precursor RNA and GAM219197 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM172367 RNA and GAM219197 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM172367 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM172367 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM172367 target RNA into GAM172367 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM219197 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM219197 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM219197 target RNA into GAM219197 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6803 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6803 gene: GAM172367 target protein and GAM219197 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM172367 and GAM219197

GR6804 BE535525 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6804(GR6804) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6804 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6804 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6804 gene encodes GR6804 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6804 precursor RNA folds spatially, forming GR6804 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6804 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6804 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6804 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM210078 precursor RNA and GAM286512 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM210078 RNA and GAM286512 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM210078 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM210078 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM210078 target RNA into GAM210078 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM286512 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM286512 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM286512 target RNA into GAM286512 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6804 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6804 gene: GAM210078 target protein and GAM286512 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM210078 and GAM286512

GR6805 AI971237 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6805(GR6805) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6805 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6805 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6805 gene encodes GR6805 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6805 precursor RNA folds spatially, forming GR6805 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6805 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6805 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6805 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM65521 precursor RNA and GAM121002 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM65521 RNA and GAM121002 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM65521 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM65521 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM65521 target RNA into GAM65521 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM121002 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM121002 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM121002 target RNA into GAM121002 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6805 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6805 gene: GAM65521 target protein and GAM121002 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM65521 and GAM121002

GR6806 BM788137 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6806(GR6806) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6806 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6806 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6806 gene encodes GR6806 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6806 precursor RNA folds spatially, forming GR6806 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6806 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6806 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6806 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM92918 precursor RNA and GAM168148 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM92918 RNA and GAM168148 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM92918 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM92918 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM92918 target RNA into GAM92918 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM168148 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM168148 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM168148 target RNA into GAM168148 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6806 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6806 gene: GAM92918 target protein and GAM168148 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM92918 and GAM168148

GR6807 R24011 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6807(GR6807) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6807 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6807 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6807 gene encodes GR6807 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6807 precursor RNA folds spatially, forming GR6807 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6807 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6807 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6807 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3985 precursor RNA, GAM5609 precursor RNA and GAM197699 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3985 RNA, GAM5609 RNA and GAM197699 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3985 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3985 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3985 target RNA into GAM3985 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5609 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5609 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5609 target RNA into GAM5609 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM197699 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM197699 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM197699 target RNA into GAM197699 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6807 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6807 gene: GAM3985 target protein, GAM5609 target protein and GAM197699 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3985, GAM5609 and GAM197699

GR6808 BG105875 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6808(GR6808) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6808 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6808 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6808 gene encodes GR6808 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6808 precursor RNA folds spatially, forming GR6808 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6808 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6808 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6808 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2259 precursor RNA and GAM5847 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2259 RNA and GAM5847 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2259 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2259 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2259 target RNA into GAM2259 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5847 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5847 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig. 8, thereby inhibiting translation of GAM5847 target RNA into GAM5847 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6808 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6808 gene: GAM2259 target protein and GAM5847 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2259 and GAM5847

GR6809 BI004435 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6809(GR6809) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6809 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6809 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6809 gene encodes GR6809 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6809 precursor RNA folds spatially, forming GR6809 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6809 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6809 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6809 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM5010 precursor RNA, GAM6156 precursor RNA and GAM148768 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5010 RNA, GAM6156 RNA and GAM148768 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5010 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5010 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5010 target RNA into GAM5010 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6156 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6156 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6156 target RNA into GAM6156 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM148768 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM148768 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM148768 target RNA into GAM148768 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6809 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6809 gene: GAM5010 target protein, GAM6156 target protein and GAM148768 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5010, GAM6156 and GAM148768

GR6810 BF197030 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6810 (GR6810) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6810 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6810 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6810 gene encodes GR6810 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6810 precursor RNA folds spatially, forming GR6810 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6810 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6810 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6810 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM122275 precursor RNA and GAM229942 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM122275 RNA and GAM229942 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM122275 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM122275 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM122275 target RNA into GAM122275 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM229942 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM229942 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM229942 target RNA into GAM229942 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6810 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6810 gene: GAM122275 target protein and GAM229942 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM122275 and GAM229942

bioinformatically detected regulatory gene, referred to here as Genomic Record 6811 (GR6811) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6811 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6811 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6811 gene encodes GR6811 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6811 precursor RNA folds spatially, forming GR6811 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6811 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6811 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6811 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM534 precursor RNA, GAM2226 precursor RNA, GAM272520 precursor RNA and GAM292857 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM534 RNA, GAM2226 RNA, GAM272520 RNA and GAM292857 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM534 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM534 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM534 target RNA into GAM534 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM2226 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2226 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig. 8, thereby inhibiting translation of GAM2226 target RNA into GAM2226 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM272520 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM272520 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM272520 target RNA into GAM272520 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM292857 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM292857 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM292857 target RNA into GAM292857 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6811 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6811 gene: GAM534 target protein, GAM2226 target protein, GAM272520 target protein and GAM292857 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM534, GAM2226, GAM272520 and GAM292857

GR6812 BG696573 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6812(GR6812) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6812 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6812 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6812 gene encodes GR6812 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6812 precursor RNA folds spatially, forming GR6812 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6812 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6812 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6812 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7906 precursor RNA and GAM148002 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7906 RNA and GAM148002 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7906 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7906 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7906 target RNA into GAM7906 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM148002 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM148002 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM148002 target RNA into GAM148002 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6812 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6812 gene: GAM7906 target protein and GAM148002 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7906 and GAM148002

GR6813 BG252629 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6813(GR6813) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6813 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6813 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6813 gene encodes GR6813 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6813 precursor RNA folds spatially, forming GR6813 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6813 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6813 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6813 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1292 precursor RNA and GAM3328 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1292 RNA and GAM3328 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1292 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1292 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1292 target RNA into GAM1292 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM3328 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3328 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3328 target RNA into GAM3328 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6813 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR6813 gene: GAM1292 target protein and GAM3328 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1292 and GAM3328

GR6814 BM467077 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6814(GR6814) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6814 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6814 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6814 gene encodes GR6814 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6814 precursor RNA folds spatially, forming GR6814 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6814 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6814 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6814 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM79320 precursor RNA, GAM109453 precursor RNA and GAM114299 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM79320 RNA, GAM109453 RNA and GAM114299 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM79320 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM79320 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM79320

target RNA into GAM79320 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM109453 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM109453 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM109453 target RNA into GAM109453 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM114299 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM114299 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM114299 target RNA into GAM114299 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6814 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6814 gene: GAM79320 target protein, GAM109453 target protein and GAM114299 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM79320, GAM109453 and GAM114299

GR6815 AA664464 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6815(GR6815) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6815 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6815 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6815 gene encodes GR6815 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6815 precursor RNA folds spatially, forming GR6815 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6815 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6815 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6815 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM47610 precursor RNA and GAM226250 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM47610 RNA and GAM226250 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM47610 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM47610 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM47610 target RNA into GAM47610 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM226250 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM226250 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM226250 target RNA into GAM226250 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6815 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6815 gene: GAM47610 target protein and GAM226250 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM47610 and GAM226250

GR6816 BF369789 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6816 (GR6816) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6816 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR6816 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6816 gene encodes GR6816 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6816 precursor RNA folds spatially, forming GR6816 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6816 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6816 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6816 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM5050 precursor RNA, GAM5828 precursor RNA and GAM224660 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5050 RNA, GAM5828 RNA and GAM224660 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5050 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5050 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5050 target RNA into GAM5050 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5828 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5828 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5828 target RNA into GAM5828 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM224660 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM224660 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM224660 target RNA into GAM224660 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6816 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6816 gene: GAM5050 target protein, GAM5828 target protein and GAM224660 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5050, GAM5828 and GAM224660

GR6817 BG120752 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6817(GR6817) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6817 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6817 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6817 gene encodes GR6817 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6817 precursor RNA folds spatially, forming GR6817 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6817 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6817 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6817 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM276531 precursor RNA and GAM330456 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM276531 RNA and GAM330456 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding

to GAM RNA of Fig. 8.

GAM276531 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM276531 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM276531 target RNA into GAM276531 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM330456 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM330456 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM330456 target RNA into GAM330456 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6817 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6817 gene: GAM276531 target protein and GAM330456 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM276531 and GAM330456

GR6818 BF795266 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6818(GR6818) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6818 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6818 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6818 gene encodes GR6818 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6818 precursor RNA folds spatially, forming GR6818 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6818 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6818 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR6818 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM73815 precursor RNA and GAM266130 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM73815 RNA and GAM266130 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM73815 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM73815 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM73815 target RNA into GAM73815 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM266130 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM266130 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM266130 target RNA into GAM266130 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6818 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6818 gene: GAM73815 target protein and GAM266130 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM73815 and GAM266130

GR6819 AI476473 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6819 (GR6819) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6819 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6819

gene was detected is described hereinabove with reference to Figs. 8-18.

GR6819 gene encodes GR6819 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6819 precursor RNA folds spatially, forming GR6819 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6819 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6819 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6819 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7670 precursor RNA and GAM169495 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7670 RNA and GAM169495 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7670 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7670 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7670 target RNA into GAM7670 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM169495 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM169495 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM169495 target RNA into GAM169495 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6819 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6819 gene: GAM7670 target protein and GAM169495 target protein, herein schematically represented by GAM1

TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7670 and GAM169495

GR6820 AW516257 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6820 (GR6820) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6820 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6820 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6820 gene encodes GR6820 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6820 precursor RNA folds spatially, forming GR6820 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6820 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6820 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6820 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2421 precursor RNA, GAM229545 precursor RNA and GAM328899 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2421 RNA, GAM229545 RNA and GAM328899 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2421 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2421 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2421 target RNA into GAM2421 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM229545 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM229545 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM229545 target RNA into GAM229545 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM328899 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM328899 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM328899 target RNA into GAM328899 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6820 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6820 gene: GAM2421 target protein, GAM229545 target protein and GAM328899 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2421, GAM229545 and GAM328899

GR6821 AI240502 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6821 (GR6821) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6821 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6821 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6821 gene encodes GR6821 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6821 precursor RNA folds spatially, forming GR6821 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6821 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6821 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6821 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM51316 precursor RNA, GAM95390 precursor RNA and GAM286240 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM51316 RNA, GAM95390 RNA and GAM286240 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM51316 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM51316 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM51316 target RNA into GAM51316 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM95390 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM95390 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM95390 target RNA into GAM95390 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM286240 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM286240 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM286240 target RNA into GAM286240 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6821 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6821 gene: GAM51316 target protein, GAM95390 target protein and GAM286240 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM51316, GAM95390 and GAM286240

GR6822 AA725366 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6822(GR6822) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6822 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6822 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6822 gene encodes GR6822 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6822 precursor RNA folds spatially, forming GR6822 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6822 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6822 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6822 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4578 precursor RNA, GAM21491 precursor RNA and GAM47245 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4578 RNA, GAM21491 RNA and GAM47245 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4578 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4578 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4578 target RNA into GAM4578 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM21491 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM21491 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM21491 target RNA into GAM21491 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM47245 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM47245 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM47245 target RNA into GAM47245 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6822 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6822 gene: GAM4578 target protein, GAM21491 target protein and GAM47245 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4578, GAM21491 and GAM47245

GR6823 BG749758 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6823(GR6823) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6823 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6823 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6823 gene encodes GR6823 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6823 precursor RNA folds spatially, forming GR6823 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6823 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6823 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6823 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM226074 precursor RNA, GAM246370 precursor RNA

and GAM267350 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM226074 RNA, GAM246370 RNA and GAM267350 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM226074 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM226074 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM226074 target RNA into GAM226074 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM246370 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM246370 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM246370 target RNA into GAM246370 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM267350 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM267350 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM267350 target RNA into GAM267350 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6823 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6823 gene: GAM226074 target protein, GAM246370 target protein and GAM267350 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM226074, GAM246370 and GAM267350

GR6824 AW886836 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6824(GR6824) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR6824 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6824 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6824 gene encodes GR6824 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6824 precursor RNA folds spatially, forming GR6824 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6824 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6824 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6824 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6551 precursor RNA and GAM278558 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6551 RNA and GAM278558 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6551 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6551 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6551 target RNA into GAM6551 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM278558 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM278558 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM278558 target RNA into GAM278558 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6824 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6824 gene: GAM6551 target protein and GAM278558 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6551 and GAM278558

GR6825 BF849221 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6825(GR6825) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6825 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6825 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6825 gene encodes GR6825 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6825 precursor RNA folds spatially, forming GR6825 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6825 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6825 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6825 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2982 precursor RNA and GAM6248 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2982 RNA and GAM6248 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2982 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2982 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds

to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2982 target RNA into GAM2982 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6248 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6248 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6248 target RNA into GAM6248 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6825 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6825 gene: GAM2982 target protein and GAM6248 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2982 and GAM6248

GR6826 BI917721 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6826(GR6826) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6826 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6826 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6826 gene encodes GR6826 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6826 precursor RNA folds spatially, forming GR6826 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6826 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6826 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6826 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM182866 precursor RNA and GAM286525 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3

FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM182866 RNA and GAM286525 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM182866 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM182866 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM182866 target RNA into GAM182866 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM286525 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM286525 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM286525 target RNA into GAM286525 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6826 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6826 gene: GAM182866 target protein and GAM286525 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM182866 and GAM286525

GR6827 BF934463 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6827(GR6827) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6827 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6827 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6827 gene encodes GR6827 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6827 precursor RNA folds spatially, forming GR6827 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6827 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6827 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6827 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM122400 precursor RNA and GAM181644 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM122400 RNA and GAM181644 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM122400 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM122400 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM122400 target RNA into GAM122400 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM181644 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM181644 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM181644 target RNA into GAM181644 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6827 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6827 gene: GAM122400 target protein and GAM181644 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM122400 and GAM181644

6828(GR6828) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6828 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6828 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6828 gene encodes GR6828 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6828 precursor RNA folds spatially, forming GR6828 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6828 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6828 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6828 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM269852 precursor RNA and GAM276169 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM269852 RNA and GAM276169 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM269852 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM269852 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM269852 target RNA into GAM269852 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM276169 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM276169 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM276169 target RNA into GAM276169 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6828 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6828 gene: GAM269852 target protein and GAM276169 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM269852 and GAM276169

GR6829 BF677983 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6829(GR6829) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6829 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6829 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6829 gene encodes GR6829 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6829 precursor RNA folds spatially, forming GR6829 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6829 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6829 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6829 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM9730 precursor RNA, GAM169490 precursor RNA, GAM185336 precursor RNA and GAM268577 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM9730 RNA, GAM169490 RNA, GAM185336 RNA and GAM268577 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM9730 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM9730 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM9730 target RNA into GAM9730 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM169490 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM169490 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM169490 target RNA into GAM169490 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM185336 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM185336 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM185336 target RNA into GAM185336 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM268577 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM268577 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM268577 target RNA into GAM268577 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6829 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6829 gene: GAM9730 target protein, GAM169490 target protein, GAM185336 target protein and GAM268577 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM9730, GAM169490, GAM185336 and GAM268577

GR6830 BI017175 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6830(GR6830) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6830 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR6830 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6830 gene encodes GR6830 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6830 precursor RNA folds spatially, forming GR6830 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6830 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6830 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6830 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7151 precursor RNA and GAM7710 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7151 RNA and GAM7710 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7151 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7151 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7151 target RNA into GAM7151 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7710 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7710 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7710 target RNA into GAM7710 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6830 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6830 gene: GAM7151 target

protein and GAM7710 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7151 and GAM7710

GR6831 BI463214 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6831 (GR6831) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6831 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6831 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6831 gene encodes GR6831 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6831 precursor RNA folds spatially, forming GR6831 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6831 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6831 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6831 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3137 precursor RNA and GAM84915 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3137 RNA and GAM84915 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3137 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3137 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3137 target RNA into GAM3137 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM84915 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM84915 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM84915 target RNA into GAM84915 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6831 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6831 gene: GAM3137 target protein and GAM84915 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3137 and GAM84915

GR6832 BM926172 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6832(GR6832) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6832 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6832 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6832 gene encodes GR6832 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6832 precursor RNA folds spatially, forming GR6832 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6832 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6832 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6832 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM270612 precursor RNA and GAM277642 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM270612 RNA and GAM277642 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM270612 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM270612 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM270612 target RNA into GAM270612 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM277642 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM277642 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM277642 target RNA into GAM277642 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6832 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6832 gene: GAM270612 target protein and GAM277642 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM270612 and GAM277642

GR6833 H92964 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6833(GR6833) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6833 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6833 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6833 gene encodes GR6833 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6833 precursor RNA folds spatially, forming GR6833 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6833 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR6833 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6833 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM75994 precursor RNA and GAM246637 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM75994 RNA and GAM246637 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM75994 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM75994 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM75994 target RNA into GAM75994 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM246637 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM246637 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM246637 target RNA into GAM246637 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6833 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6833 gene: GAM75994 target protein and GAM246637 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM75994 and GAM246637

GR6834 AW673181 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6834(GR6834) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6834 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6834 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6834 gene encodes GR6834 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6834 precursor RNA folds spatially, forming GR6834 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6834 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6834 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6834 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2334 precursor RNA, GAM7265 precursor RNA and GAM96498 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2334 RNA, GAM7265 RNA and GAM96498 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2334 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2334 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2334 target RNA into GAM2334 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7265 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7265 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7265 target RNA into GAM7265 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM96498 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM96498 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM96498 target RNA into GAM96498 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6834 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6834 gene: GAM2334 target protein, GAM7265 target protein and GAM96498 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2334, GAM7265 and GAM96498

GR6835 BF761969 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6835(GR6835) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6835 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6835 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6835 gene encodes GR6835 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6835 precursor RNA folds spatially, forming GR6835 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6835 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6835 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6835 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM327 precursor RNA and GAM181850 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM327 RNA and GAM181850 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM327 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM327 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM327 target RNA into GAM327 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM181850 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM181850 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM181850 target RNA into GAM181850 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6835 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6835 gene: GAM327 target protein and GAM181850 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM327 and GAM181850

GR6836 R08714 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6836(GR6836) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6836 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6836 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6836 gene encodes GR6836 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6836 precursor RNA folds spatially, forming GR6836 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6836 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6836 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6836 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM7755 precursor RNA, GAM309004 precursor RNA and GAM330869 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7755 RNA, GAM309004 RNA and GAM330869 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7755 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7755 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7755 target RNA into GAM7755 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM309004 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM309004 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM309004 target RNA into GAM309004 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM330869 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM330869 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM330869 target RNA into GAM330869 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6836 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6836 gene: GAM7755 target protein, GAM309004 target protein and GAM330869 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6,

hereby incorporated by reference, with references to GAM7755, GAM309004 and GAM330869

GR6837 AW468146 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6837 (GR6837) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6837 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6837 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6837 gene encodes GR6837 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6837 precursor RNA folds spatially, forming GR6837 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6837 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6837 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6837 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM105539 precursor RNA, GAM268978 precursor RNA and GAM326430 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM105539 RNA, GAM268978 RNA and GAM326430 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM105539 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM105539 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM105539 target RNA into GAM105539 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM268978 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM268978 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM268978 target RNA into GAM268978 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM326430 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM326430 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM326430 target RNA into GAM326430 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6837 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6837 gene: GAM105539 target protein, GAM268978 target protein and GAM326430 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM105539, GAM268978 and GAM326430

GR6838 H66726 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6838(GR6838) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6838 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6838 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6838 gene encodes GR6838 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6838 precursor RNA folds spatially, forming GR6838 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6838 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6838 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6838 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM20254 precursor RNA, GAM79535 precursor RNA and GAM203412 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM20254 RNA, GAM79535 RNA and GAM203412 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM20254 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM20254 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM20254 target RNA into GAM20254 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM79535 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM79535 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM79535 target RNA into GAM79535 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM203412 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM203412 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM203412 target RNA into GAM203412 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6838 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6838 gene: GAM20254 target protein, GAM79535 target protein and GAM203412 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM20254, GAM79535 and GAM203412

bioinformatically detected regulatory gene, referred to here as Genomic Record 6839 (GR6839) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6839 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6839 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6839 gene encodes GR6839 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6839 precursor RNA folds spatially, forming GR6839 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6839 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6839 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6839 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM80567 precursor RNA and GAM213151 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM80567 RNA and GAM213151 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM80567 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM80567 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM80567 target RNA into GAM80567 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM213151 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM213151 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM213151

target RNA into GAM213151 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6839 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6839 gene: GAM80567 target protein and GAM213151 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM80567 and GAM213151

GR6840 BM823039 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6840(GR6840) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6840 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6840 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6840 gene encodes GR6840 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6840 precursor RNA folds spatially, forming GR6840 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6840 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6840 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6840 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7597 precursor RNA and GAM322461 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7597 RNA and GAM322461 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7597 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7597 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7597 target RNA into GAM7597 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM322461 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM322461 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM322461 target RNA into GAM322461 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6840 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6840 gene: GAM7597 target protein and GAM322461 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7597 and GAM322461

GR6841 AA455921 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6841 (GR6841) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6841 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6841 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6841 gene encodes GR6841 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6841 precursor RNA folds spatially, forming GR6841 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6841 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6841 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6841 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM157983 precursor RNA and GAM169416 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM157983 RNA and GAM169416 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM157983 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM157983 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM157983 target RNA into GAM157983 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM169416 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM169416 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM169416 target RNA into GAM169416 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6841 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6841 gene: GAM157983 target protein and GAM169416 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM157983 and GAM169416

GR6842 BF205581 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6842(GR6842) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6842 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6842 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6842 gene encodes GR6842 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6842 precursor RNA folds spatially, forming GR6842 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6842 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6842 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6842 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM73204 precursor RNA and GAM200208 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM73204 RNA and GAM200208 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM73204 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM73204 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM73204 target RNA into GAM73204 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM200208 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM200208 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM200208 target RNA into GAM200208 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6842 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6842 gene: GAM73204 target protein and GAM200208 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM73204 and GAM200208

GR6843 R82873 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6843(GR6843) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6843 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6843 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6843 gene encodes GR6843 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6843 precursor RNA folds spatially, forming GR6843 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6843 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6843 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6843 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM900 precursor RNA and GAM118560 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM900 RNA and GAM118560 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM900 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM900 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM900 target RNA into GAM900 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM118560 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM118560 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM118560 target RNA into GAM118560 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6843 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6843 gene: GAM900 target protein and GAM118560 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM900 and GAM118560

GR6844 AU125679 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6844(GR6844) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6844 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6844 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6844 gene encodes GR6844 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6844 precursor RNA folds spatially, forming GR6844 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6844 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6844 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6844 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3186 precursor RNA and GAM213973 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3186 RNA and GAM213973 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3186 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3186 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3186 target RNA into GAM3186 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM213973 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM213973 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM213973 target RNA into GAM213973 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6844 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6844 gene: GAM3186 target protein and GAM213973 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3186 and GAM213973

GR6845 BI195045 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6845(GR6845) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6845 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6845 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6845 gene encodes GR6845 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6845 precursor RNA folds spatially, forming GR6845 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6845 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6845 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6845 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM48279 precursor RNA, GAM83973 precursor RNA and GAM207701 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM48279 RNA, GAM83973 RNA and GAM207701 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM48279 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM48279 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM48279 target RNA into GAM48279 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM83973 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM83973 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM83973 target RNA into GAM83973 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM207701 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM207701 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM207701 target RNA into GAM207701 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6845 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6845 gene: GAM48279 target protein, GAM83973 target protein and GAM207701 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM48279, GAM83973 and GAM207701

GR6846 BQ081912 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6846(GR6846) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6846 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6846 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6846 gene encodes GR6846 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6846 precursor RNA folds spatially, forming GR6846 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6846 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6846 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6846 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8390 precursor RNA and GAM41960 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8390 RNA and GAM41960 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8390 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8390 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8390 target RNA into GAM8390 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM41960 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM41960 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM41960 target RNA into GAM41960 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6846 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6846 gene: GAM8390 target protein and GAM41960 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8390 and GAM41960

GR6847 BI038627 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6847(GR6847) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6847 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6847 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6847 gene encodes GR6847 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6847 precursor RNA folds spatially, forming GR6847 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6847 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6847 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6847 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM206384 precursor RNA, GAM245353 precursor RNA and GAM257071 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM206384 RNA, GAM245353 RNA and GAM257071 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM206384 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM206384 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM206384 target RNA into GAM206384 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM245353 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM245353 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM245353 target RNA into GAM245353 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM257071 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM257071 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM257071 target RNA into GAM257071 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6847 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6847 gene: GAM206384 target protein, GAM245353 target protein and GAM257071 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM206384, GAM245353 and GAM257071

GR6848 BM541974 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6848(GR6848) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6848 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6848 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6848 gene encodes GR6848 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6848 precursor RNA folds spatially, forming GR6848 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6848 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6848 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6848 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM616 precursor RNA, GAM4053 precursor RNA and GAM118909 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM616 RNA, GAM4053 RNA and GAM118909 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM616 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM616 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM616 target RNA into GAM616 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM4053 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4053 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4053 target RNA into GAM4053 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM118909 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM118909 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM118909 target RNA into GAM118909 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly

utilities, of GR6848 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6848 gene: GAM616 target protein, GAM4053 target protein and GAM118909 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM616, GAM4053 and GAM118909

GR6849 BG399757 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6849(GR6849) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6849 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6849 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6849 gene encodes GR6849 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6849 precursor RNA folds spatially, forming GR6849 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6849 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6849 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6849 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM18827 precursor RNA and GAM102932 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM18827 RNA and GAM102932 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM18827 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM18827 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM18827 target RNA into GAM18827 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM102932 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM102932 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM102932 target RNA into GAM102932 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6849 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6849 gene: GAM18827 target protein and GAM102932 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM18827 and GAM102932

GR6850 AA324940 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6850(GR6850) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6850 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6850 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6850 gene encodes GR6850 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6850 precursor RNA folds spatially, forming GR6850 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6850 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6850 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6850 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM152832 precursor RNA and GAM219315 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3

FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM152832 RNA and GAM219315 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM152832 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM152832 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM152832 target RNA into GAM152832 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM219315 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM219315 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM219315 target RNA into GAM219315 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6850 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6850 gene: GAM152832 target protein and GAM219315 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM152832 and GAM219315

GR6851 BM761029 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6851 (GR6851) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6851 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6851 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6851 gene encodes GR6851 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6851 precursor RNA folds spatially, forming GR6851 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6851 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6851 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6851 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM219442 precursor RNA and GAM243647 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM219442 RNA and GAM243647 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM219442 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM219442 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM219442 target RNA into GAM219442 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM243647 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM243647 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM243647 target RNA into GAM243647 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6851 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6851 gene: GAM219442 target protein and GAM243647 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM219442 and GAM243647

6852(GR6852) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6852 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6852 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6852 gene encodes GR6852 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6852 precursor RNA folds spatially, forming GR6852 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6852 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6852 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6852 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM152 precursor RNA and GAM96279 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM152 RNA and GAM96279 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM152 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM152 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM152 target RNA into GAM152 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM96279 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM96279 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM96279 target RNA into GAM96279 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6852 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6852 gene: GAM152 target protein and GAM96279 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM152 and GAM96279

GR6853 AW328068 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6853(GR6853) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6853 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6853 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6853 gene encodes GR6853 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6853 precursor RNA folds spatially, forming GR6853 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6853 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6853 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6853 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4463 precursor RNA and GAM18076 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4463 RNA and GAM18076 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4463 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM4463 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4463 target RNA into GAM4463 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM18076 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM18076 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM18076 target RNA into GAM18076 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6853 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6853 gene: GAM4463 target protein and GAM18076 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4463 and GAM18076

GR6854 AA586920 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6854(GR6854) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6854 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6854 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6854 gene encodes GR6854 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6854 precursor RNA folds spatially, forming GR6854 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6854 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6854 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6854 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2

separate GAM precursor RNAs, GAM164501 precursor RNA and GAM217004 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM164501 RNA and GAM217004 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM164501 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM164501 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM164501 target RNA into GAM164501 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM217004 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM217004 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM217004 target RNA into GAM217004 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6854 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6854 gene: GAM164501 target protein and GAM217004 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM164501 and GAM217004

GR6855 AW138132 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6855(GR6855) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6855 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6855 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6855 gene encodes GR6855 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR6855 precursor RNA folds spatially, forming GR6855 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6855 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6855 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6855 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1705 precursor RNA and GAM28278 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1705 RNA and GAM28278 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1705 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1705 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1705 target RNA into GAM1705 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM28278 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM28278 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM28278 target RNA into GAM28278 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6855 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6855 gene: GAM1705 target protein and GAM28278 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1705 and GAM28278

GR6856 AW902638 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6856 (GR6856) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6856 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6856 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6856 gene encodes GR6856 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6856 precursor RNA folds spatially, forming GR6856 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6856 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6856 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6856 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM28211 precursor RNA and GAM290036 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM28211 RNA and GAM290036 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM28211 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM28211 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM28211 target RNA into GAM28211 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM290036 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM290036 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM290036 target RNA into GAM290036 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6856 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6856 gene: GAM28211 target protein and GAM290036 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM28211 and GAM290036

GR6857 AA948208 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6857 (GR6857) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6857 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6857 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6857 gene encodes GR6857 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6857 precursor RNA folds spatially, forming GR6857 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6857 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6857 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6857 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM38384 precursor RNA and GAM54943 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM38384 RNA and GAM54943 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM38384 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM38384 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM38384 target RNA into GAM38384 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM54943 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM54943 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM54943 target RNA into GAM54943 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6857 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6857 gene: GAM38384 target protein and GAM54943 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM38384 and GAM54943

GR6858 BI223591 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6858(GR6858) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6858 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6858 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6858 gene encodes GR6858 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6858 precursor RNA folds spatially, forming GR6858 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6858 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6858 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6858 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM5376 precursor RNA, GAM5824 precursor RNA and GAM63992 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5376 RNA, GAM5824 RNA and GAM63992 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5376 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5376 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5376 target RNA into GAM5376 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5824 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5824 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5824 target RNA into GAM5824 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM63992 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM63992 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM63992 target RNA into GAM63992 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6858 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6858 gene: GAM5376 target protein, GAM5824 target protein and GAM63992 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5376, GAM5824 and GAM63992

bioinformatically detected regulatory gene, referred to here as Genomic Record 6859(GR6859) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6859 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6859 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6859 gene encodes GR6859 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6859 precursor RNA folds spatially, forming GR6859 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6859 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6859 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6859 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM32769 precursor RNA and GAM105078 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM32769 RNA and GAM105078 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM32769 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM32769 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM32769 target RNA into GAM32769 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM105078 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM105078 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM105078

target RNA into GAM105078 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6859 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6859 gene: GAM32769 target protein and GAM105078 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM32769 and GAM105078

GR6860 AI204988 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6860(GR6860) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6860 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6860 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6860 gene encodes GR6860 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6860 precursor RNA folds spatially, forming GR6860 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6860 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6860 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6860 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4934 precursor RNA, GAM8655 precursor RNA and GAM12316 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4934 RNA, GAM8655 RNA and GAM12316 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4934 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4934 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4934 target RNA into GAM4934 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8655 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8655 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8655 target RNA into GAM8655 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM12316 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM12316 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM12316 target RNA into GAM12316 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6860 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6860 gene: GAM4934 target protein, GAM8655 target protein and GAM12316 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4934, GAM8655 and GAM12316

GR6861 BQ014319 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6861 (GR6861) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6861 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6861 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6861 gene encodes GR6861 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6861 precursor RNA folds spatially, forming GR6861 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6861 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6861 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6861 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM34299 precursor RNA, GAM58899 precursor RNA and GAM65293 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM34299 RNA, GAM58899 RNA and GAM65293 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM34299 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM34299 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM34299 target RNA into GAM34299 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM58899 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM58899 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM58899 target RNA into GAM58899 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM65293 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM65293 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM65293 target RNA into GAM65293 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6861 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6861 gene: GAM34299 target protein, GAM58899 target protein and GAM65293 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM34299, GAM58899 and GAM65293

GR6862 BF213922 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6862(GR6862) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6862 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6862 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6862 gene encodes GR6862 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6862 precursor RNA folds spatially, forming GR6862 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6862 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6862 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6862 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1848 precursor RNA and GAM2728 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1848 RNA and GAM2728 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1848 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1848 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig. 8, thereby inhibiting translation of GAM1848 target RNA into GAM1848 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM2728 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2728 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2728 target RNA into GAM2728 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6862 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6862 gene: GAM1848 target protein and GAM2728 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1848 and GAM2728

GR6863 BF951730 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6863(GR6863) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6863 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6863 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6863 gene encodes GR6863 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6863 precursor RNA folds spatially, forming GR6863 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6863 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6863 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6863 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3557 precursor RNA and GAM5627 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin

shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3557 RNA and GAM5627 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3557 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3557 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3557 target RNA into GAM3557 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5627 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5627 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5627 target RNA into GAM5627 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6863 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6863 gene: GAM3557 target protein and GAM5627 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3557 and GAM5627

GR6864 BG901153 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6864(GR6864) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6864 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6864 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6864 gene encodes GR6864 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6864 precursor RNA folds spatially, forming GR6864 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6864 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6864 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6864 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM100195 precursor RNA and GAM128188 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM100195 RNA and GAM128188 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM100195 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM100195 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM100195 target RNA into GAM100195 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM128188 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM128188 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM128188 target RNA into GAM128188 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6864 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6864 gene: GAM100195 target protein and GAM128188 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM100195 and GAM128188

GR6865 BG261360 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6865(GR6865) gene, which encodes an `operon-like` cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6865 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6865 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6865 gene encodes GR6865 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6865 precursor RNA folds spatially, forming GR6865 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6865 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6865 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6865 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4138 precursor RNA, GAM6047 precursor RNA and GAM17594 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4138 RNA, GAM6047 RNA and GAM17594 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4138 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4138 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4138 target RNA into GAM4138 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6047 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6047 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6047 target RNA into GAM6047 target protein, herein schematically represented by GAM1 TARGET

PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM17594 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM17594 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM17594 target RNA into GAM17594 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6865 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6865 gene: GAM4138 target protein, GAM6047 target protein and GAM17594 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4138, GAM6047 and GAM17594

GR6866 AA469074 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6866(GR6866) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6866 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6866 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6866 gene encodes GR6866 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6866 precursor RNA folds spatially, forming GR6866 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6866 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6866 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6866 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM153459 precursor RNA and GAM297193 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM153459 RNA and GAM297193 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM153459 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM153459 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM153459 target RNA into GAM153459 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM297193 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM297193 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM297193 target RNA into GAM297193 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6866 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6866 gene: GAM153459 target protein and GAM297193 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM153459 and GAM297193

GR6867 BF996327 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6867(GR6867) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6867 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6867 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6867 gene encodes GR6867 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6867 precursor RNA folds spatially, forming GR6867 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated

that GR6867 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6867 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6867 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM9973 precursor RNA and GAM227090 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM9973 RNA and GAM227090 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM9973 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM9973 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM9973 target RNA into GAM9973 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM227090 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM227090 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM227090 target RNA into GAM227090 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6867 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6867 gene: GAM9973 target protein and GAM227090 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM9973 and GAM227090

GR6868 BI829228 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6868(GR6868) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR6868 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6868 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6868 gene encodes GR6868 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6868 precursor RNA folds spatially, forming GR6868 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6868 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6868 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6868 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2355 precursor RNA and GAM183483 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2355 RNA and GAM183483 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2355 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2355 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2355 target RNA into GAM2355 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM183483 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM183483 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM183483 target RNA into GAM183483 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6868 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6868 gene: GAM2355 target protein and GAM183483 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2355 and GAM183483

GR6869 BM048789 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6869(GR6869) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6869 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6869 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6869 gene encodes GR6869 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6869 precursor RNA folds spatially, forming GR6869 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6869 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6869 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6869 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6288 precursor RNA and GAM231017 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6288 RNA and GAM231017 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6288 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6288 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds

to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6288 target RNA into GAM6288 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM231017 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM231017 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM231017 target RNA into GAM231017 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6869 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6869 gene: GAM6288 target protein and GAM231017 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6288 and GAM231017

GR6870 BM970740 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6870(GR6870) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6870 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6870 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6870 gene encodes GR6870 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6870 precursor RNA folds spatially, forming GR6870 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6870 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6870 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6870 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM255209 precursor RNA and GAM335828 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3

FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM255209 RNA and GAM335828 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM255209 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM255209 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM255209 target RNA into GAM255209 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM335828 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM335828 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM335828 target RNA into GAM335828 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6870 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6870 gene: GAM255209 target protein and GAM335828 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM255209 and GAM335828

GR6871 BF872712 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6871(GR6871) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6871 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6871 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6871 gene encodes GR6871 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6871 precursor RNA folds spatially, forming GR6871 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6871 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6871 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6871 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6112 precursor RNA and GAM75299 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6112 RNA and GAM75299 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6112 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6112 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6112 target RNA into GAM6112 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM75299 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM75299 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM75299 target RNA into GAM75299 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6871 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6871 gene: GAM6112 target protein and GAM75299 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6112 and GAM75299

6872(GR6872) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6872 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6872 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6872 gene encodes GR6872 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6872 precursor RNA folds spatially, forming GR6872 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6872 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6872 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6872 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4499 precursor RNA, GAM24018 precursor RNA and GAM234726 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4499 RNA, GAM24018 RNA and GAM234726 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4499 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4499 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4499 target RNA into GAM4499 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM24018 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM24018 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM24018

target RNA into GAM24018 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM234726 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM234726 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM234726 target RNA into GAM234726 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6872 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6872 gene: GAM4499 target protein, GAM24018 target protein and GAM234726 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4499, GAM24018 and GAM234726

GR6873 AI797713 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6873(GR6873) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6873 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6873 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6873 gene encodes GR6873 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6873 precursor RNA folds spatially, forming GR6873 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6873 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6873 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6873 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM423 precursor RNA and GAM32176 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin

shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM423 RNA and GAM32176 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM423 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM423 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM423 target RNA into GAM423 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM32176 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM32176 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM32176 target RNA into GAM32176 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6873 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6873 gene: GAM423 target protein and GAM32176 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM423 and GAM32176

GR6874 AA808488 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6874(GR6874) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6874 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6874 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6874 gene encodes GR6874 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6874 precursor RNA folds spatially, forming GR6874 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6874 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6874 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6874 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM49043 precursor RNA and GAM82836 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM49043 RNA and GAM82836 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM49043 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM49043 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM49043 target RNA into GAM49043 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM82836 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM82836 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM82836 target RNA into GAM82836 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6874 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6874 gene: GAM49043 target protein and GAM82836 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM49043 and GAM82836

GR6875 BE734291 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6875(GR6875) gene, which encodes an `operon-like` cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6875 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6875 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6875 gene encodes GR6875 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6875 precursor RNA folds spatially, forming GR6875 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6875 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6875 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6875 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM212 precursor RNA and GAM31354 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM212 RNA and GAM31354 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM212 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM212 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM212 target RNA into GAM212 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM31354 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM31354 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM31354 target RNA into GAM31354 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6875 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6875 gene: GAM212 target protein and GAM31354 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM212 and GAM31354

GR6876 AI359724 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6876(GR6876) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6876 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6876 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6876 gene encodes GR6876 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6876 precursor RNA folds spatially, forming GR6876 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6876 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6876 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6876 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2872 precursor RNA and GAM19084 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2872 RNA and GAM19084 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2872 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2872 target RNA, herein schematically represented by

GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2872 target RNA into GAM2872 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM19084 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM19084 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM19084 target RNA into GAM19084 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6876 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6876 gene: GAM2872 target protein and GAM19084 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2872 and GAM19084

GR6877 BF313844 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6877(GR6877) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6877 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6877 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6877 gene encodes GR6877 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6877 precursor RNA folds spatially, forming GR6877 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6877 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6877 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6877 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2883 precursor RNA and GAM7299 precursor

RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2883 RNA and GAM7299 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2883 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2883 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2883 target RNA into GAM2883 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7299 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7299 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7299 target RNA into GAM7299 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6877 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6877 gene: GAM2883 target protein and GAM7299 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2883 and GAM7299

GR6878 BG563543 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6878(GR6878) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6878 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6878 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6878 gene encodes GR6878 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6878 precursor RNA folds spatially, forming GR6878 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6878 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6878 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6878 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM149 precursor RNA and GAM7850 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM149 RNA and GAM7850 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM149 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM149 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM149 target RNA into GAM149 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7850 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7850 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7850 target RNA into GAM7850 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6878 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6878 gene: GAM149 target protein and GAM7850 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM149 and GAM7850

bioinformatically detected regulatory gene, referred to here as Genomic Record 6879 (GR6879) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6879 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6879 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6879 gene encodes GR6879 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6879 precursor RNA folds spatially, forming GR6879 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6879 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6879 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6879 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM108190 precursor RNA and GAM166293 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM108190 RNA and GAM166293 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM108190 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM108190 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM108190 target RNA into GAM108190 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM166293 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM166293 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM166293

target RNA into GAM166293 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6879 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6879 gene: GAM108190 target protein and GAM166293 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM108190 and GAM166293

GR6880 BE066039 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6880(GR6880) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6880 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6880 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6880 gene encodes GR6880 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6880 precursor RNA folds spatially, forming GR6880 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6880 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6880 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6880 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM219963 precursor RNA, GAM241473 precursor RNA and GAM298437 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM219963 RNA, GAM241473 RNA and GAM298437 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM219963 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM219963 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM219963 target RNA into GAM219963 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM241473 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM241473 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM241473 target RNA into GAM241473 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM298437 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM298437 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM298437 target RNA into GAM298437 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6880 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6880 gene: GAM219963 target protein, GAM241473 target protein and GAM298437 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM219963, GAM241473 and GAM298437

GR6881 AU141927 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6881 (GR6881) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6881 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6881 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6881 gene encodes GR6881 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6881 precursor RNA folds spatially, forming GR6881 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6881 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6881 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6881 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM77323 precursor RNA and GAM180933 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM77323 RNA and GAM180933 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM77323 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM77323 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM77323 target RNA into GAM77323 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM180933 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM180933 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM180933 target RNA into GAM180933 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6881 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6881 gene: GAM77323 target protein and GAM180933 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM77323 and GAM180933

6882(GR6882) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6882 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6882 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6882 gene encodes GR6882 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6882 precursor RNA folds spatially, forming GR6882 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6882 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6882 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6882 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM544 precursor RNA, GAM2969 precursor RNA, GAM136779 precursor RNA and GAM181950 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM544 RNA, GAM2969 RNA, GAM136779 RNA and GAM181950 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM544 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM544 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM544 target RNA into GAM544 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM2969 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2969 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2969 target RNA into

GAM2969 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM136779 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM136779 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM136779 target RNA into GAM136779 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM181950 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM181950 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM181950 target RNA into GAM181950 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6882 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6882 gene: GAM544 target protein, GAM2969 target protein, GAM136779 target protein and GAM181950 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM544, GAM2969, GAM136779 and GAM181950

GR6883 BE314676 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6883(GR6883) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6883 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6883 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6883 gene encodes GR6883 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6883 precursor RNA folds spatially, forming GR6883 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6883 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6883 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6883 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM464 precursor RNA, GAM5577 precursor RNA, GAM6474 precursor RNA and GAM209696 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM464 RNA, GAM5577 RNA, GAM6474 RNA and GAM209696 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM464 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM464 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM464 target RNA into GAM464 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5577 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5577 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5577 target RNA into GAM5577 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6474 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6474 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6474 target RNA into GAM6474 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM209696 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM209696 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM209696 target RNA into GAM209696 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6883 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6883 gene: GAM464 target protein, GAM5577 target protein, GAM6474 target protein and GAM209696 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM464, GAM5577, GAM6474 and GAM209696

GR6884 BG212791 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6884(GR6884) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6884 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6884 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6884 gene encodes GR6884 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6884 precursor RNA folds spatially, forming GR6884 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6884 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6884 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6884 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM42290 precursor RNA and GAM253672 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM42290 RNA and GAM253672 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM42290 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM42290 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM42290 target RNA into GAM42290 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM253672 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM253672 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM253672 target RNA into GAM253672 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6884 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6884 gene: GAM42290 target protein and GAM253672 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM42290 and GAM253672

GR6885 BG774239 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6885(GR6885) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6885 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6885 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6885 gene encodes GR6885 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6885 precursor RNA folds spatially, forming GR6885 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6885 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6885 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6885 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM7154 precursor RNA, GAM99880 precursor RNA and

GAM211672 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7154 RNA, GAM99880 RNA and GAM211672 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7154 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7154 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7154 target RNA into GAM7154 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM99880 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM99880 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM99880 target RNA into GAM99880 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM211672 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM211672 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM211672 target RNA into GAM211672 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6885 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6885 gene: GAM7154 target protein, GAM99880 target protein and GAM211672 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7154, GAM99880 and GAM211672

GR6886 BQ023732 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6886(GR6886) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR6886 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6886 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6886 gene encodes GR6886 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6886 precursor RNA folds spatially, forming GR6886 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6886 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6886 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6886 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5633 precursor RNA and GAM140790 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5633 RNA and GAM140790 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5633 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5633 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5633 target RNA into GAM5633 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM140790 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM140790 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM140790 target RNA into GAM140790 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6886 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6886 gene: GAM5633 target protein and GAM140790 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5633 and GAM140790

GR6887 BE900698 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6887(GR6887) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6887 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6887 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6887 gene encodes GR6887 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6887 precursor RNA folds spatially, forming GR6887 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6887 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6887 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6887 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM634 precursor RNA, GAM223731 precursor RNA and GAM239074 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM634 RNA, GAM223731 RNA and GAM239074 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM634 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM634 target RNA, herein schematically represented by

GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM634 target RNA into GAM634 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM223731 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM223731 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM223731 target RNA into GAM223731 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM239074 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM239074 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM239074 target RNA into GAM239074 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6887 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6887 gene: GAM634 target protein, GAM223731 target protein and GAM239074 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM634, GAM223731 and GAM239074

GR6888 BF858624 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6888(GR6888) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6888 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6888 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6888 gene encodes GR6888 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6888 precursor RNA folds spatially, forming GR6888 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6888 folded precursor RNA comprises a plurality of what is known in the

art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6888 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6888 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM490 precursor RNA and GAM302956 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM490 RNA and GAM302956 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM490 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM490 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM490 target RNA into GAM490 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM302956 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM302956 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM302956 target RNA into GAM302956 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6888 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6888 gene: GAM490 target protein and GAM302956 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM490 and GAM302956

GR6889 AW340678 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6889(GR6889) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR6889 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6889 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6889 gene encodes GR6889 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6889 precursor RNA folds spatially, forming GR6889 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6889 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6889 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6889 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM1396 precursor RNA, GAM116553 precursor RNA, GAM175832 precursor RNA and GAM258989 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1396 RNA, GAM116553 RNA, GAM175832 RNA and GAM258989 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1396 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1396 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1396 target RNA into GAM1396 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM116553 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM116553 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM116553 target RNA into GAM116553 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM175832 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM175832 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM175832 target RNA into GAM175832 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM258989 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM258989 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM258989 target RNA into GAM258989 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6889 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6889 gene: GAM1396 target protein, GAM116553 target protein, GAM175832 target protein and GAM258989 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1396, GAM116553, GAM175832 and GAM258989

GR6890 BI827667 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6890(GR6890) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6890 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6890 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6890 gene encodes GR6890 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6890 precursor RNA folds spatially, forming GR6890 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6890 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6890 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6890 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM48 precursor RNA, GAM257172 precursor RNA and GAM274253 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM48 RNA, GAM257172 RNA and GAM274253 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM48 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM48 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM48 target RNA into GAM48 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM257172 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM257172 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM257172 target RNA into GAM257172 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM274253 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM274253 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM274253 target RNA into GAM274253 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6890 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6890 gene: GAM48 target protein, GAM257172 target protein and GAM274253 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM48, GAM257172 and GAM274253

bioinformatically detected regulatory gene, referred to here as Genomic Record 6891 (GR6891) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6891 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6891 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6891 gene encodes GR6891 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6891 precursor RNA folds spatially, forming GR6891 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6891 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6891 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6891 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM3901 precursor RNA, GAM64627 precursor RNA, GAM107454 precursor RNA and GAM218651 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3901 RNA, GAM64627 RNA, GAM107454 RNA and GAM218651 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3901 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3901 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3901 target RNA into GAM3901 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM64627 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM64627 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM64627 target RNA into GAM64627 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM107454 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM107454 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM107454 target RNA into GAM107454 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM218651 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM218651 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM218651 target RNA into GAM218651 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6891 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6891 gene: GAM3901 target protein, GAM64627 target protein, GAM107454 target protein and GAM218651 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3901, GAM64627, GAM107454 and GAM218651

GR6892 BF686118 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6892(GR6892) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6892 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6892 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6892 gene encodes GR6892 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6892 precursor RNA folds spatially, forming GR6892 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6892 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6892 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6892 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1213 precursor RNA and GAM76406 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1213 RNA and GAM76406 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1213 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1213 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1213 target RNA into GAM1213 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM76406 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM76406 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM76406 target RNA into GAM76406 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6892 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6892 gene: GAM1213 target protein and GAM76406 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1213 and GAM76406

GR6893 BQ045448 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6893(GR6893) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6893 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6893 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6893 gene encodes GR6893 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6893 precursor RNA folds spatially, forming GR6893 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6893 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6893 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6893 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM7981 precursor RNA, GAM70138 precursor RNA, GAM75124 precursor RNA and GAM83836 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7981 RNA, GAM70138 RNA, GAM75124 RNA and GAM83836 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7981 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7981 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7981 target RNA into GAM7981 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM70138 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM70138 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM70138 target RNA into GAM70138 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM75124 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM75124 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM75124 target RNA into GAM75124 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM83836 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM83836 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM83836 target RNA into GAM83836 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6893 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6893 gene: GAM7981 target protein, GAM70138 target protein, GAM75124 target protein and GAM83836 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7981, GAM70138, GAM75124 and GAM83836

GR6894 BG219547 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6894(GR6894) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6894 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6894 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6894 gene encodes GR6894 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6894 precursor RNA folds spatially, forming GR6894 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6894 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6894 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6894 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2

separate GAM precursor RNAs, GAM52611 precursor RNA and GAM310652 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM52611 RNA and GAM310652 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM52611 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM52611 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM52611 target RNA into GAM52611 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM310652 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM310652 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM310652 target RNA into GAM310652 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6894 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6894 gene: GAM52611 target protein and GAM310652 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM52611 and GAM310652

GR6895 BI057838 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6895(GR6895) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6895 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6895 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6895 gene encodes GR6895 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR6895 precursor RNA folds spatially, forming GR6895 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6895 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6895 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6895 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4617 precursor RNA and GAM42948 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4617 RNA and GAM42948 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4617 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4617 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4617 target RNA into GAM4617 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM42948 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM42948 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM42948 target RNA into GAM42948 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6895 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6895 gene: GAM4617 target protein and GAM42948 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4617 and GAM42948

GR6896 BG037115 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6896(GR6896) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6896 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6896 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6896 gene encodes GR6896 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6896 precursor RNA folds spatially, forming GR6896 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6896 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6896 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6896 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM19563 precursor RNA and GAM58918 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM19563 RNA and GAM58918 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM19563 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM19563 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM19563 target RNA into GAM19563 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM58918 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM58918 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM58918 target RNA into GAM58918 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6896 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6896 gene: GAM19563 target protein and GAM58918 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM19563 and GAM58918

GR6897 BI833962 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6897(GR6897) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6897 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6897 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6897 gene encodes GR6897 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6897 precursor RNA folds spatially, forming GR6897 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6897 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6897 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6897 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM217924 precursor RNA and GAM273351 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM217924 RNA and GAM273351 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM217924 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM217924 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM217924 target RNA into GAM217924 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM273351 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM273351 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM273351 target RNA into GAM273351 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6897 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6897 gene: GAM217924 target protein and GAM273351 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM217924 and GAM273351

GR6898 BF240048 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6898(GR6898) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6898 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6898 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6898 gene encodes GR6898 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6898 precursor RNA folds spatially, forming GR6898 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6898 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6898 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6898 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM32098 precursor RNA, GAM191282 precursor RNA and GAM283181 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM32098 RNA, GAM191282 RNA and GAM283181 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM32098 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM32098 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM32098 target RNA into GAM32098 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM191282 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM191282 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM191282 target RNA into GAM191282 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM283181 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM283181 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM283181 target RNA into GAM283181 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6898 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6898 gene: GAM32098 target protein, GAM191282 target protein and GAM283181 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM32098, GAM191282 and GAM283181

bioinformatically detected regulatory gene, referred to here as Genomic Record 6899(GR6899) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6899 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6899 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6899 gene encodes GR6899 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6899 precursor RNA folds spatially, forming GR6899 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6899 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6899 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6899 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM84667 precursor RNA, GAM197927 precursor RNA and GAM208632 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM84667 RNA, GAM197927 RNA and GAM208632 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM84667 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM84667 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM84667 target RNA into GAM84667 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM197927 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM197927 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM197927 target RNA into GAM197927 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM208632 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM208632 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM208632 target RNA into GAM208632 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6899 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6899 gene: GAM84667 target protein, GAM197927 target protein and GAM208632 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM84667, GAM197927 and GAM208632

GR6900 BG434115 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6900(GR6900) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6900 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6900 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6900 gene encodes GR6900 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6900 precursor RNA folds spatially, forming GR6900 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6900 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6900 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6900 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4972 precursor RNA and GAM6788 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3

FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4972 RNA and GAM6788 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4972 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4972 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4972 target RNA into GAM4972 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6788 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6788 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6788 target RNA into GAM6788 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6900 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6900 gene: GAM4972 target protein and GAM6788 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4972 and GAM6788

GR6901 BE382784 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6901 (GR6901) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6901 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6901 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6901 gene encodes GR6901 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6901 precursor RNA folds spatially, forming GR6901 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6901 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6901 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6901 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM64243 precursor RNA and GAM100151 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM64243 RNA and GAM100151 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM64243 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM64243 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM64243 target RNA into GAM64243 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM100151 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM100151 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM100151 target RNA into GAM100151 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6901 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6901 gene: GAM64243 target protein and GAM100151 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM64243 and GAM100151

6902(GR6902) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6902 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6902 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6902 gene encodes GR6902 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6902 precursor RNA folds spatially, forming GR6902 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6902 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6902 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6902 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM254355 precursor RNA and GAM255954 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM254355 RNA and GAM255954 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM254355 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM254355 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM254355 target RNA into GAM254355 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM255954 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM255954 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM255954 target RNA into GAM255954 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6902 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6902 gene: GAM254355 target protein and GAM255954 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM254355 and GAM255954

GR6903 AI361459 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6903(GR6903) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6903 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6903 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6903 gene encodes GR6903 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6903 precursor RNA folds spatially, forming GR6903 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6903 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6903 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6903 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2651 precursor RNA, GAM153999 precursor RNA and GAM161820 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2651 RNA, GAM153999 RNA and GAM161820 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2651 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2651 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2651 target RNA into GAM2651 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM153999 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM153999 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM153999 target RNA into GAM153999 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM161820 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM161820 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM161820 target RNA into GAM161820 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6903 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6903 gene: GAM2651 target protein, GAM153999 target protein and GAM161820 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2651, GAM153999 and GAM161820

GR6904 BF183561 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6904(GR6904) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6904 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6904 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6904 gene encodes GR6904 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6904 precursor RNA folds spatially, forming GR6904 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6904 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6904 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6904 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM22381 precursor RNA and GAM177927 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM22381 RNA and GAM177927 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM22381 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM22381 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM22381 target RNA into GAM22381 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM177927 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM177927 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM177927 target RNA into GAM177927 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6904 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6904 gene: GAM22381 target protein and GAM177927 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM22381 and GAM177927

GR6905 BE930633 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6905(GR6905) gene, which encodes an `operon-like` cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6905 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6905 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6905 gene encodes GR6905 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6905 precursor RNA folds spatially, forming GR6905 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6905 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6905 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6905 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1773 precursor RNA and GAM4997 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1773 RNA and GAM4997 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1773 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1773 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1773 target RNA into GAM1773 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM4997 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4997 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4997 target RNA into GAM4997 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6905 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6905 gene: GAM1773 target protein and GAM4997 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1773 and GAM4997

GR6906 BE562822 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6906(GR6906) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6906 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6906 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6906 gene encodes GR6906 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6906 precursor RNA folds spatially, forming GR6906 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6906 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6906 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6906 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM7378 precursor RNA, GAM62812 precursor RNA and GAM271223 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7378 RNA, GAM62812 RNA and GAM271223 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7378 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM7378 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7378 target RNA into GAM7378 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM62812 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM62812 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM62812 target RNA into GAM62812 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM271223 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM271223 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM271223 target RNA into GAM271223 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6906 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6906 gene: GAM7378 target protein, GAM62812 target protein and GAM271223 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7378, GAM62812 and GAM271223

GR6907 AU098429 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6907(GR6907) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6907 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6907 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6907 gene encodes GR6907 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6907 precursor RNA folds spatially, forming GR6907 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated

that GR6907 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6907 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6907 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6964 precursor RNA and GAM223293 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6964 RNA and GAM223293 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6964 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6964 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6964 target RNA into GAM6964 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM223293 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM223293 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM223293 target RNA into GAM223293 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6907 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6907 gene: GAM6964 target protein and GAM223293 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6964 and GAM223293

GR6908 AA599358 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6908(GR6908) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR6908 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6908 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6908 gene encodes GR6908 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6908 precursor RNA folds spatially, forming GR6908 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6908 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6908 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6908 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM128116 precursor RNA, GAM168456 precursor RNA and GAM295604 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM128116 RNA, GAM168456 RNA and GAM295604 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM128116 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM128116 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM128116 target RNA into GAM128116 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM168456 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM168456 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM168456 target RNA into GAM168456 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM295604 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM295604 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM295604 target RNA into GAM295604 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6908 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6908 gene: GAM128116 target protein, GAM168456 target protein and GAM295604 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM128116, GAM168456 and GAM295604

GR6909 BF828350 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6909 (GR6909) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6909 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6909 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6909 gene encodes GR6909 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6909 precursor RNA folds spatially, forming GR6909 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6909 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6909 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6909 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM66099 precursor RNA and GAM250357 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM66099 RNA and GAM250357 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM66099 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM66099 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM66099 target RNA into GAM66099 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM250357 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM250357 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM250357 target RNA into GAM250357 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6909 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6909 gene: GAM66099 target protein and GAM250357 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM66099 and GAM250357

GR6910 AA551367 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6910(GR6910) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6910 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6910 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6910 gene encodes GR6910 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6910 precursor RNA folds spatially, forming GR6910 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6910 folded precursor RNA comprises a plurality of what is known in the

art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6910 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6910 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM26912 precursor RNA and GAM204681 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM26912 RNA and GAM204681 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM26912 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM26912 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM26912 target RNA into GAM26912 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM204681 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM204681 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM204681 target RNA into GAM204681 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6910 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6910 gene: GAM26912 target protein and GAM204681 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM26912 and GAM204681

GR6911 BE865537 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6911(GR6911) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR6911 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6911 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6911 gene encodes GR6911 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6911 precursor RNA folds spatially, forming GR6911 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6911 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6911 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6911 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM88530 precursor RNA, GAM161109 precursor RNA and GAM168315 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM88530 RNA, GAM161109 RNA and GAM168315 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM88530 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM88530 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM88530 target RNA into GAM88530 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM161109 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM161109 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM161109 target RNA into GAM161109 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM168315 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM168315 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM168315 target RNA into GAM168315 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6911 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6911 gene: GAM88530 target protein, GAM161109 target protein and GAM168315 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM88530, GAM161109 and GAM168315

GR6912 BG723132 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6912(GR6912) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6912 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6912 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6912 gene encodes GR6912 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6912 precursor RNA folds spatially, forming GR6912 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6912 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6912 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6912 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8582 precursor RNA and GAM285849 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8582 RNA and GAM285849 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8582 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8582 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8582 target RNA into GAM8582 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM285849 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM285849 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM285849 target RNA into GAM285849 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6912 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6912 gene: GAM8582 target protein and GAM285849 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8582 and GAM285849

GR6913 AA761292 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6913(GR6913) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6913 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6913 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6913 gene encodes GR6913 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6913 precursor RNA folds spatially, forming GR6913 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6913 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR6913 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6913 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1498 precursor RNA, GAM2371 precursor RNA and GAM22901 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1498 RNA, GAM2371 RNA and GAM22901 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1498 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1498 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1498 target RNA into GAM1498 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM2371 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2371 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2371 target RNA into GAM2371 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM22901 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM22901 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM22901 target RNA into GAM22901 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6913 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6913 gene: GAM1498 target protein, GAM2371 target protein and GAM22901 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN.

The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1498, GAM2371 and GAM22901

GR6914 AI889929 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6914 (GR6914) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6914 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6914 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6914 gene encodes GR6914 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6914 precursor RNA folds spatially, forming GR6914 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6914 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6914 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6914 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM198955 precursor RNA and GAM275462 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM198955 RNA and GAM275462 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM198955 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM198955 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM198955 target RNA into GAM198955 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM275462 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM275462 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM275462 target RNA into GAM275462 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6914 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6914 gene: GAM198955 target protein and GAM275462 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM198955 and GAM275462

GR6915 BM041112 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6915(GR6915) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6915 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6915 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6915 gene encodes GR6915 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6915 precursor RNA folds spatially, forming GR6915 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6915 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6915 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6915 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4781 precursor RNA and GAM58524 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM4781 RNA and GAM58524 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4781 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4781 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4781 target RNA into GAM4781 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM58524 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM58524 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM58524 target RNA into GAM58524 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6915 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6915 gene: GAM4781 target protein and GAM58524 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4781 and GAM58524

GR6916 BM722772 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6916 (GR6916) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6916 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6916 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6916 gene encodes GR6916 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6916 precursor RNA folds spatially, forming GR6916 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6916 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6916 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6916 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM63189 precursor RNA and GAM332060 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM63189 RNA and GAM332060 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM63189 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM63189 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM63189 target RNA into GAM63189 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM332060 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM332060 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM332060 target RNA into GAM332060 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6916 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6916 gene: GAM63189 target protein and GAM332060 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM63189 and GAM332060

GR6917 BG768896 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6917(GR6917) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6917 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6917 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6917 gene encodes GR6917 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6917 precursor RNA folds spatially, forming GR6917 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6917 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6917 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6917 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM212411 precursor RNA, GAM277577 precursor RNA and GAM320045 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM212411 RNA, GAM277577 RNA and GAM320045 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM212411 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM212411 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM212411 target RNA into GAM212411 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM277577 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM277577 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM277577 target RNA into GAM277577 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM320045 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM320045 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM320045 target RNA into GAM320045 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6917 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6917 gene: GAM212411 target protein, GAM277577 target protein and GAM320045 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM212411, GAM277577 and GAM320045

GR6918 AI419262 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6918(GR6918) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6918 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6918 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6918 gene encodes GR6918 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6918 precursor RNA folds spatially, forming GR6918 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6918 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6918 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6918 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2044 precursor RNA, GAM6069 precursor RNA and GAM59046 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM2044 RNA, GAM6069 RNA and GAM59046 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2044 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2044 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2044 target RNA into GAM2044 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6069 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6069 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6069 target RNA into GAM6069 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM59046 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM59046 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM59046 target RNA into GAM59046 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6918 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6918 gene: GAM2044 target protein, GAM6069 target protein and GAM59046 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2044, GAM6069 and GAM59046

GR6919 BM851743 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6919 (GR6919) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6919 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6919 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6919 gene encodes GR6919 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6919 precursor RNA folds spatially, forming GR6919 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6919 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6919 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6919 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6143 precursor RNA and GAM134624 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6143 RNA and GAM134624 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6143 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6143 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6143 target RNA into GAM6143 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM134624 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM134624 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM134624 target RNA into GAM134624 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6919 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6919 gene: GAM6143 target protein and GAM134624 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference,

with references to GAM6143 and GAM134624

GR6920 N84052 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6920 (GR6920) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6920 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6920 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6920 gene encodes GR6920 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6920 precursor RNA folds spatially, forming GR6920 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6920 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6920 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6920 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM341 precursor RNA and GAM2589 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM341 RNA and GAM2589 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM341 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM341 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM341 target RNA into GAM341 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM2589 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2589 target RNA, herein schematically represented by

GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2589 target RNA into GAM2589 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6920 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6920 gene: GAM341 target protein and GAM2589 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM341 and GAM2589

GR6921 AA071432 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6921 (GR6921) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6921 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6921 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6921 gene encodes GR6921 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6921 precursor RNA folds spatially, forming GR6921 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6921 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6921 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6921 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM42143 precursor RNA and GAM290407 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM42143 RNA and GAM290407 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding

to GAM RNA of Fig. 8.

GAM42143 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM42143 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM42143 target RNA into GAM42143 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM290407 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM290407 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM290407 target RNA into GAM290407 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6921 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6921 gene: GAM42143 target protein and GAM290407 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM42143 and GAM290407

GR6922 AI097493 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6922(GR6922) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6922 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6922 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6922 gene encodes GR6922 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6922 precursor RNA folds spatially, forming GR6922 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6922 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6922 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR6922 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4585 precursor RNA and GAM8063 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4585 RNA and GAM8063 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4585 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4585 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4585 target RNA into GAM4585 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8063 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8063 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8063 target RNA into GAM8063 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6922 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6922 gene: GAM4585 target protein and GAM8063 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4585 and GAM8063

GR6923 BF222075 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6923(GR6923) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6923 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6923

gene was detected is described hereinabove with reference to Figs. 8-18.

GR6923 gene encodes GR6923 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6923 precursor RNA folds spatially, forming GR6923 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6923 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6923 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6923 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM824 precursor RNA and GAM7819 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM824 RNA and GAM7819 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM824 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM824 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM824 target RNA into GAM824 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7819 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7819 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7819 target RNA into GAM7819 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6923 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6923 gene: GAM824 target protein and GAM7819 target protein, herein schematically represented by GAM1

TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM824 and GAM7819

GR6924 R87800 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6924(GR6924) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6924 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6924 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6924 gene encodes GR6924 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6924 precursor RNA folds spatially, forming GR6924 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6924 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6924 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6924 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3598 precursor RNA and GAM267828 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3598 RNA and GAM267828 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3598 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3598 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3598 target RNA into GAM3598 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM267828 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM267828 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM267828 target RNA into GAM267828 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6924 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6924 gene: GAM3598 target protein and GAM267828 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3598 and GAM267828

GR6925 BG828624 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6925(GR6925) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6925 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6925 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6925 gene encodes GR6925 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6925 precursor RNA folds spatially, forming GR6925 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6925 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6925 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6925 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM7418 precursor RNA, GAM70134 precursor RNA, GAM110481 precursor RNA and GAM277308 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7418 RNA, GAM70134 RNA, GAM110481 RNA and GAM277308 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7418 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7418 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7418 target RNA into GAM7418 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM70134 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM70134 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM70134 target RNA into GAM70134 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM110481 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM110481 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM110481 target RNA into GAM110481 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM277308 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM277308 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM277308 target RNA into GAM277308 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6925 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6925 gene: GAM7418 target protein, GAM70134 target protein, GAM110481 target protein and GAM277308 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7418, GAM70134, GAM110481 and GAM277308

6926(GR6926) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6926 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6926 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6926 gene encodes GR6926 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6926 precursor RNA folds spatially, forming GR6926 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6926 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6926 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6926 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM98396 precursor RNA, GAM129068 precursor RNA, GAM225254 precursor RNA and GAM241667 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM98396 RNA, GAM129068 RNA, GAM225254 RNA and GAM241667 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM98396 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM98396 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM98396 target RNA into GAM98396 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM129068 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM129068 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM129068

target RNA into GAM129068 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM225254 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM225254 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM225254 target RNA into GAM225254 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM241667 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM241667 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM241667 target RNA into GAM241667 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6926 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6926 gene: GAM98396 target protein, GAM129068 target protein, GAM225254 target protein and GAM241667 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM98396, GAM129068, GAM225254 and GAM241667

GR6927 BG257649 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6927(GR6927) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6927 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6927 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6927 gene encodes GR6927 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6927 precursor RNA folds spatially, forming GR6927 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6927 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6927 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6927 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5189 precursor RNA and GAM7195 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5189 RNA and GAM7195 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5189 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5189 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5189 target RNA into GAM5189 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7195 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7195 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7195 target RNA into GAM7195 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6927 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6927 gene: GAM5189 target protein and GAM7195 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5189 and GAM7195

GR6928 BF815530 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6928(GR6928) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6928 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR6928 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6928 gene encodes GR6928 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6928 precursor RNA folds spatially, forming GR6928 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6928 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6928 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6928 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM277581 precursor RNA and GAM303679 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM277581 RNA and GAM303679 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM277581 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM277581 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM277581 target RNA into GAM277581 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM303679 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM303679 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM303679 target RNA into GAM303679 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6928 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6928 gene: GAM277581 target

protein and GAM303679 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM277581 and GAM303679

GR6929 AW816010 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6929 (GR6929) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6929 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6929 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6929 gene encodes GR6929 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6929 precursor RNA folds spatially, forming GR6929 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6929 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6929 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6929 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM47295 precursor RNA and GAM139959 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM47295 RNA and GAM139959 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM47295 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM47295 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM47295 target RNA into GAM47295 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM139959 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM139959 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM139959 target RNA into GAM139959 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6929 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6929 gene: GAM47295 target protein and GAM139959 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM47295 and GAM139959

GR6930 BI869320 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6930(GR6930) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6930 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6930 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6930 gene encodes GR6930 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6930 precursor RNA folds spatially, forming GR6930 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6930 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6930 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6930 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6810 precursor RNA and GAM102172 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6810 RNA and GAM102172 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6810 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6810 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6810 target RNA into GAM6810 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM102172 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM102172 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM102172 target RNA into GAM102172 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6930 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6930 gene: GAM6810 target protein and GAM102172 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6810 and GAM102172

GR6931 AA419619 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6931 (GR6931) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6931 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6931 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6931 gene encodes GR6931 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6931 precursor RNA folds spatially, forming GR6931 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6931 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR6931 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6931 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5002 precursor RNA and GAM103697 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5002 RNA and GAM103697 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5002 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5002 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5002 target RNA into GAM5002 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM103697 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM103697 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM103697 target RNA into GAM103697 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6931 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6931 gene: GAM5002 target protein and GAM103697 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5002 and GAM103697

GR6932 BQ064096 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6932(GR6932) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6932 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6932 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6932 gene encodes GR6932 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6932 precursor RNA folds spatially, forming GR6932 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6932 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6932 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6932 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM2946 precursor RNA, GAM61634 precursor RNA, GAM71688 precursor RNA and GAM247044 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2946 RNA, GAM61634 RNA, GAM71688 RNA and GAM247044 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2946 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2946 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2946 target RNA into GAM2946 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM61634 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM61634 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM61634 target RNA into GAM61634 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM71688 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM71688 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM71688 target RNA into GAM71688 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM247044 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM247044 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM247044 target RNA into GAM247044 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6932 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6932 gene: GAM2946 target protein, GAM61634 target protein, GAM71688 target protein and GAM247044 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2946, GAM61634, GAM71688 and GAM247044

GR6933 BE833903 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6933(GR6933) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6933 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6933 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6933 gene encodes GR6933 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6933 precursor RNA folds spatially, forming GR6933 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6933 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6933 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6933 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM29797 precursor RNA and GAM331299 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM29797 RNA and GAM331299 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM29797 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM29797 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM29797 target RNA into GAM29797 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM331299 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM331299 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM331299 target RNA into GAM331299 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6933 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6933 gene: GAM29797 target protein and GAM331299 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM29797 and GAM331299

GR6934 AA732393 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6934(GR6934) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6934 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6934 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6934 gene encodes GR6934 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6934 precursor RNA folds spatially, forming GR6934 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6934 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6934 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6934 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM888 precursor RNA and GAM140680 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM888 RNA and GAM140680 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM888 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM888 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM888 target RNA into GAM888 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM140680 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM140680 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM140680 target RNA into GAM140680 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6934 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6934 gene: GAM888 target protein and GAM140680 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM888 and GAM140680

GR6935 BG530050 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6935(GR6935) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6935 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6935 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6935 gene encodes GR6935 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6935 precursor RNA folds spatially, forming GR6935 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6935 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6935 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6935 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM58577 precursor RNA and GAM286452 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM58577 RNA and GAM286452 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM58577 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM58577 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM58577 target RNA into GAM58577 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM286452 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM286452 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM286452 target RNA into GAM286452 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6935 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6935 gene: GAM58577 target protein and GAM286452 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM58577 and GAM286452

GR6936 BI549105 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6936(GR6936) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6936 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6936 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6936 gene encodes GR6936 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6936 precursor RNA folds spatially, forming GR6936 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6936 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6936 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6936 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM84954 precursor RNA and GAM108299 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM84954 RNA and GAM108299 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM84954 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM84954 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM84954 target RNA into GAM84954 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM108299 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM108299 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM108299 target RNA into GAM108299 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6936 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6936 gene: GAM84954 target protein and GAM108299 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM84954 and GAM108299

GR6937 BM924549 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6937(GR6937) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6937 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6937 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6937 gene encodes GR6937 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6937 precursor RNA folds spatially, forming GR6937 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6937 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6937 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6937 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM763 precursor RNA and GAM208453 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM763 RNA and GAM208453 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM763 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM763 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM763 target RNA into GAM763 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM208453 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM208453 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM208453 target RNA into GAM208453 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6937 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6937 gene: GAM763 target protein and GAM208453 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM763 and GAM208453

GR6938 BG474695 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6938(GR6938) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6938 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6938 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6938 gene encodes GR6938 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6938 precursor RNA folds spatially, forming GR6938 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6938 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6938 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6938 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4610 precursor RNA and GAM42749 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4610 RNA and GAM42749 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4610 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4610 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4610 target RNA into GAM4610 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM42749 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM42749 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM42749 target RNA into GAM42749 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6938 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6938 gene: GAM4610 target protein and GAM42749 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes

is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4610 and GAM42749

GR6939 AW378245 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6939 (GR6939) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6939 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6939 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6939 gene encodes GR6939 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6939 precursor RNA folds spatially, forming GR6939 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6939 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6939 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6939 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM775 precursor RNA and GAM76246 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM775 RNA and GAM76246 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM775 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM775 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM775 target RNA into GAM775 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM76246 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM76246 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM76246 target RNA into GAM76246 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6939 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6939 gene: GAM775 target protein and GAM76246 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM775 and GAM76246

GR6940 AI147314 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6940 (GR6940) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6940 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6940 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6940 gene encodes GR6940 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6940 precursor RNA folds spatially, forming GR6940 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6940 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6940 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6940 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4259 precursor RNA and GAM178235 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4259 RNA and GAM178235 RNA, herein schematically

represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4259 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4259 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4259 target RNA into GAM4259 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM178235 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM178235 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM178235 target RNA into GAM178235 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6940 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6940 gene: GAM4259 target protein and GAM178235 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4259 and GAM178235

GR6941 BF361427 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6941 (GR6941) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6941 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6941 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6941 gene encodes GR6941 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6941 precursor RNA folds spatially, forming GR6941 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6941 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6941 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6941 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM56785 precursor RNA and GAM302894 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM56785 RNA and GAM302894 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM56785 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM56785 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM56785 target RNA into GAM56785 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM302894 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM302894 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM302894 target RNA into GAM302894 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6941 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6941 gene: GAM56785 target protein and GAM302894 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM56785 and GAM302894

GR6942 BG617507 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6942(GR6942) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6942 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR6942 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6942 gene encodes GR6942 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6942 precursor RNA folds spatially, forming GR6942 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6942 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6942 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6942 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM54041 precursor RNA and GAM118564 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM54041 RNA and GAM118564 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM54041 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM54041 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM54041 target RNA into GAM54041 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM118564 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM118564 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM118564 target RNA into GAM118564 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6942 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6942 gene: GAM54041 target

protein and GAM118564 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM54041 and GAM118564

GR6943 BF672786 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6943(GR6943) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6943 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6943 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6943 gene encodes GR6943 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6943 precursor RNA folds spatially, forming GR6943 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6943 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6943 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6943 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5159 precursor RNA and GAM229118 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5159 RNA and GAM229118 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5159 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5159 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5159 target RNA into GAM5159 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM229118 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM229118 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM229118 target RNA into GAM229118 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6943 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6943 gene: GAM5159 target protein and GAM229118 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5159 and GAM229118

GR6944 BE270728 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6944(GR6944) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6944 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6944 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6944 gene encodes GR6944 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6944 precursor RNA folds spatially, forming GR6944 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6944 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6944 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6944 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM61248 precursor RNA, GAM257348 precursor RNA and GAM309322 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM61248 RNA, GAM257348 RNA and GAM309322 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM61248 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM61248 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM61248 target RNA into GAM61248 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM257348 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM257348 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM257348 target RNA into GAM257348 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM309322 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM309322 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM309322 target RNA into GAM309322 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6944 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6944 gene: GAM61248 target protein, GAM257348 target protein and GAM309322 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM61248, GAM257348 and GAM309322

GR6945 BF902815 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6945(GR6945) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6945 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6945

gene was detected is described hereinabove with reference to Figs. 8-18.

GR6945 gene encodes GR6945 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6945 precursor RNA folds spatially, forming GR6945 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6945 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6945 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6945 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM43040 precursor RNA, GAM189973 precursor RNA and GAM279375 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM43040 RNA, GAM189973 RNA and GAM279375 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM43040 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM43040 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM43040 target RNA into GAM43040 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM189973 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM189973 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM189973 target RNA into GAM189973 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM279375 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM279375 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM279375 target RNA into GAM279375 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6945 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6945 gene: GAM43040 target protein, GAM189973 target protein and GAM279375 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM43040, GAM189973 and GAM279375

GR6946 AA115976 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6946(GR6946) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6946 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6946 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6946 gene encodes GR6946 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6946 precursor RNA folds spatially, forming GR6946 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6946 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6946 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6946 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2414 precursor RNA and GAM229782 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2414 RNA and GAM229782 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2414 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2414 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2414 target RNA into GAM2414 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM229782 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM229782 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM229782 target RNA into GAM229782 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6946 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6946 gene: GAM2414 target protein and GAM229782 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2414 and GAM229782

GR6947 AA291050 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6947(GR6947) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6947 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6947 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6947 gene encodes GR6947 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6947 precursor RNA folds spatially, forming GR6947 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6947 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6947 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6947 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3904 precursor RNA and GAM316201 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3904 RNA and GAM316201 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3904 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3904 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3904 target RNA into GAM3904 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM316201 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM316201 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM316201 target RNA into GAM316201 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6947 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6947 gene: GAM3904 target protein and GAM316201 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3904 and GAM316201

GR6948 BG189591 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6948(GR6948) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6948 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6948 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6948 gene encodes GR6948 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6948 precursor RNA folds spatially, forming GR6948 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6948 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6948 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6948 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM12768 precursor RNA and GAM20225 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM12768 RNA and GAM20225 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM12768 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM12768 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM12768 target RNA into GAM12768 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM20225 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM20225 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM20225 target RNA into GAM20225 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6948 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6948 gene: GAM12768 target protein and GAM20225 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes

is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM12768 and GAM20225

GR6949 AI339683 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6949 (GR6949) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6949 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6949 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6949 gene encodes GR6949 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6949 precursor RNA folds spatially, forming GR6949 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6949 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6949 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6949 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4391 precursor RNA and GAM114107 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4391 RNA and GAM114107 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4391 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4391 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4391 target RNA into GAM4391 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM114107 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM114107 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM114107 target RNA into GAM114107 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6949 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6949 gene: GAM4391 target protein and GAM114107 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4391 and GAM114107

GR6950 AL702674 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6950 (GR6950) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6950 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6950 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6950 gene encodes GR6950 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6950 precursor RNA folds spatially, forming GR6950 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6950 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6950 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6950 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4372 precursor RNA, GAM9191 precursor RNA and GAM38052 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22

nucleotides in length, GAM4372 RNA, GAM9191 RNA and GAM38052 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4372 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4372 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4372 target RNA into GAM4372 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM9191 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM9191 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM9191 target RNA into GAM9191 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM38052 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM38052 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM38052 target RNA into GAM38052 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6950 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6950 gene: GAM4372 target protein, GAM9191 target protein and GAM38052 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4372, GAM9191 and GAM38052

GR6951 BE389823 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6951 (GR6951) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6951 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6951 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6951 gene encodes GR6951 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6951 precursor RNA folds spatially, forming GR6951 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6951 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6951 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6951 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3400 precursor RNA and GAM4242 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3400 RNA and GAM4242 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3400 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3400 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3400 target RNA into GAM3400 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM4242 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4242 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4242 target RNA into GAM4242 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6951 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6951 gene: GAM3400 target protein and GAM4242 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference,

with references to GAM3400 and GAM4242

GR6952 BQ004735 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6952(GR6952) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6952 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6952 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6952 gene encodes GR6952 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6952 precursor RNA folds spatially, forming GR6952 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6952 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6952 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6952 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4540 precursor RNA, GAM119066 precursor RNA and GAM268604 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4540 RNA, GAM119066 RNA and GAM268604 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4540 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4540 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4540 target RNA into GAM4540 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM119066 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM119066 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM119066 target RNA into GAM119066 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM268604 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM268604 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM268604 target RNA into GAM268604 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6952 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6952 gene: GAM4540 target protein, GAM119066 target protein and GAM268604 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4540, GAM119066 and GAM268604

GR6953 AI870599 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6953(GR6953) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6953 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6953 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6953 gene encodes GR6953 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6953 precursor RNA folds spatially, forming GR6953 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6953 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6953 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6953 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM258518 precursor RNA and GAM335073 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM258518 RNA and GAM335073 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM258518 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM258518 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM258518 target RNA into GAM258518 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM335073 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM335073 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM335073 target RNA into GAM335073 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6953 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6953 gene: GAM258518 target protein and GAM335073 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM258518 and GAM335073

GR6954 BE148909 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6954(GR6954) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6954 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6954 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6954 gene encodes GR6954 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6954 precursor RNA folds spatially, forming GR6954 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6954 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6954 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6954 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM6415 precursor RNA, GAM173469 precursor RNA and GAM175880 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6415 RNA, GAM173469 RNA and GAM175880 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6415 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6415 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6415 target RNA into GAM6415 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM173469 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM173469 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM173469 target RNA into GAM173469 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM175880 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM175880 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM175880 target RNA into GAM175880 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6954 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6954 gene: GAM6415 target protein, GAM173469 target protein and GAM175880 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6415, GAM173469 and GAM175880

GR6955 AA824234 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6955(GR6955) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6955 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6955 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6955 gene encodes GR6955 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6955 precursor RNA folds spatially, forming GR6955 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6955 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6955 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6955 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM254667 precursor RNA and GAM292637 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM254667 RNA and GAM292637 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM254667 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM254667 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM254667 target RNA into GAM254667 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM292637 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM292637 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM292637 target RNA into GAM292637 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6955 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6955 gene: GAM254667 target protein and GAM292637 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM254667 and GAM292637

GR6956 AU157455 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6956(GR6956) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6956 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6956 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6956 gene encodes GR6956 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6956 precursor RNA folds spatially, forming GR6956 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6956 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6956 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6956 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2

separate GAM precursor RNAs, GAM52980 precursor RNA and GAM121026 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM52980 RNA and GAM121026 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM52980 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM52980 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM52980 target RNA into GAM52980 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM121026 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM121026 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM121026 target RNA into GAM121026 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6956 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6956 gene: GAM52980 target protein and GAM121026 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM52980 and GAM121026

GR6957 AA614457 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6957(GR6957) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6957 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6957 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6957 gene encodes GR6957 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR6957 precursor RNA folds spatially, forming GR6957 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6957 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6957 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6957 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6663 precursor RNA and GAM213175 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6663 RNA and GAM213175 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6663 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6663 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6663 target RNA into GAM6663 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM213175 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM213175 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM213175 target RNA into GAM213175 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6957 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6957 gene: GAM6663 target protein and GAM213175 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6663 and GAM213175

GR6958 AI671448 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6958(GR6958) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6958 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6958 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6958 gene encodes GR6958 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6958 precursor RNA folds spatially, forming GR6958 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6958 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6958 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6958 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM64158 precursor RNA and GAM336004 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM64158 RNA and GAM336004 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM64158 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM64158 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM64158 target RNA into GAM64158 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336004 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336004 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336004 target RNA into GAM336004 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6958 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6958 gene: GAM64158 target protein and GAM336004 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM64158 and GAM336004

GR6959 BI763889 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6959 (GR6959) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6959 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6959 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6959 gene encodes GR6959 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6959 precursor RNA folds spatially, forming GR6959 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6959 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6959 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6959 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8055 precursor RNA and GAM101166 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8055 RNA and GAM101166 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8055 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8055 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8055 target RNA into GAM8055 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM101166 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM101166 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM101166 target RNA into GAM101166 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6959 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6959 gene: GAM8055 target protein and GAM101166 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8055 and GAM101166

GR6960 AI720440 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6960 (GR6960) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6960 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6960 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6960 gene encodes GR6960 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6960 precursor RNA folds spatially, forming GR6960 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6960 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6960 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6960 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1242 precursor RNA and GAM296030 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1242 RNA and GAM296030 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1242 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1242 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1242 target RNA into GAM1242 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM296030 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM296030 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM296030 target RNA into GAM296030 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6960 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6960 gene: GAM1242 target protein and GAM296030 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1242 and GAM296030

GR6961 BM017180 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6961 (GR6961) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6961 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6961 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6961 gene encodes GR6961 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6961 precursor RNA folds spatially, forming GR6961 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6961 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6961 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6961 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3076 precursor RNA and GAM209750 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3076 RNA and GAM209750 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3076 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3076 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3076 target RNA into GAM3076 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM209750 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM209750 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM209750 target RNA into GAM209750 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6961 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6961 gene: GAM3076 target protein and GAM209750 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference,

with references to GAM3076 and GAM209750

GR6962 AA086281 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6962(GR6962) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6962 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6962 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6962 gene encodes GR6962 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6962 precursor RNA folds spatially, forming GR6962 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6962 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6962 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6962 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM179114 precursor RNA and GAM321416 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM179114 RNA and GAM321416 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM179114 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM179114 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM179114 target RNA into GAM179114 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM321416 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM321416 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM321416 target RNA into GAM321416 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6962 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6962 gene: GAM179114 target protein and GAM321416 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM179114 and GAM321416

GR6963 AI014658 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6963(GR6963) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6963 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6963 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6963 gene encodes GR6963 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6963 precursor RNA folds spatially, forming GR6963 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6963 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6963 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6963 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM77882 precursor RNA and GAM79962 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM77882 RNA and GAM79962 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding

to GAM RNA of Fig. 8.

GAM77882 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM77882 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM77882 target RNA into GAM77882 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM79962 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM79962 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM79962 target RNA into GAM79962 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6963 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6963 gene: GAM77882 target protein and GAM79962 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM77882 and GAM79962

GR6964 AW590940 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6964(GR6964) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6964 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6964 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6964 gene encodes GR6964 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6964 precursor RNA folds spatially, forming GR6964 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6964 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6964 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR6964 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM89868 precursor RNA and GAM236303 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM89868 RNA and GAM236303 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM89868 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM89868 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM89868 target RNA into GAM89868 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM236303 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM236303 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM236303 target RNA into GAM236303 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6964 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6964 gene: GAM89868 target protein and GAM236303 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM89868 and GAM236303

GR6965 AI436603 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6965(GR6965) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6965 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6965

gene was detected is described hereinabove with reference to Figs. 8-18.

GR6965 gene encodes GR6965 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6965 precursor RNA folds spatially, forming GR6965 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6965 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6965 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6965 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM142112 precursor RNA and GAM333145 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM142112 RNA and GAM333145 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM142112 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM142112 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM142112 target RNA into GAM142112 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM333145 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM333145 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM333145 target RNA into GAM333145 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6965 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6965 gene: GAM142112 target protein and GAM333145 target protein, herein schematically represented by GAM1

TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM142112 and GAM333145

GR6966 AW964303 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6966(GR6966) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6966 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6966 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6966 gene encodes GR6966 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6966 precursor RNA folds spatially, forming GR6966 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6966 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6966 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6966 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM997 precursor RNA, GAM28001 precursor RNA and GAM336063 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM997 RNA, GAM28001 RNA and GAM336063 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM997 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM997 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM997 target RNA into GAM997 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM28001 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM28001 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM28001 target RNA into GAM28001 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336063 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336063 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336063 target RNA into GAM336063 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6966 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6966 gene: GAM997 target protein, GAM28001 target protein and GAM336063 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM997, GAM28001 and GAM336063

GR6967 BG717457 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6967(GR6967) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6967 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6967 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6967 gene encodes GR6967 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6967 precursor RNA folds spatially, forming GR6967 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6967 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6967 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6967 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3159 precursor RNA, GAM5369 precursor RNA and GAM5804 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3159 RNA, GAM5369 RNA and GAM5804 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3159 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3159 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3159 target RNA into GAM3159 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5369 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5369 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5369 target RNA into GAM5369 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5804 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5804 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5804 target RNA into GAM5804 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6967 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6967 gene: GAM3159 target protein, GAM5369 target protein and GAM5804 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3159, GAM5369 and GAM5804

GR6968 BF979532 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6968(GR6968) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6968 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6968 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6968 gene encodes GR6968 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6968 precursor RNA folds spatially, forming GR6968 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6968 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6968 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6968 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM64978 precursor RNA, GAM278283 precursor RNA and GAM293726 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM64978 RNA, GAM278283 RNA and GAM293726 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM64978 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM64978 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM64978 target RNA into GAM64978 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM278283 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM278283 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM278283 target RNA into GAM278283 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM293726 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM293726 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM293726 target RNA into GAM293726 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6968 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6968 gene: GAM64978 target protein, GAM278283 target protein and GAM293726 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM64978, GAM278283 and GAM293726

GR6969 AW007188 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6969(GR6969) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6969 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6969 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6969 gene encodes GR6969 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6969 precursor RNA folds spatially, forming GR6969 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6969 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6969 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6969 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7354 precursor RNA and GAM129867 precursor

RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7354 RNA and GAM129867 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7354 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7354 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7354 target RNA into GAM7354 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM129867 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM129867 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM129867 target RNA into GAM129867 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6969 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6969 gene: GAM7354 target protein and GAM129867 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7354 and GAM129867

GR6970 BF344666 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6970 (GR6970) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6970 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6970 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6970 gene encodes GR6970 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6970 precursor RNA folds spatially, forming GR6970 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6970 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6970 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6970 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM33213 precursor RNA and GAM97660 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM33213 RNA and GAM97660 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM33213 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM33213 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM33213 target RNA into GAM33213 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM97660 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM97660 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM97660 target RNA into GAM97660 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6970 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6970 gene: GAM33213 target protein and GAM97660 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM33213 and GAM97660

bioinformatically detected regulatory gene, referred to here as Genomic Record 6971 (GR6971) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6971 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6971 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6971 gene encodes GR6971 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6971 precursor RNA folds spatially, forming GR6971 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6971 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6971 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6971 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM55312 precursor RNA and GAM95095 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM55312 RNA and GAM95095 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM55312 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM55312 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM55312 target RNA into GAM55312 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM95095 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM95095 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM95095

target RNA into GAM95095 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6971 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6971 gene: GAM55312 target protein and GAM95095 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM55312 and GAM95095

GR6972 BG505490 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6972(GR6972) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6972 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6972 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6972 gene encodes GR6972 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6972 precursor RNA folds spatially, forming GR6972 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6972 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6972 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6972 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM162347 precursor RNA and GAM234484 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM162347 RNA and GAM234484 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM162347 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM162347 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM162347 target RNA into GAM162347 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM234484 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM234484 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM234484 target RNA into GAM234484 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6972 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6972 gene: GAM162347 target protein and GAM234484 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM162347 and GAM234484

GR6973 AU143982 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6973(GR6973) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6973 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6973 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6973 gene encodes GR6973 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6973 precursor RNA folds spatially, forming GR6973 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6973 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6973 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6973 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM57414 precursor RNA and GAM212670 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM57414 RNA and GAM212670 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM57414 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM57414 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM57414 target RNA into GAM57414 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM212670 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM212670 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM212670 target RNA into GAM212670 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6973 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6973 gene: GAM57414 target protein and GAM212670 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM57414 and GAM212670

GR6974 H14593 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6974(GR6974) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6974 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6974 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6974 gene encodes GR6974 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6974 precursor RNA folds spatially, forming GR6974 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6974 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6974 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6974 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM92559 precursor RNA and GAM215976 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM92559 RNA and GAM215976 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM92559 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM92559 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM92559 target RNA into GAM92559 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM215976 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM215976 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM215976 target RNA into GAM215976 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6974 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6974 gene: GAM92559 target protein and GAM215976 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM92559 and GAM215976

GR6975 BG106301 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6975(GR6975) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6975 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6975 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6975 gene encodes GR6975 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6975 precursor RNA folds spatially, forming GR6975 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6975 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6975 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6975 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4488 precursor RNA, GAM123841 precursor RNA and GAM168833 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4488 RNA, GAM123841 RNA and GAM168833 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4488 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4488 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4488 target RNA into GAM4488 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM123841 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM123841 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM123841 target RNA into GAM123841 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM168833 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM168833 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM168833 target RNA into GAM168833 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6975 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6975 gene: GAM4488 target protein, GAM123841 target protein and GAM168833 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4488, GAM123841 and GAM168833

GR6976 BM475051 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6976(GR6976) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6976 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6976 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6976 gene encodes GR6976 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6976 precursor RNA folds spatially, forming GR6976 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6976 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6976 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6976 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4

separate GAM precursor RNAs, GAM2836 precursor RNA, GAM49651 precursor RNA, GAM59993 precursor RNA and GAM126273 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2836 RNA, GAM49651 RNA, GAM59993 RNA and GAM126273 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2836 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2836 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2836 target RNA into GAM2836 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM49651 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM49651 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM49651 target RNA into GAM49651 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM59993 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM59993 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM59993 target RNA into GAM59993 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM126273 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM126273 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM126273 target RNA into GAM126273 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6976 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6976 gene: GAM2836 target protein, GAM49651 target protein, GAM59993 target protein and GAM126273 target

protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2836, GAM49651, GAM59993 and GAM126273

GR6977 BG251024 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6977(GR6977) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6977 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6977 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6977 gene encodes GR6977 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6977 precursor RNA folds spatially, forming GR6977 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6977 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6977 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6977 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7324 precursor RNA and GAM284056 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7324 RNA and GAM284056 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7324 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7324 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7324 target RNA into GAM7324 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM284056 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM284056 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM284056 target RNA into GAM284056 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6977 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6977 gene: GAM7324 target protein and GAM284056 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7324 and GAM284056

GR6978 BG707890 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6978(GR6978) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6978 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6978 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6978 gene encodes GR6978 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6978 precursor RNA folds spatially, forming GR6978 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6978 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6978 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6978 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM190484 precursor RNA and GAM233774 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM190484 RNA and GAM233774 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM190484 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM190484 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM190484 target RNA into GAM190484 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM233774 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM233774 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM233774 target RNA into GAM233774 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6978 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6978 gene: GAM190484 target protein and GAM233774 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM190484 and GAM233774

GR6979 BF974781 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6979(GR6979) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6979 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6979 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6979 gene encodes GR6979 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6979 precursor RNA folds spatially, forming GR6979 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6979 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR6979 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6979 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5432 precursor RNA and GAM318039 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5432 RNA and GAM318039 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5432 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5432 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5432 target RNA into GAM5432 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM318039 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM318039 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM318039 target RNA into GAM318039 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6979 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6979 gene: GAM5432 target protein and GAM318039 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5432 and GAM318039

GR6980 BI545524 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6980 (GR6980) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6980 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6980 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6980 gene encodes GR6980 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6980 precursor RNA folds spatially, forming GR6980 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6980 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6980 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6980 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM103 precursor RNA and GAM2752 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM103 RNA and GAM2752 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM103 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM103 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM103 target RNA into GAM103 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM2752 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2752 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2752 target RNA into GAM2752 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6980 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6980 gene: GAM103 target protein and GAM2752 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM103 and GAM2752

GR6981 T23837 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6981 (GR6981) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6981 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6981 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6981 gene encodes GR6981 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6981 precursor RNA folds spatially, forming GR6981 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6981 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6981 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6981 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3361 precursor RNA, GAM6750 precursor RNA and GAM274327 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3361 RNA, GAM6750 RNA and GAM274327 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3361 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3361 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig. 8, thereby inhibiting translation of GAM3361 target RNA into GAM3361 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6750 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6750 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6750 target RNA into GAM6750 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM274327 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM274327 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM274327 target RNA into GAM274327 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6981 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6981 gene: GAM3361 target protein, GAM6750 target protein and GAM274327 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3361, GAM6750 and GAM274327

GR6982 BI086180 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6982(GR6982) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6982 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6982 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6982 gene encodes GR6982 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6982 precursor RNA folds spatially, forming GR6982 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6982 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6982 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6982 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM46863 precursor RNA and GAM257757 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM46863 RNA and GAM257757 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM46863 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM46863 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM46863 target RNA into GAM46863 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM257757 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM257757 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM257757 target RNA into GAM257757 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6982 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6982 gene: GAM46863 target protein and GAM257757 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM46863 and GAM257757

GR6983 BF515184 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6983(GR6983) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6983 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6983 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6983 gene encodes GR6983 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6983 precursor RNA folds spatially, forming GR6983 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6983 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6983 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6983 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM94275 precursor RNA and GAM299453 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM94275 RNA and GAM299453 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM94275 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM94275 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM94275 target RNA into GAM94275 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM299453 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM299453 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM299453 target RNA into GAM299453 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6983 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR6983 gene: GAM94275 target protein and GAM299453 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM94275 and GAM299453

GR6984 BG611874 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6984(GR6984) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6984 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6984 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6984 gene encodes GR6984 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6984 precursor RNA folds spatially, forming GR6984 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6984 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6984 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6984 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM48415 precursor RNA, GAM99972 precursor RNA and GAM107333 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM48415 RNA, GAM99972 RNA and GAM107333 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM48415 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM48415 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM48415

target RNA into GAM48415 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM99972 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM99972 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM99972 target RNA into GAM99972 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM107333 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM107333 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM107333 target RNA into GAM107333 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6984 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6984 gene: GAM48415 target protein, GAM99972 target protein and GAM107333 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM48415, GAM99972 and GAM107333

GR6985 W40533 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6985(GR6985) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6985 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6985 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6985 gene encodes GR6985 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6985 precursor RNA folds spatially, forming GR6985 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6985 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6985 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6985 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3130 precursor RNA and GAM144149 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3130 RNA and GAM144149 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3130 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3130 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3130 target RNA into GAM3130 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM144149 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM144149 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM144149 target RNA into GAM144149 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6985 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6985 gene: GAM3130 target protein and GAM144149 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3130 and GAM144149

GR6986 AI302218 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6986(GR6986) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6986 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR6986 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6986 gene encodes GR6986 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6986 precursor RNA folds spatially, forming GR6986 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6986 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6986 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6986 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM145627 precursor RNA and GAM186528 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM145627 RNA and GAM186528 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM145627 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM145627 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM145627 target RNA into GAM145627 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM186528 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM186528 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM186528 target RNA into GAM186528 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6986 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6986 gene: GAM145627 target

protein and GAM186528 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM145627 and GAM186528

GR6987 BF695973 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6987(GR6987) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6987 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6987 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6987 gene encodes GR6987 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6987 precursor RNA folds spatially, forming GR6987 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6987 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6987 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6987 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM7399 precursor RNA, GAM7891 precursor RNA and GAM206131 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7399 RNA, GAM7891 RNA and GAM206131 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7399 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7399 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7399 target RNA into GAM7399 target protein, herein schematically represented by GAM1 TARGET

PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7891 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7891 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7891 target RNA into GAM7891 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM206131 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM206131 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM206131 target RNA into GAM206131 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6987 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6987 gene: GAM7399 target protein, GAM7891 target protein and GAM206131 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7399, GAM7891 and GAM206131

GR6988 AI651546 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6988(GR6988) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6988 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6988 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6988 gene encodes GR6988 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6988 precursor RNA folds spatially, forming GR6988 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6988 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6988 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR6988 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3056 precursor RNA and GAM151148 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3056 RNA and GAM151148 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3056 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3056 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3056 target RNA into GAM3056 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM151148 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM151148 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM151148 target RNA into GAM151148 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6988 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6988 gene: GAM3056 target protein and GAM151148 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3056 and GAM151148

GR6989 BG469952 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6989(GR6989) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6989 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6989

gene was detected is described hereinabove with reference to Figs. 8-18.

GR6989 gene encodes GR6989 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6989 precursor RNA folds spatially, forming GR6989 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6989 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6989 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6989 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3903 precursor RNA, GAM127962 precursor RNA and GAM300979 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3903 RNA, GAM127962 RNA and GAM300979 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3903 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3903 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3903 target RNA into GAM3903 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM127962 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM127962 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM127962 target RNA into GAM127962 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM300979 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM300979 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM300979 target RNA into GAM300979 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6989 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6989 gene: GAM3903 target protein, GAM127962 target protein and GAM300979 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3903, GAM127962 and GAM300979

GR6990 BF892032 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6990 (GR6990) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6990 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6990 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6990 gene encodes GR6990 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6990 precursor RNA folds spatially, forming GR6990 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6990 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6990 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6990 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM242365 precursor RNA and GAM333483 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM242365 RNA and GAM333483 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM242365 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM242365 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM242365 target RNA into GAM242365 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM333483 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM333483 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM333483 target RNA into GAM333483 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6990 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6990 gene: GAM242365 target protein and GAM333483 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM242365 and GAM333483

GR6991 AI859998 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6991 (GR6991) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6991 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6991 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6991 gene encodes GR6991 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6991 precursor RNA folds spatially, forming GR6991 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6991 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6991 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6991 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5901 precursor RNA and GAM188882 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5901 RNA and GAM188882 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5901 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5901 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5901 target RNA into GAM5901 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM188882 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM188882 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM188882 target RNA into GAM188882 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6991 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6991 gene: GAM5901 target protein and GAM188882 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5901 and GAM188882

GR6992 BG954492 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6992(GR6992) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6992 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6992 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6992 gene encodes GR6992 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6992 precursor RNA folds spatially, forming GR6992 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6992 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6992 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6992 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM111266 precursor RNA and GAM293026 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM111266 RNA and GAM293026 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM111266 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM111266 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM111266 target RNA into GAM111266 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM293026 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM293026 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM293026 target RNA into GAM293026 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6992 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6992 gene: GAM111266 target protein and GAM293026 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes

is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM111266 and GAM293026

GR6993 BM683732 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6993 (GR6993) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6993 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6993 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6993 gene encodes GR6993 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6993 precursor RNA folds spatially, forming GR6993 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6993 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6993 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6993 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM124340 precursor RNA and GAM285100 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM124340 RNA and GAM285100 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM124340 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM124340 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM124340 target RNA into GAM124340 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM285100 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM285100 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM285100 target RNA into GAM285100 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6993 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6993 gene: GAM124340 target protein and GAM285100 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM124340 and GAM285100

GR6994 AW572080 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6994(GR6994) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6994 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6994 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6994 gene encodes GR6994 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6994 precursor RNA folds spatially, forming GR6994 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6994 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6994 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6994 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4797 precursor RNA and GAM321616 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4797 RNA and GAM321616 RNA, herein schematically

represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4797 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4797 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4797 target RNA into GAM4797 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM321616 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM321616 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM321616 target RNA into GAM321616 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6994 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6994 gene: GAM4797 target protein and GAM321616 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4797 and GAM321616

GR6995 AA835332 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6995(GR6995) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6995 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6995 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6995 gene encodes GR6995 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6995 precursor RNA folds spatially, forming GR6995 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6995 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6995 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6995 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4370 precursor RNA and GAM49093 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4370 RNA and GAM49093 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4370 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4370 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4370 target RNA into GAM4370 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM49093 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM49093 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM49093 target RNA into GAM49093 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6995 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6995 gene: GAM4370 target protein and GAM49093 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4370 and GAM49093

GR6996 BF799289 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6996 (GR6996) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6996 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR6996 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6996 gene encodes GR6996 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6996 precursor RNA folds spatially, forming GR6996 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6996 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6996 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6996 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1913 precursor RNA and GAM7947 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1913 RNA and GAM7947 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1913 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1913 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1913 target RNA into GAM1913 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7947 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7947 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7947 target RNA into GAM7947 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6996 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6996 gene: GAM1913 target

protein and GAM7947 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1913 and GAM7947

GR6997 AV723213 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6997 (GR6997) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6997 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6997 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6997 gene encodes GR6997 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6997 precursor RNA folds spatially, forming GR6997 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6997 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6997 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6997 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4268 precursor RNA, GAM24005 precursor RNA and GAM329814 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4268 RNA, GAM24005 RNA and GAM329814 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4268 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4268 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4268 target RNA into GAM4268 target protein, herein schematically represented by GAM1 TARGET

PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM24005 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM24005 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM24005 target RNA into GAM24005 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM329814 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM329814 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM329814 target RNA into GAM329814 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6997 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6997 gene: GAM4268 target protein, GAM24005 target protein and GAM329814 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4268, GAM24005 and GAM329814

GR6998 BE961636 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6998(GR6998) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6998 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6998 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6998 gene encodes GR6998 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6998 precursor RNA folds spatially, forming GR6998 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6998 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6998 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR6998 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM909 precursor RNA, GAM22482 precursor RNA, GAM123204 precursor RNA and GAM277689 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM909 RNA, GAM22482 RNA, GAM123204 RNA and GAM277689 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM909 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM909 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM909 target RNA into GAM909 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM22482 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM22482 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM22482 target RNA into GAM22482 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM123204 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM123204 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM123204 target RNA into GAM123204 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM277689 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM277689 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM277689 target RNA into GAM277689 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly

utilities, of GR6998 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6998 gene: GAM909 target protein, GAM22482 target protein, GAM123204 target protein and GAM277689 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM909, GAM22482, GAM123204 and GAM277689

GR6999 AA256391 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 6999(GR6999) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR6999 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR6999 gene was detected is described hereinabove with reference to Figs. 8-18.

GR6999 gene encodes GR6999 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR6999 precursor RNA folds spatially, forming GR6999 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR6999 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR6999 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR6999 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM48361 precursor RNA and GAM69749 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM48361 RNA and GAM69749 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM48361 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM48361 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM48361 target RNA into GAM48361 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM69749 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM69749 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM69749 target RNA into GAM69749 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR6999 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR6999 gene: GAM48361 target protein and GAM69749 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM48361 and GAM69749

GR7000 BM806950 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7000(GR7000) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7000 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7000 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7000 gene encodes GR7000 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7000 precursor RNA folds spatially, forming GR7000 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7000 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7000 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7000 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3689 precursor RNA, GAM8051 precursor RNA and GAM189341 precursor RNA, herein schematically represented by GAM1 FOLDED

PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3689 RNA, GAM8051 RNA and GAM189341 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3689 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3689 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3689 target RNA into GAM3689 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8051 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8051 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8051 target RNA into GAM8051 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM189341 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM189341 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM189341 target RNA into GAM189341 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7000 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7000 gene: GAM3689 target protein, GAM8051 target protein and GAM189341 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3689, GAM8051 and GAM189341

GR7001 BI261420 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7001(GR7001) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR7001 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7001 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7001 gene encodes GR7001 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7001 precursor RNA folds spatially, forming GR7001 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7001 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7001 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7001 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM31645 precursor RNA and GAM68194 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM31645 RNA and GAM68194 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM31645 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM31645 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM31645 target RNA into GAM31645 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM68194 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM68194 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM68194 target RNA into GAM68194 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly

utilities, of GR7001 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7001 gene: GAM31645 target protein and GAM68194 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM31645 and GAM68194

GR7002 BG391103 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7002(GR7002) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7002 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7002 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7002 gene encodes GR7002 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7002 precursor RNA folds spatially, forming GR7002 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7002 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7002 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7002 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM334 precursor RNA, GAM128356 precursor RNA, GAM172819 precursor RNA and GAM217993 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM334 RNA, GAM128356 RNA, GAM172819 RNA and GAM217993 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM334 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM334 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds

to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM334 target RNA into GAM334 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM128356 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM128356 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM128356 target RNA into GAM128356 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM172819 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM172819 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM172819 target RNA into GAM172819 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM217993 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM217993 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM217993 target RNA into GAM217993 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7002 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7002 gene: GAM334 target protein, GAM128356 target protein, GAM172819 target protein and GAM217993 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM334, GAM128356, GAM172819 and GAM217993

GR7003 BM984154 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7003(GR7003) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7003 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7003 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7003 gene encodes GR7003 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7003 precursor RNA folds spatially, forming GR7003 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7003 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7003 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7003 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM429 precursor RNA, GAM154964 precursor RNA, GAM169523 precursor RNA and GAM187420 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM429 RNA, GAM154964 RNA, GAM169523 RNA and GAM187420 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM429 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM429 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM429 target RNA into GAM429 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM154964 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM154964 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM154964 target RNA into GAM154964 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM169523 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM169523 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM169523 target RNA into GAM169523 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM187420 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM187420 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM187420 target RNA into GAM187420 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7003 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7003 gene: GAM429 target protein, GAM154964 target protein, GAM169523 target protein and GAM187420 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM429, GAM154964, GAM169523 and GAM187420

GR7004 BF092760 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7004(GR7004) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7004 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7004 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7004 gene encodes GR7004 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7004 precursor RNA folds spatially, forming GR7004 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7004 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7004 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7004 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2773 precursor RNA, GAM19367 precursor RNA and GAM263974 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED

PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2773 RNA, GAM19367 RNA and GAM263974 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2773 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2773 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2773 target RNA into GAM2773 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM19367 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM19367 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM19367 target RNA into GAM19367 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM263974 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM263974 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM263974 target RNA into GAM263974 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7004 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7004 gene: GAM2773 target protein, GAM19367 target protein and GAM263974 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2773, GAM19367 and GAM263974

GR7005 AW451812 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7005(GR7005) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7005 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7005 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7005 gene encodes GR7005 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7005 precursor RNA folds spatially, forming GR7005 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7005 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7005 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7005 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2649 precursor RNA, GAM108609 precursor RNA and GAM147217 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2649 RNA, GAM108609 RNA and GAM147217 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2649 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2649 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2649 target RNA into GAM2649 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM108609 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM108609 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM108609 target RNA into GAM108609 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM147217 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM147217 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM147217 target RNA into GAM147217 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7005 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7005 gene: GAM2649 target protein, GAM108609 target protein and GAM147217 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2649, GAM108609 and GAM147217

GR7006 BI254443 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7006(GR7006) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7006 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7006 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7006 gene encodes GR7006 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7006 precursor RNA folds spatially, forming GR7006 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7006 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7006 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7006 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM709 precursor RNA, GAM1711 precursor RNA and GAM3867 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM709 RNA, GAM1711 RNA and GAM3867 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM709 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM709 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM709 target RNA into GAM709 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM1711 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1711 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1711 target RNA into GAM1711 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM3867 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3867 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3867 target RNA into GAM3867 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7006 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7006 gene: GAM709 target protein, GAM1711 target protein and GAM3867 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM709, GAM1711 and GAM3867

GR7007 AW151854 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7007(GR7007) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7007 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7007 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7007 gene encodes GR7007 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7007 precursor RNA folds spatially, forming GR7007 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7007 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7007 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7007 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM96632 precursor RNA and GAM136087 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM96632 RNA and GAM136087 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM96632 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM96632 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM96632 target RNA into GAM96632 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM136087 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM136087 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM136087 target RNA into GAM136087 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7007 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7007 gene: GAM96632 target protein and GAM136087 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference,

with references to GAM96632 and GAM136087

GR7008 BF949717 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7008(GR7008) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7008 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7008 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7008 gene encodes GR7008 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7008 precursor RNA folds spatially, forming GR7008 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7008 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7008 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7008 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2573 precursor RNA and GAM6909 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2573 RNA and GAM6909 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2573 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2573 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2573 target RNA into GAM2573 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6909 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6909 target RNA, herein schematically represented by

GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6909 target RNA into GAM6909 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7008 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7008 gene: GAM2573 target protein and GAM6909 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2573 and GAM6909

GR7009 AV690331 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7009(GR7009) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7009 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7009 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7009 gene encodes GR7009 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7009 precursor RNA folds spatially, forming GR7009 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7009 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7009 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7009 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM65023 precursor RNA and GAM115792 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM65023 RNA and GAM115792 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding

to GAM RNA of Fig. 8.

GAM65023 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM65023 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM65023 target RNA into GAM65023 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM115792 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM115792 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM115792 target RNA into GAM115792 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7009 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7009 gene: GAM65023 target protein and GAM115792 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM65023 and GAM115792

GR7010 BE742256 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7010(GR7010) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7010 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7010 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7010 gene encodes GR7010 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7010 precursor RNA folds spatially, forming GR7010 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7010 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7010 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR7010 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1069 precursor RNA and GAM182892 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1069 RNA and GAM182892 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1069 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1069 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1069 target RNA into GAM1069 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM182892 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM182892 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM182892 target RNA into GAM182892 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7010 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7010 gene: GAM1069 target protein and GAM182892 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1069 and GAM182892

GR7011 BF665216 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7011(GR7011) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7011 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7011

gene was detected is described hereinabove with reference to Figs. 8-18.

GR7011 gene encodes GR7011 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7011 precursor RNA folds spatially, forming GR7011 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7011 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7011 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7011 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5194 precursor RNA and GAM255255 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5194 RNA and GAM255255 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5194 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5194 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5194 target RNA into GAM5194 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM255255 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM255255 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM255255 target RNA into GAM255255 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7011 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7011 gene: GAM5194 target protein and GAM255255 target protein, herein schematically represented by GAM1

TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5194 and GAM255255

GR7012 BG336364 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7012(GR7012) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7012 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7012 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7012 gene encodes GR7012 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7012 precursor RNA folds spatially, forming GR7012 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7012 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7012 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7012 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3510 precursor RNA, GAM151814 precursor RNA and GAM227395 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3510 RNA, GAM151814 RNA and GAM227395 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3510 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3510 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3510 target RNA into GAM3510 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM151814 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM151814 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM151814 target RNA into GAM151814 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM227395 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM227395 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM227395 target RNA into GAM227395 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7012 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7012 gene: GAM3510 target protein, GAM151814 target protein and GAM227395 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3510, GAM151814 and GAM227395

GR7013 BF315218 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7013(GR7013) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7013 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7013 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7013 gene encodes GR7013 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7013 precursor RNA folds spatially, forming GR7013 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7013 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7013 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7013 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM10215 precursor RNA and GAM224235 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM10215 RNA and GAM224235 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM10215 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM10215 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM10215 target RNA into GAM10215 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM224235 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM224235 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM224235 target RNA into GAM224235 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7013 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7013 gene: GAM10215 target protein and GAM224235 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM10215 and GAM224235

GR7014 AW877706 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7014(GR7014) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7014 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7014 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7014 gene encodes GR7014 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7014 precursor RNA folds spatially, forming GR7014 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7014 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7014 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7014 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM127003 precursor RNA and GAM202344 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM127003 RNA and GAM202344 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM127003 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM127003 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM127003 target RNA into GAM127003 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM202344 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM202344 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM202344 target RNA into GAM202344 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7014 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7014 gene: GAM127003 target protein and GAM202344 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes

is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM127003 and GAM202344

GR7015 BI916210 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7015(GR7015) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7015 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7015 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7015 gene encodes GR7015 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7015 precursor RNA folds spatially, forming GR7015 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7015 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7015 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7015 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3408 precursor RNA and GAM304988 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3408 RNA and GAM304988 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3408 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3408 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3408 target RNA into GAM3408 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM304988 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM304988 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM304988 target RNA into GAM304988 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7015 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7015 gene: GAM3408 target protein and GAM304988 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3408 and GAM304988

GR7016 AA160184 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7016(GR7016) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7016 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7016 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7016 gene encodes GR7016 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7016 precursor RNA folds spatially, forming GR7016 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7016 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7016 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7016 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM162692 precursor RNA and GAM203155 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM162692 RNA and GAM203155 RNA, herein schematically

represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM162692 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM162692 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM162692 target RNA into GAM162692 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM203155 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM203155 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM203155 target RNA into GAM203155 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7016 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7016 gene: GAM162692 target protein and GAM203155 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM162692 and GAM203155

GR7017 AL596696 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7017(GR7017) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7017 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7017 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7017 gene encodes GR7017 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7017 precursor RNA folds spatially, forming GR7017 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7017 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7017 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7017 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM75473 precursor RNA, GAM114899 precursor RNA and GAM231858 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM75473 RNA, GAM114899 RNA and GAM231858 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM75473 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM75473 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM75473 target RNA into GAM75473 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM114899 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM114899 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM114899 target RNA into GAM114899 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM231858 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM231858 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM231858 target RNA into GAM231858 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7017 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7017 gene: GAM75473 target protein, GAM114899 target protein and GAM231858 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM75473, GAM114899 and

GR7018 BI224518 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7018(GR7018) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7018 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7018 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7018 gene encodes GR7018 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7018 precursor RNA folds spatially, forming GR7018 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7018 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7018 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7018 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1812 precursor RNA and GAM3166 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1812 RNA and GAM3166 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1812 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1812 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1812 target RNA into GAM1812 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM3166 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3166 target RNA, herein schematically represented by

GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3166 target RNA into GAM3166 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7018 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7018 gene: GAM1812 target protein and GAM3166 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1812 and GAM3166

GR7019 BG911055 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7019(GR7019) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7019 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7019 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7019 gene encodes GR7019 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7019 precursor RNA folds spatially, forming GR7019 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7019 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7019 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7019 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM131650 precursor RNA and GAM301294 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM131650 RNA and GAM301294 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding

to GAM RNA of Fig. 8.

GAM131650 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM131650 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM131650 target RNA into GAM131650 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM301294 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM301294 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM301294 target RNA into GAM301294 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7019 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7019 gene: GAM131650 target protein and GAM301294 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM131650 and GAM301294

GR7020 BG687671 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7020(GR7020) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7020 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7020 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7020 gene encodes GR7020 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7020 precursor RNA folds spatially, forming GR7020 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7020 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7020 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR7020 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3820 precursor RNA and GAM105119 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3820 RNA and GAM105119 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3820 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3820 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3820 target RNA into GAM3820 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM105119 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM105119 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM105119 target RNA into GAM105119 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7020 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7020 gene: GAM3820 target protein and GAM105119 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3820 and GAM105119

GR7021 AA658035 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7021(GR7021) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7021 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7021

gene was detected is described hereinabove with reference to Figs. 8-18.

GR7021 gene encodes GR7021 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7021 precursor RNA folds spatially, forming GR7021 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7021 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7021 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7021 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM14743 precursor RNA and GAM251949 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM14743 RNA and GAM251949 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM14743 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM14743 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM14743 target RNA into GAM14743 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM251949 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM251949 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM251949 target RNA into GAM251949 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7021 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7021 gene: GAM14743 target protein and GAM251949 target protein, herein schematically represented by GAM1

TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM14743 and GAM251949

GR7022 BE732459 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7022(GR7022) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7022 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7022 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7022 gene encodes GR7022 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7022 precursor RNA folds spatially, forming GR7022 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7022 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7022 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7022 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM35704 precursor RNA and GAM40498 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM35704 RNA and GAM40498 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM35704 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM35704 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM35704 target RNA into GAM35704 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM40498 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM40498 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM40498 target RNA into GAM40498 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7022 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7022 gene: GAM35704 target protein and GAM40498 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM35704 and GAM40498

GR7023 AI784447 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7023(GR7023) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7023 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7023 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7023 gene encodes GR7023 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7023 precursor RNA folds spatially, forming GR7023 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7023 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7023 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7023 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4533 precursor RNA and GAM137583 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM4533 RNA and GAM137583 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4533 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4533 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4533 target RNA into GAM4533 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM137583 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM137583 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM137583 target RNA into GAM137583 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7023 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7023 gene: GAM4533 target protein and GAM137583 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4533 and GAM137583

GR7024 AA487586 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7024(GR7024) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7024 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7024 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7024 gene encodes GR7024 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7024 precursor RNA folds spatially, forming GR7024 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7024 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7024 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7024 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1290 precursor RNA and GAM158900 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1290 RNA and GAM158900 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1290 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1290 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1290 target RNA into GAM1290 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM158900 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM158900 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM158900 target RNA into GAM158900 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7024 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7024 gene: GAM1290 target protein and GAM158900 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1290 and GAM158900

GR7025 H42705 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7025(GR7025) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7025 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7025 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7025 gene encodes GR7025 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7025 precursor RNA folds spatially, forming GR7025 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7025 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7025 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7025 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM49810 precursor RNA and GAM281733 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM49810 RNA and GAM281733 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM49810 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM49810 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM49810 target RNA into GAM49810 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM281733 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM281733 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM281733 target RNA into GAM281733 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7025 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR7025 gene: GAM49810 target protein and GAM281733 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM49810 and GAM281733

GR7026 AW946255 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7026(GR7026) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7026 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7026 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7026 gene encodes GR7026 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7026 precursor RNA folds spatially, forming GR7026 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7026 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7026 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7026 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM122042 precursor RNA, GAM155132 precursor RNA and GAM175184 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM122042 RNA, GAM155132 RNA and GAM175184 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM122042 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM122042 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM122042

target RNA into GAM122042 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM155132 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM155132 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM155132 target RNA into GAM155132 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM175184 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM175184 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM175184 target RNA into GAM175184 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7026 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7026 gene: GAM122042 target protein, GAM155132 target protein and GAM175184 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM122042, GAM155132 and GAM175184

GR7027 BM793177 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7027(GR7027) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7027 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7027 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7027 gene encodes GR7027 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7027 precursor RNA folds spatially, forming GR7027 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7027 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7027 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7027 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM227715 precursor RNA and GAM247616 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM227715 RNA and GAM247616 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM227715 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM227715 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM227715 target RNA into GAM227715 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM247616 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM247616 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM247616 target RNA into GAM247616 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7027 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7027 gene: GAM227715 target protein and GAM247616 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM227715 and GAM247616

GR7028 AI817580 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7028(GR7028) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7028 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR7028 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7028 gene encodes GR7028 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7028 precursor RNA folds spatially, forming GR7028 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7028 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7028 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7028 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM87125 precursor RNA, GAM95547 precursor RNA and GAM260191 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM87125 RNA, GAM95547 RNA and GAM260191 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM87125 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM87125 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM87125 target RNA into GAM87125 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM95547 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM95547 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM95547 target RNA into GAM95547 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM260191 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM260191 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM260191 target RNA into GAM260191 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7028 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7028 gene: GAM87125 target protein, GAM95547 target protein and GAM260191 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM87125, GAM95547 and GAM260191

GR7029 AA705677 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7029(GR7029) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7029 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7029 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7029 gene encodes GR7029 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7029 precursor RNA folds spatially, forming GR7029 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7029 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7029 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7029 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6801 precursor RNA and GAM277480 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6801 RNA and GAM277480 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding

to GAM RNA of Fig. 8.

GAM6801 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6801 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6801 target RNA into GAM6801 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM277480 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM277480 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM277480 target RNA into GAM277480 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7029 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7029 gene: GAM6801 target protein and GAM277480 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6801 and GAM277480

GR7030 AA448211 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7030(GR7030) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7030 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7030 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7030 gene encodes GR7030 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7030 precursor RNA folds spatially, forming GR7030 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7030 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7030 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR7030 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1524 precursor RNA and GAM175423 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1524 RNA and GAM175423 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1524 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1524 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1524 target RNA into GAM1524 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM175423 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM175423 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM175423 target RNA into GAM175423 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7030 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7030 gene: GAM1524 target protein and GAM175423 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1524 and GAM175423

GR7031 AA644273 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7031(GR7031) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7031 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7031

gene was detected is described hereinabove with reference to Figs. 8-18.

GR7031 gene encodes GR7031 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7031 precursor RNA folds spatially, forming GR7031 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7031 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7031 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7031 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM27666 precursor RNA and GAM63227 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM27666 RNA and GAM63227 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM27666 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM27666 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM27666 target RNA into GAM27666 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM63227 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM63227 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM63227 target RNA into GAM63227 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7031 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7031 gene: GAM27666 target protein and GAM63227 target protein, herein schematically represented by GAM1

TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM27666 and GAM63227

GR7032 AW389151 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7032(GR7032) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7032 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7032 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7032 gene encodes GR7032 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7032 precursor RNA folds spatially, forming GR7032 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7032 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7032 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7032 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7130 precursor RNA and GAM119159 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7130 RNA and GAM119159 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7130 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7130 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7130 target RNA into GAM7130 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM119159 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM119159 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM119159 target RNA into GAM119159 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7032 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7032 gene: GAM7130 target protein and GAM119159 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7130 and GAM119159

GR7033 BG987871 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7033(GR7033) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7033 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7033 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7033 gene encodes GR7033 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7033 precursor RNA folds spatially, forming GR7033 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7033 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7033 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7033 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM122767 precursor RNA and GAM155394 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM122767 RNA and GAM155394 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM122767 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM122767 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM122767 target RNA into GAM122767 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM155394 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM155394 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM155394 target RNA into GAM155394 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7033 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7033 gene: GAM122767 target protein and GAM155394 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM122767 and GAM155394

GR7034 BF769575 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7034(GR7034) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7034 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7034 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7034 gene encodes GR7034 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7034 precursor RNA folds spatially, forming GR7034 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7034 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7034 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7034 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM57047 precursor RNA and GAM90347 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM57047 RNA and GAM90347 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM57047 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM57047 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM57047 target RNA into GAM57047 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM90347 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM90347 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM90347 target RNA into GAM90347 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7034 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7034 gene: GAM57047 target protein and GAM90347 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM57047 and GAM90347

GR7035 BE256118 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7035(GR7035) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7035 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7035 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7035 gene encodes GR7035 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7035 precursor RNA folds spatially, forming GR7035 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7035 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7035 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7035 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM128743 precursor RNA and GAM158618 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM128743 RNA and GAM158618 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM128743 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM128743 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM128743 target RNA into GAM128743 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM158618 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM158618 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM158618 target RNA into GAM158618 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7035 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR7035 gene: GAM128743 target protein and GAM158618 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM128743 and GAM158618

GR7036 BF965466 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7036(GR7036) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7036 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7036 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7036 gene encodes GR7036 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7036 precursor RNA folds spatially, forming GR7036 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7036 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7036 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7036 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2176 precursor RNA and GAM120623 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2176 RNA and GAM120623 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2176 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2176 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2176 target RNA into GAM2176 target protein, herein schematically represented by GAM1 TARGET

PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM120623 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM120623 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM120623 target RNA into GAM120623 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7036 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7036 gene: GAM2176 target protein and GAM120623 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2176 and GAM120623

GR7037 R25555 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7037(GR7037) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7037 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7037 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7037 gene encodes GR7037 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7037 precursor RNA folds spatially, forming GR7037 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7037 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7037 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7037 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM57296 precursor RNA and GAM323621 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM57296 RNA and GAM323621 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM57296 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM57296 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM57296 target RNA into GAM57296 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM323621 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM323621 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM323621 target RNA into GAM323621 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7037 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7037 gene: GAM57296 target protein and GAM323621 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM57296 and GAM323621

GR7038 BE712776 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7038(GR7038) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7038 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7038 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7038 gene encodes GR7038 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7038 precursor RNA folds spatially, forming GR7038 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7038 folded precursor RNA comprises a plurality of what is known in the

art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7038 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7038 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3342 precursor RNA and GAM204602 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3342 RNA and GAM204602 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3342 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3342 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3342 target RNA into GAM3342 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM204602 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM204602 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM204602 target RNA into GAM204602 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7038 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7038 gene: GAM3342 target protein and GAM204602 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3342 and GAM204602

GR7039 BM006879 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7039(GR7039) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR7039 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7039 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7039 gene encodes GR7039 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7039 precursor RNA folds spatially, forming GR7039 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7039 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7039 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7039 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM940 precursor RNA and GAM98857 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM940 RNA and GAM98857 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM940 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM940 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM940 target RNA into GAM940 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM98857 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM98857 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM98857 target RNA into GAM98857 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly

utilities, of GR7039 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7039 gene: GAM940 target protein and GAM98857 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM940 and GAM98857

GR7040 BG703131 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7040(GR7040) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7040 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7040 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7040 gene encodes GR7040 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7040 precursor RNA folds spatially, forming GR7040 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7040 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7040 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7040 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6766 precursor RNA and GAM246141 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6766 RNA and GAM246141 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6766 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6766 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig. 8, thereby inhibiting translation of GAM6766 target RNA into GAM6766 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM246141 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM246141 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM246141 target RNA into GAM246141 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7040 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7040 gene: GAM6766 target protein and GAM246141 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6766 and GAM246141

GR7041 BG622726 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7041(GR7041) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7041 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7041 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7041 gene encodes GR7041 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7041 precursor RNA folds spatially, forming GR7041 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7041 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7041 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7041 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5286 precursor RNA and GAM111899 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin

shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5286 RNA and GAM111899 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5286 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5286 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5286 target RNA into GAM5286 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM111899 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM111899 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM111899 target RNA into GAM111899 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7041 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7041 gene: GAM5286 target protein and GAM111899 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5286 and GAM111899

GR7042 BF335192 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7042(GR7042) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7042 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7042 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7042 gene encodes GR7042 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7042 precursor RNA folds spatially, forming GR7042 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7042 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7042 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7042 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8419 precursor RNA and GAM277187 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8419 RNA and GAM277187 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8419 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8419 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8419 target RNA into GAM8419 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM277187 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM277187 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM277187 target RNA into GAM277187 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7042 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7042 gene: GAM8419 target protein and GAM277187 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8419 and GAM277187

GR7043 AA136113 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7043(GR7043) gene, which encodes an `operon-like` cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7043 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7043 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7043 gene encodes GR7043 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7043 precursor RNA folds spatially, forming GR7043 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7043 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7043 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7043 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8620 precursor RNA and GAM103814 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8620 RNA and GAM103814 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8620 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8620 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8620 target RNA into GAM8620 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM103814 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM103814 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM103814 target RNA into GAM103814 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7043 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7043 gene: GAM8620 target protein and GAM103814 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8620 and GAM103814

GR7044 BI601129 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7044(GR7044) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7044 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7044 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7044 gene encodes GR7044 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7044 precursor RNA folds spatially, forming GR7044 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7044 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7044 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7044 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM806 precursor RNA, GAM118395 precursor RNA and GAM330259 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM806 RNA, GAM118395 RNA and GAM330259 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM806 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM806 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM806 target RNA into GAM806 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM118395 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM118395 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM118395 target RNA into GAM118395 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM330259 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM330259 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM330259 target RNA into GAM330259 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7044 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7044 gene: GAM806 target protein, GAM118395 target protein and GAM330259 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM806, GAM118395 and GAM330259

GR7045 BE173273 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7045(GR7045) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7045 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7045 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7045 gene encodes GR7045 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7045 precursor RNA folds spatially, forming GR7045 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated

that GR7045 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7045 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7045 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM536 precursor RNA and GAM303039 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM536 RNA and GAM303039 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM536 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM536 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM536 target RNA into GAM536 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM303039 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM303039 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM303039 target RNA into GAM303039 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7045 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7045 gene: GAM536 target protein and GAM303039 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM536 and GAM303039

GR7046 AW853743 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7046(GR7046) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR7046 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7046 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7046 gene encodes GR7046 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7046 precursor RNA folds spatially, forming GR7046 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7046 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7046 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7046 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM4768 precursor RNA, GAM28350 precursor RNA, GAM36152 precursor RNA and GAM163228 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4768 RNA, GAM28350 RNA, GAM36152 RNA and GAM163228 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4768 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4768 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4768 target RNA into GAM4768 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM28350 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM28350 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM28350 target RNA into GAM28350 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM36152 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM36152 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM36152 target RNA into GAM36152 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM163228 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM163228 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM163228 target RNA into GAM163228 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7046 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7046 gene: GAM4768 target protein, GAM28350 target protein, GAM36152 target protein and GAM163228 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4768, GAM28350, GAM36152 and GAM163228

GR7047 BG744763 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7047(GR7047) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7047 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7047 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7047 gene encodes GR7047 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7047 precursor RNA folds spatially, forming GR7047 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7047 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7047 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7047 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM6662 precursor RNA, GAM35872 precursor RNA and GAM270459 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6662 RNA, GAM35872 RNA and GAM270459 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6662 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6662 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6662 target RNA into GAM6662 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM35872 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM35872 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM35872 target RNA into GAM35872 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM270459 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM270459 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM270459 target RNA into GAM270459 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7047 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7047 gene: GAM6662 target protein, GAM35872 target protein and GAM270459 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6662, GAM35872 and GAM270459

GR7048 BM050801 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7048(GR7048) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7048 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7048 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7048 gene encodes GR7048 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7048 precursor RNA folds spatially, forming GR7048 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7048 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7048 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7048 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM46348 precursor RNA, GAM64997 precursor RNA and GAM262565 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM46348 RNA, GAM64997 RNA and GAM262565 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM46348 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM46348 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM46348 target RNA into GAM46348 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM64997 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM64997 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM64997 target RNA into GAM64997 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM262565 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM262565 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM262565 target RNA into GAM262565 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7048 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7048 gene: GAM46348 target protein, GAM64997 target protein and GAM262565 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM46348, GAM64997 and GAM262565

GR7049 BI458158 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7049(GR7049) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7049 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7049 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7049 gene encodes GR7049 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7049 precursor RNA folds spatially, forming GR7049 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7049 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7049 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7049 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 5 separate GAM precursor RNAs, GAM1690 precursor RNA, GAM2203 precursor RNA,

GAM2566 precursor RNA, GAM97356 precursor RNA and GAM195519 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1690 RNA, GAM2203 RNA, GAM2566 RNA, GAM97356 RNA and GAM195519 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1690 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1690 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1690 target RNA into GAM1690 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM2203 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2203 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2203 target RNA into GAM2203 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM2566 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2566 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2566 target RNA into GAM2566 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM97356 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM97356 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM97356 target RNA into GAM97356 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM195519 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM195519 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM195519 target RNA into GAM195519 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7049 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7049 gene: GAM1690 target protein, GAM2203 target protein, GAM2566 target protein, GAM97356 target protein and GAM195519 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1690, GAM2203, GAM2566, GAM97356 and GAM195519

GR7050 R13003 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7050(GR7050) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7050 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7050 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7050 gene encodes GR7050 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7050 precursor RNA folds spatially, forming GR7050 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7050 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7050 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7050 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM35328 precursor RNA, GAM175520 precursor RNA and GAM330080 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM35328 RNA, GAM175520 RNA and GAM330080 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM35328 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM35328 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM35328 target RNA into GAM35328 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM175520 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM175520 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM175520 target RNA into GAM175520 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM330080 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM330080 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM330080 target RNA into GAM330080 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7050 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7050 gene: GAM35328 target protein, GAM175520 target protein and GAM330080 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM35328, GAM175520 and GAM330080

GR7051 T57841 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7051 (GR7051) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7051 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7051 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7051 gene encodes GR7051 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7051 precursor RNA folds spatially, forming GR7051 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7051 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7051 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7051 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM261210 precursor RNA and GAM267156 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM261210 RNA and GAM267156 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM261210 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM261210 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM261210 target RNA into GAM261210 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM267156 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM267156 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM267156 target RNA into GAM267156 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7051 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7051 gene: GAM261210 target protein and GAM267156 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM261210 and GAM267156

7052(GR7052) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7052 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7052 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7052 gene encodes GR7052 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7052 precursor RNA folds spatially, forming GR7052 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7052 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7052 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7052 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM85462 precursor RNA and GAM294107 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM85462 RNA and GAM294107 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM85462 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM85462 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM85462 target RNA into GAM85462 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM294107 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM294107 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM294107 target RNA into GAM294107 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7052 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7052 gene: GAM85462 target protein and GAM294107 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM85462 and GAM294107

GR7053 BM968195 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7053(GR7053) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7053 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7053 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7053 gene encodes GR7053 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7053 precursor RNA folds spatially, forming GR7053 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7053 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7053 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7053 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM177969 precursor RNA and GAM189606 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM177969 RNA and GAM189606 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM177969 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM177969 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM177969 target RNA into GAM177969 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM189606 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM189606 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM189606 target RNA into GAM189606 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7053 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7053 gene: GAM177969 target protein and GAM189606 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM177969 and GAM189606

GR7054 BI770557 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7054(GR7054) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7054 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7054 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7054 gene encodes GR7054 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7054 precursor RNA folds spatially, forming GR7054 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7054 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7054 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7054 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2

separate GAM precursor RNAs, GAM118963 precursor RNA and GAM189797 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM118963 RNA and GAM189797 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM118963 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM118963 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM118963 target RNA into GAM118963 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM189797 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM189797 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM189797 target RNA into GAM189797 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7054 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7054 gene: GAM118963 target protein and GAM189797 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM118963 and GAM189797

GR7055 BI552925 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7055(GR7055) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7055 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7055 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7055 gene encodes GR7055 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR7055 precursor RNA folds spatially, forming GR7055 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7055 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7055 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7055 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM40422 precursor RNA and GAM298017 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM40422 RNA and GAM298017 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM40422 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM40422 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM40422 target RNA into GAM40422 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM298017 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM298017 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM298017 target RNA into GAM298017 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7055 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7055 gene: GAM40422 target protein and GAM298017 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM40422 and GAM298017

GR7056 BE279264 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7056(GR7056) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7056 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7056 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7056 gene encodes GR7056 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7056 precursor RNA folds spatially, forming GR7056 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7056 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7056 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7056 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1054 precursor RNA, GAM2919 precursor RNA and GAM206340 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1054 RNA, GAM2919 RNA and GAM206340 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1054 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1054 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1054 target RNA into GAM1054 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM2919 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2919 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds

to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2919 target RNA into GAM2919 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM206340 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM206340 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM206340 target RNA into GAM206340 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7056 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7056 gene: GAM1054 target protein, GAM2919 target protein and GAM206340 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1054, GAM2919 and GAM206340

GR7057 R19224 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7057(GR7057) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7057 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7057 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7057 gene encodes GR7057 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7057 precursor RNA folds spatially, forming GR7057 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7057 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7057 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7057 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM45937 precursor RNA, GAM247515 precursor RNA

and GAM277284 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM45937 RNA, GAM247515 RNA and GAM277284 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM45937 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM45937 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM45937 target RNA into GAM45937 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM247515 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM247515 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM247515 target RNA into GAM247515 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM277284 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM277284 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM277284 target RNA into GAM277284 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7057 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7057 gene: GAM45937 target protein, GAM247515 target protein and GAM277284 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM45937, GAM247515 and GAM277284

GR7058 R66493 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7058(GR7058) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR7058 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7058 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7058 gene encodes GR7058 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7058 precursor RNA folds spatially, forming GR7058 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7058 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7058 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7058 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM39766 precursor RNA and GAM310342 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM39766 RNA and GAM310342 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM39766 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM39766 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM39766 target RNA into GAM39766 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM310342 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM310342 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM310342 target RNA into GAM310342 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7058 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7058 gene: GAM39766 target protein and GAM310342 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM39766 and GAM310342

GR7059 BI006517 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7059(GR7059) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7059 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7059 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7059 gene encodes GR7059 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7059 precursor RNA folds spatially, forming GR7059 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7059 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7059 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7059 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM7278 precursor RNA, GAM257656 precursor RNA and GAM260204 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7278 RNA, GAM257656 RNA and GAM260204 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7278 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7278 target RNA, herein schematically represented by

GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7278 target RNA into GAM7278 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM257656 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM257656 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM257656 target RNA into GAM257656 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM260204 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM260204 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM260204 target RNA into GAM260204 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7059 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7059 gene: GAM7278 target protein, GAM257656 target protein and GAM260204 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7278, GAM257656 and GAM260204

GR7060 BG677373 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7060(GR7060) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7060 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7060 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7060 gene encodes GR7060 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7060 precursor RNA folds spatially, forming GR7060 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7060 folded precursor RNA comprises a plurality of what is known in the

art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7060 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7060 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM26310 precursor RNA and GAM242496 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM26310 RNA and GAM242496 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM26310 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM26310 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM26310 target RNA into GAM26310 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM242496 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM242496 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM242496 target RNA into GAM242496 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7060 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7060 gene: GAM26310 target protein and GAM242496 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM26310 and GAM242496

GR7061 BM664605 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7061 (GR7061) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR7061 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7061 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7061 gene encodes GR7061 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7061 precursor RNA folds spatially, forming GR7061 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7061 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7061 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7061 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6314 precursor RNA and GAM243082 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6314 RNA and GAM243082 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6314 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6314 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6314 target RNA into GAM6314 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM243082 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM243082 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM243082 target RNA into GAM243082 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly

utilities, of GR7061 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7061 gene: GAM6314 target protein and GAM243082 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6314 and GAM243082

GR7062 BI461931 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7062(GR7062) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7062 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7062 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7062 gene encodes GR7062 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7062 precursor RNA folds spatially, forming GR7062 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7062 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7062 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7062 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM8050 precursor RNA, GAM76853 precursor RNA and GAM217971 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8050 RNA, GAM76853 RNA and GAM217971 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8050 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8050 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds

to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8050 target RNA into GAM8050 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM76853 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM76853 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM76853 target RNA into GAM76853 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM217971 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM217971 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM217971 target RNA into GAM217971 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7062 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7062 gene: GAM8050 target protein, GAM76853 target protein and GAM217971 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8050, GAM76853 and GAM217971

GR7063 BI026200 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7063(GR7063) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7063 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7063 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7063 gene encodes GR7063 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7063 precursor RNA folds spatially, forming GR7063 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7063 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR7063 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7063 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM89840 precursor RNA, GAM173114 precursor RNA and GAM300297 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM89840 RNA, GAM173114 RNA and GAM300297 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM89840 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM89840 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM89840 target RNA into GAM89840 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM173114 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM173114 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM173114 target RNA into GAM173114 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM300297 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM300297 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM300297 target RNA into GAM300297 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7063 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7063 gene: GAM89840 target protein, GAM173114 target protein and GAM300297 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN.

The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM89840, GAM173114 and GAM300297

GR7064 BG403754 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7064(GR7064) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7064 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7064 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7064 gene encodes GR7064 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7064 precursor RNA folds spatially, forming GR7064 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7064 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7064 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7064 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM41389 precursor RNA and GAM104016 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM41389 RNA and GAM104016 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM41389 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM41389 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM41389 target RNA into GAM41389 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM104016 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM104016 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM104016 target RNA into GAM104016 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7064 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7064 gene: GAM41389 target protein and GAM104016 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM41389 and GAM104016

GR7065 BE501964 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7065(GR7065) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7065 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7065 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7065 gene encodes GR7065 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7065 precursor RNA folds spatially, forming GR7065 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7065 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7065 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7065 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM142499 precursor RNA and GAM259429 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM142499 RNA and GAM259429 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM142499 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM142499 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM142499 target RNA into GAM142499 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM259429 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM259429 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM259429 target RNA into GAM259429 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7065 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7065 gene: GAM142499 target protein and GAM259429 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM142499 and GAM259429

GR7066 BM714917 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7066(GR7066) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7066 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7066 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7066 gene encodes GR7066 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7066 precursor RNA folds spatially, forming GR7066 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7066 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7066 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7066 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM64829 precursor RNA and GAM305413 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM64829 RNA and GAM305413 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM64829 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM64829 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM64829 target RNA into GAM64829 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM305413 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM305413 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM305413 target RNA into GAM305413 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7066 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7066 gene: GAM64829 target protein and GAM305413 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM64829 and GAM305413

GR7067 BM975884 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7067(GR7067) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7067 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7067 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7067 gene encodes GR7067 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7067 precursor RNA folds spatially, forming GR7067 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7067 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7067 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7067 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1394 precursor RNA and GAM310572 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1394 RNA and GAM310572 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1394 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1394 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1394 target RNA into GAM1394 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM310572 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM310572 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM310572 target RNA into GAM310572 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7067 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR7067 gene: GAM1394 target protein and GAM310572 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1394 and GAM310572

GR7068 AI217523 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7068(GR7068) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7068 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7068 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7068 gene encodes GR7068 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7068 precursor RNA folds spatially, forming GR7068 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7068 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7068 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7068 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM50732 precursor RNA, GAM82676 precursor RNA and GAM209311 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM50732 RNA, GAM82676 RNA and GAM209311 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM50732 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM50732 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM50732

target RNA into GAM50732 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM82676 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM82676 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM82676 target RNA into GAM82676 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM209311 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM209311 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM209311 target RNA into GAM209311 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7068 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7068 gene: GAM50732 target protein, GAM82676 target protein and GAM209311 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM50732, GAM82676 and GAM209311

GR7069 BF677081 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7069(GR7069) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7069 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7069 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7069 gene encodes GR7069 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7069 precursor RNA folds spatially, forming GR7069 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7069 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7069 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7069 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM6386 precursor RNA, GAM32411 precursor RNA, GAM55871 precursor RNA and GAM198037 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6386 RNA, GAM32411 RNA, GAM55871 RNA and GAM198037 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6386 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6386 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6386 target RNA into GAM6386 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM32411 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM32411 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM32411 target RNA into GAM32411 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM55871 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM55871 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM55871 target RNA into GAM55871 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM198037 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM198037 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM198037 target RNA into GAM198037 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7069 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7069 gene: GAM6386 target protein, GAM32411 target protein, GAM55871 target protein and GAM198037 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6386, GAM32411, GAM55871 and GAM198037

GR7070 BF930317 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7070(GR7070) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7070 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7070 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7070 gene encodes GR7070 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7070 precursor RNA folds spatially, forming GR7070 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7070 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7070 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7070 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3870 precursor RNA, GAM5869 precursor RNA and GAM7618 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3870 RNA, GAM5869 RNA and GAM7618 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3870 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM3870 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3870 target RNA into GAM3870 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5869 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5869 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5869 target RNA into GAM5869 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7618 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7618 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7618 target RNA into GAM7618 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7070 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7070 gene: GAM3870 target protein, GAM5869 target protein and GAM7618 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3870, GAM5869 and GAM7618

GR7071 BG116521 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7071(GR7071) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7071 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7071 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7071 gene encodes GR7071 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7071 precursor RNA folds spatially, forming GR7071 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated

that GR7071 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7071 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7071 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1582 precursor RNA, GAM130322 precursor RNA and GAM291192 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1582 RNA, GAM130322 RNA and GAM291192 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1582 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1582 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1582 target RNA into GAM1582 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM130322 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM130322 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM130322 target RNA into GAM130322 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM291192 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM291192 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM291192 target RNA into GAM291192 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7071 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7071 gene: GAM1582 target

protein, GAM130322 target protein and GAM291192 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1582, GAM130322 and GAM291192

GR7072 BE219821 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7072(GR7072) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7072 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7072 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7072 gene encodes GR7072 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7072 precursor RNA folds spatially, forming GR7072 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7072 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7072 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7072 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2708 precursor RNA and GAM47021 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2708 RNA and GAM47021 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2708 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2708 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2708 target RNA into GAM2708 target protein, herein schematically represented by GAM1 TARGET

PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM47021 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM47021 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM47021 target RNA into GAM47021 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7072 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7072 gene: GAM2708 target protein and GAM47021 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2708 and GAM47021

GR7073 BI596895 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7073(GR7073) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7073 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7073 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7073 gene encodes GR7073 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7073 precursor RNA folds spatially, forming GR7073 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7073 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7073 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7073 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM161984 precursor RNA and GAM313239 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM161984 RNA and GAM313239 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM161984 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM161984 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM161984 target RNA into GAM161984 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM313239 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM313239 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM313239 target RNA into GAM313239 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7073 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7073 gene: GAM161984 target protein and GAM313239 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM161984 and GAM313239

GR7074 D29560 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7074(GR7074) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7074 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7074 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7074 gene encodes GR7074 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7074 precursor RNA folds spatially, forming GR7074 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7074 folded precursor RNA comprises a plurality of what is known in the

art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7074 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7074 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM14098 precursor RNA, GAM100423 precursor RNA and GAM129541 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM14098 RNA, GAM100423 RNA and GAM129541 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM14098 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM14098 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM14098 target RNA into GAM14098 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM100423 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM100423 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM100423 target RNA into GAM100423 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM129541 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM129541 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM129541 target RNA into GAM129541 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7074 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7074 gene: GAM14098 target protein, GAM100423 target protein and GAM129541 target protein, herein

schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM14098, GAM100423 and GAM129541

GR7075 BI912602 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7075(GR7075) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7075 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7075 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7075 gene encodes GR7075 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7075 precursor RNA folds spatially, forming GR7075 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7075 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7075 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7075 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM59981 precursor RNA and GAM87199 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM59981 RNA and GAM87199 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM59981 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM59981 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM59981 target RNA into GAM59981 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM87199 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM87199 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM87199 target RNA into GAM87199 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7075 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7075 gene: GAM59981 target protein and GAM87199 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM59981 and GAM87199

GR7076 AA457635 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7076(GR7076) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7076 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7076 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7076 gene encodes GR7076 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7076 precursor RNA folds spatially, forming GR7076 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7076 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7076 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7076 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM182316 precursor RNA and GAM187833 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM182316 RNA and GAM187833 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM182316 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM182316 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM182316 target RNA into GAM182316 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM187833 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM187833 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM187833 target RNA into GAM187833 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7076 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7076 gene: GAM182316 target protein and GAM187833 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM182316 and GAM187833

GR7077 BM782106 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7077(GR7077) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7077 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7077 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7077 gene encodes GR7077 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7077 precursor RNA folds spatially, forming GR7077 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7077 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR7077 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7077 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM8064 precursor RNA, GAM58903 precursor RNA and GAM274816 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8064 RNA, GAM58903 RNA and GAM274816 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8064 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8064 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8064 target RNA into GAM8064 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM58903 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM58903 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM58903 target RNA into GAM58903 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM274816 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM274816 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM274816 target RNA into GAM274816 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7077 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7077 gene: GAM8064 target protein, GAM58903 target protein and GAM274816 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN.

The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8064, GAM58903 and GAM274816

GR7078 BI197185 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7078(GR7078) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7078 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7078 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7078 gene encodes GR7078 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7078 precursor RNA folds spatially, forming GR7078 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7078 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7078 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7078 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM83096 precursor RNA, GAM124610 precursor RNA and GAM217826 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM83096 RNA, GAM124610 RNA and GAM217826 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM83096 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM83096 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM83096 target RNA into GAM83096 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM124610 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM124610 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM124610 target RNA into GAM124610 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM217826 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM217826 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM217826 target RNA into GAM217826 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7078 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7078 gene: GAM83096 target protein, GAM124610 target protein and GAM217826 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM83096, GAM124610 and GAM217826

GR7079 BE297813 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7079(GR7079) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7079 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7079 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7079 gene encodes GR7079 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7079 precursor RNA folds spatially, forming GR7079 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7079 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7079 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7079 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM151948 precursor RNA, GAM209462 precursor RNA and GAM228075 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM151948 RNA, GAM209462 RNA and GAM228075 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM151948 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM151948 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM151948 target RNA into GAM151948 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM209462 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM209462 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM209462 target RNA into GAM209462 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM228075 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM228075 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM228075 target RNA into GAM228075 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7079 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7079 gene: GAM151948 target protein, GAM209462 target protein and GAM228075 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM151948, GAM209462 and GAM228075

GR7080 W87846 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7080(GR7080) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7080 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7080 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7080 gene encodes GR7080 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7080 precursor RNA folds spatially, forming GR7080 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7080 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7080 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7080 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2835 precursor RNA, GAM87315 precursor RNA and GAM128852 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2835 RNA, GAM87315 RNA and GAM128852 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2835 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2835 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2835 target RNA into GAM2835 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM87315 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM87315 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM87315 target RNA into GAM87315 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM128852 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM128852 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM128852 target RNA into GAM128852 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7080 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7080 gene: GAM2835 target protein, GAM87315 target protein and GAM128852 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2835, GAM87315 and GAM128852

GR7081 AW661999 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7081 (GR7081) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7081 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7081 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7081 gene encodes GR7081 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7081 precursor RNA folds spatially, forming GR7081 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7081 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7081 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7081 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM24587 precursor RNA, GAM88249 precursor RNA

and GAM311012 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM24587 RNA, GAM88249 RNA and GAM311012 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM24587 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM24587 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM24587 target RNA into GAM24587 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM88249 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM88249 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM88249 target RNA into GAM88249 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM311012 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM311012 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM311012 target RNA into GAM311012 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7081 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7081 gene: GAM24587 target protein, GAM88249 target protein and GAM311012 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM24587, GAM88249 and GAM311012

GR7082 BG752041 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7082(GR7082) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR7082 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7082 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7082 gene encodes GR7082 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7082 precursor RNA folds spatially, forming GR7082 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7082 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7082 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7082 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2953 precursor RNA and GAM7291 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2953 RNA and GAM7291 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2953 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2953 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2953 target RNA into GAM2953 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7291 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7291 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7291 target RNA into GAM7291 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7082 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7082 gene: GAM2953 target protein and GAM7291 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2953 and GAM7291

GR7083 BE007421 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7083(GR7083) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7083 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7083 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7083 gene encodes GR7083 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7083 precursor RNA folds spatially, forming GR7083 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7083 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7083 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7083 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM90105 precursor RNA and GAM279129 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM90105 RNA and GAM279129 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM90105 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM90105 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM90105 target RNA into GAM90105 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM279129 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM279129 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM279129 target RNA into GAM279129 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7083 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7083 gene: GAM90105 target protein and GAM279129 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM90105 and GAM279129

GR7084 AA010628 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7084(GR7084) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7084 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7084 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7084 gene encodes GR7084 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7084 precursor RNA folds spatially, forming GR7084 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7084 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7084 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7084 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8033 precursor RNA and GAM329737 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3

FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8033 RNA and GAM329737 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8033 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8033 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8033 target RNA into GAM8033 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM329737 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM329737 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM329737 target RNA into GAM329737 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7084 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7084 gene: GAM8033 target protein and GAM329737 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8033 and GAM329737

GR7085 BE884286 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7085(GR7085) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7085 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7085 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7085 gene encodes GR7085 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7085 precursor RNA folds spatially, forming GR7085 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7085 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7085 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7085 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3135 precursor RNA and GAM3974 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3135 RNA and GAM3974 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3135 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3135 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3135 target RNA into GAM3135 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM3974 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3974 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3974 target RNA into GAM3974 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7085 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7085 gene: GAM3135 target protein and GAM3974 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3135 and GAM3974

7086(GR7086) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7086 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7086 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7086 gene encodes GR7086 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7086 precursor RNA folds spatially, forming GR7086 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7086 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7086 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7086 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM54894 precursor RNA and GAM209667 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM54894 RNA and GAM209667 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM54894 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM54894 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM54894 target RNA into GAM54894 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM209667 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM209667 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM209667 target RNA into GAM209667 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7086 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7086 gene: GAM54894 target protein and GAM209667 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM54894 and GAM209667

GR7087 BF844125 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7087(GR7087) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7087 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7087 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7087 gene encodes GR7087 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7087 precursor RNA folds spatially, forming GR7087 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7087 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7087 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7087 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3179 precursor RNA and GAM14086 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3179 RNA and GAM14086 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3179 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM3179 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3179 target RNA into GAM3179 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM14086 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM14086 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM14086 target RNA into GAM14086 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7087 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7087 gene: GAM3179 target protein and GAM14086 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3179 and GAM14086

GR7088 BG541711 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7088(GR7088) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7088 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7088 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7088 gene encodes GR7088 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7088 precursor RNA folds spatially, forming GR7088 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7088 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7088 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7088 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3

separate GAM precursor RNAs, GAM42491 precursor RNA, GAM152372 precursor RNA and GAM159808 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM42491 RNA, GAM152372 RNA and GAM159808 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM42491 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM42491 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM42491 target RNA into GAM42491 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM152372 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM152372 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM152372 target RNA into GAM152372 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM159808 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM159808 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM159808 target RNA into GAM159808 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7088 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7088 gene: GAM42491 target protein, GAM152372 target protein and GAM159808 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM42491, GAM152372 and GAM159808

GR7089 AA595559 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7089 (GR7089) gene, which encodes an `operon-like` cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7089 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7089 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7089 gene encodes GR7089 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7089 precursor RNA folds spatially, forming GR7089 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7089 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7089 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7089 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM153120 precursor RNA and GAM252109 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM153120 RNA and GAM252109 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM153120 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM153120 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM153120 target RNA into GAM153120 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM252109 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM252109 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM252109 target RNA into GAM252109 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7089 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7089 gene: GAM153120 target protein and GAM252109 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM153120 and GAM252109

GR7090 BG569894 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7090(GR7090) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7090 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7090 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7090 gene encodes GR7090 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7090 precursor RNA folds spatially, forming GR7090 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7090 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7090 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7090 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1127 precursor RNA, GAM62402 precursor RNA and GAM131663 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1127 RNA, GAM62402 RNA and GAM131663 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1127 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM1127 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1127 target RNA into GAM1127 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM62402 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM62402 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM62402 target RNA into GAM62402 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM131663 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM131663 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM131663 target RNA into GAM131663 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7090 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7090 gene: GAM1127 target protein, GAM62402 target protein and GAM131663 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1127, GAM62402 and GAM131663

GR7091 AI921720 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7091 (GR7091) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7091 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7091 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7091 gene encodes GR7091 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7091 precursor RNA folds spatially, forming GR7091 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated

that GR7091 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7091 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7091 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM53123 precursor RNA, GAM55544 precursor RNA and GAM263894 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM53123 RNA, GAM55544 RNA and GAM263894 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM53123 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM53123 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM53123 target RNA into GAM53123 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM55544 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM55544 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM55544 target RNA into GAM55544 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM263894 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM263894 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM263894 target RNA into GAM263894 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7091 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7091 gene: GAM53123 target

protein, GAM55544 target protein and GAM263894 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM53123, GAM55544 and GAM263894

GR7092 BE300075 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7092(GR7092) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7092 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7092 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7092 gene encodes GR7092 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7092 precursor RNA folds spatially, forming GR7092 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7092 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7092 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7092 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM597 precursor RNA, GAM29670 precursor RNA and GAM62421 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM597 RNA, GAM29670 RNA and GAM62421 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM597 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM597 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM597 target RNA into

GAM597 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM29670 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM29670 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM29670 target RNA into GAM29670 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM62421 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM62421 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM62421 target RNA into GAM62421 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7092 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7092 gene: GAM597 target protein, GAM29670 target protein and GAM62421 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM597, GAM29670 and GAM62421

GR7093 AA781920 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7093(GR7093) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7093 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7093 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7093 gene encodes GR7093 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7093 precursor RNA folds spatially, forming GR7093 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7093 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7093 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7093 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM154005 precursor RNA, GAM256433 precursor RNA and GAM309536 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM154005 RNA, GAM256433 RNA and GAM309536 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM154005 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM154005 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM154005 target RNA into GAM154005 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM256433 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM256433 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM256433 target RNA into GAM256433 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM309536 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM309536 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM309536 target RNA into GAM309536 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7093 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7093 gene: GAM154005 target protein, GAM256433 target protein and GAM309536 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM154005, GAM256433 and

GR7094 N32618 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7094(GR7094) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7094 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7094 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7094 gene encodes GR7094 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7094 precursor RNA folds spatially, forming GR7094 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7094 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7094 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7094 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM213540 precursor RNA, GAM236078 precursor RNA and GAM300848 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM213540 RNA, GAM236078 RNA and GAM300848 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM213540 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM213540 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM213540 target RNA into GAM213540 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM236078 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM236078 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM236078 target RNA into GAM236078 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM300848 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM300848 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM300848 target RNA into GAM300848 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7094 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7094 gene: GAM213540 target protein, GAM236078 target protein and GAM300848 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM213540, GAM236078 and GAM300848

GR7095 BF436457 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7095(GR7095) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7095 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7095 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7095 gene encodes GR7095 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7095 precursor RNA folds spatially, forming GR7095 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7095 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7095 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7095 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM38665 precursor RNA, GAM77849 precursor RNA and GAM200169 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM38665 RNA, GAM77849 RNA and GAM200169 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM38665 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM38665 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM38665 target RNA into GAM38665 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM77849 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM77849 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM77849 target RNA into GAM77849 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM200169 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM200169 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM200169 target RNA into GAM200169 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7095 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7095 gene: GAM38665 target protein, GAM77849 target protein and GAM200169 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM38665, GAM77849 and GAM200169

7096(GR7096) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7096 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7096 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7096 gene encodes GR7096 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7096 precursor RNA folds spatially, forming GR7096 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7096 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7096 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7096 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM214516 precursor RNA and GAM293223 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM214516 RNA and GAM293223 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM214516 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM214516 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM214516 target RNA into GAM214516 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM293223 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM293223 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM293223 target RNA into GAM293223 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7096 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7096 gene: GAM214516 target protein and GAM293223 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM214516 and GAM293223

GR7097 AI681068 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7097(GR7097) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7097 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7097 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7097 gene encodes GR7097 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7097 precursor RNA folds spatially, forming GR7097 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7097 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7097 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7097 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM206722 precursor RNA and GAM233808 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM206722 RNA and GAM233808 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM206722 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM206722 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM206722 target RNA into GAM206722 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM233808 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM233808 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM233808 target RNA into GAM233808 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7097 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7097 gene: GAM206722 target protein and GAM233808 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM206722 and GAM233808

GR7098 AW748563 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7098(GR7098) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7098 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7098 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7098 gene encodes GR7098 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7098 precursor RNA folds spatially, forming GR7098 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7098 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7098 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7098 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2

separate GAM precursor RNAs, GAM7955 precursor RNA and GAM184642 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7955 RNA and GAM184642 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7955 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7955 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7955 target RNA into GAM7955 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM184642 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM184642 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM184642 target RNA into GAM184642 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7098 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7098 gene: GAM7955 target protein and GAM184642 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7955 and GAM184642

GR7099 BM724195 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7099(GR7099) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7099 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7099 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7099 gene encodes GR7099 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR7099 precursor RNA folds spatially, forming GR7099 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7099 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7099 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7099 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1713 precursor RNA, GAM118490 precursor RNA and GAM306300 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1713 RNA, GAM118490 RNA and GAM306300 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1713 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1713 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1713 target RNA into GAM1713 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM118490 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM118490 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM118490 target RNA into GAM118490 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM306300 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM306300 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM306300 target RNA into GAM306300 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7099 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7099 gene: GAM1713 target protein, GAM118490 target protein and GAM306300 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1713, GAM118490 and GAM306300

GR7100 AI694645 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7100(GR7100) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7100 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7100 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7100 gene encodes GR7100 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7100 precursor RNA folds spatially, forming GR7100 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7100 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7100 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7100 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM11735 precursor RNA and GAM165796 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM11735 RNA and GAM165796 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM11735 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM11735 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM11735 target RNA into GAM11735 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM165796 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM165796 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM165796 target RNA into GAM165796 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7100 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7100 gene: GAM11735 target protein and GAM165796 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM11735 and GAM165796

GR7101 BG027378 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7101(GR7101) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7101 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7101 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7101 gene encodes GR7101 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7101 precursor RNA folds spatially, forming GR7101 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7101 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7101 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7101 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM142011 precursor RNA and GAM318019 precursor

RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM142011 RNA and GAM318019 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM142011 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM142011 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM142011 target RNA into GAM142011 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM318019 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM318019 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM318019 target RNA into GAM318019 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7101 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7101 gene: GAM142011 target protein and GAM318019 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM142011 and GAM318019

GR7102 BE896140 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7102(GR7102) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7102 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7102 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7102 gene encodes GR7102 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7102 precursor RNA folds spatially, forming GR7102 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7102 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7102 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7102 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1505 precursor RNA, GAM88189 precursor RNA and GAM223470 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1505 RNA, GAM88189 RNA and GAM223470 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1505 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1505 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1505 target RNA into GAM1505 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM88189 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM88189 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM88189 target RNA into GAM88189 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM223470 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM223470 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM223470 target RNA into GAM223470 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly

utilities, of GR7102 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7102 gene: GAM1505 target protein, GAM88189 target protein and GAM223470 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1505, GAM88189 and GAM223470

GR7103 BM909811 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7103(GR7103) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7103 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7103 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7103 gene encodes GR7103 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7103 precursor RNA folds spatially, forming GR7103 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7103 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7103 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7103 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7343 precursor RNA and GAM90315 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7343 RNA and GAM90315 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7343 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7343 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds

to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7343 target RNA into GAM7343 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM90315 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM90315 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM90315 target RNA into GAM90315 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7103 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7103 gene: GAM7343 target protein and GAM90315 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7343 and GAM90315

GR7104 AA559172 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7104(GR7104) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7104 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7104 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7104 gene encodes GR7104 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7104 precursor RNA folds spatially, forming GR7104 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7104 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7104 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7104 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1165 precursor RNA, GAM148547 precursor RNA and GAM239818 precursor RNA, herein schematically represented by GAM1 FOLDED

PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1165 RNA, GAM148547 RNA and GAM239818 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1165 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1165 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1165 target RNA into GAM1165 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM148547 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM148547 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM148547 target RNA into GAM148547 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM239818 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM239818 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM239818 target RNA into GAM239818 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7104 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7104 gene: GAM1165 target protein, GAM148547 target protein and GAM239818 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1165, GAM148547 and GAM239818

GR7105 BE616799 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7105(GR7105) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR7105 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7105 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7105 gene encodes GR7105 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7105 precursor RNA folds spatially, forming GR7105 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7105 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7105 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7105 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6359 precursor RNA and GAM156052 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6359 RNA and GAM156052 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6359 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6359 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6359 target RNA into GAM6359 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM156052 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM156052 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM156052 target RNA into GAM156052 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly

utilities, of GR7105 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7105 gene: GAM6359 target protein and GAM156052 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6359 and GAM156052

GR7106 BG214335 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7106(GR7106) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7106 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7106 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7106 gene encodes GR7106 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7106 precursor RNA folds spatially, forming GR7106 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7106 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7106 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7106 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM413 precursor RNA and GAM173580 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM413 RNA and GAM173580 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM413 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM413 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig. 8, thereby inhibiting translation of GAM413 target RNA into GAM413 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM173580 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM173580 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM173580 target RNA into GAM173580 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7106 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7106 gene: GAM413 target protein and GAM173580 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM413 and GAM173580

GR7107 BG761327 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7107(GR7107) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7107 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7107 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7107 gene encodes GR7107 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7107 precursor RNA folds spatially, forming GR7107 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7107 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7107 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7107 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM812 precursor RNA and GAM82539 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin

shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM812 RNA and GAM82539 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM812 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM812 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM812 target RNA into GAM812 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM82539 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM82539 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM82539 target RNA into GAM82539 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7107 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7107 gene: GAM812 target protein and GAM82539 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM812 and GAM82539

GR7108 AA334766 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7108(GR7108) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7108 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7108 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7108 gene encodes GR7108 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7108 precursor RNA folds spatially, forming GR7108 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7108 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7108 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7108 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6178 precursor RNA and GAM228078 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6178 RNA and GAM228078 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6178 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6178 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6178 target RNA into GAM6178 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM228078 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM228078 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM228078 target RNA into GAM228078 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7108 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7108 gene: GAM6178 target protein and GAM228078 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6178 and GAM228078

GR7109 BG033027 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7109(GR7109) gene, which encodes an `operon-like` cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7109 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7109 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7109 gene encodes GR7109 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7109 precursor RNA folds spatially, forming GR7109 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7109 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7109 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7109 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4181 precursor RNA, GAM80964 precursor RNA and GAM205282 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4181 RNA, GAM80964 RNA and GAM205282 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4181 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4181 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4181 target RNA into GAM4181 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM80964 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM80964 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM80964 target RNA into GAM80964 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM205282 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM205282 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM205282 target RNA into GAM205282 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7109 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7109 gene: GAM4181 target protein, GAM80964 target protein and GAM205282 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4181, GAM80964 and GAM205282

GR7110 BI838656 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7110(GR7110) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7110 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7110 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7110 gene encodes GR7110 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7110 precursor RNA folds spatially, forming GR7110 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7110 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7110 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7110 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM109246 precursor RNA, GAM251501 precursor RNA and GAM259135 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED

PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM109246 RNA, GAM251501 RNA and GAM259135 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM109246 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM109246 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM109246 target RNA into GAM109246 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM251501 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM251501 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM251501 target RNA into GAM251501 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM259135 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM259135 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM259135 target RNA into GAM259135 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7110 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7110 gene: GAM109246 target protein, GAM251501 target protein and GAM259135 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM109246, GAM251501 and GAM259135

GR7111 BF685182 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7111(GR7111) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7111 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7111 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7111 gene encodes GR7111 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7111 precursor RNA folds spatially, forming GR7111 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7111 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7111 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7111 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM5155 precursor RNA, GAM145152 precursor RNA and GAM207885 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5155 RNA, GAM145152 RNA and GAM207885 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5155 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5155 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5155 target RNA into GAM5155 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM145152 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM145152 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM145152 target RNA into GAM145152 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM207885 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM207885 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM207885 target RNA into GAM207885 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7111 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7111 gene: GAM5155 target protein, GAM145152 target protein and GAM207885 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5155, GAM145152 and GAM207885

GR7112 BE066782 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7112(GR7112) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7112 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7112 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7112 gene encodes GR7112 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7112 precursor RNA folds spatially, forming GR7112 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7112 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7112 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7112 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM170357 precursor RNA and GAM310608 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM170357 RNA and GAM310608 RNA, herein schematically

represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM170357 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM170357 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM170357 target RNA into GAM170357 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM310608 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM310608 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM310608 target RNA into GAM310608 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7112 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7112 gene: GAM170357 target protein and GAM310608 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM170357 and GAM310608

GR7113 AA046371 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7113(GR7113) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7113 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7113 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7113 gene encodes GR7113 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7113 precursor RNA folds spatially, forming GR7113 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7113 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7113 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7113 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM36493 precursor RNA, GAM126065 precursor RNA and GAM332268 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM36493 RNA, GAM126065 RNA and GAM332268 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM36493 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM36493 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM36493 target RNA into GAM36493 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM126065 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM126065 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM126065 target RNA into GAM126065 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM332268 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM332268 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM332268 target RNA into GAM332268 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7113 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7113 gene: GAM36493 target protein, GAM126065 target protein and GAM332268 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM36493, GAM126065 and

GR7114 AV759679 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7114(GR7114) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7114 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7114 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7114 gene encodes GR7114 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7114 precursor RNA folds spatially, forming GR7114 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7114 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7114 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7114 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2007 precursor RNA and GAM3185 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2007 RNA and GAM3185 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2007 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2007 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2007 target RNA into GAM2007 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM3185 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3185 target RNA, herein schematically represented by

GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3185 target RNA into GAM3185 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7114 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7114 gene: GAM2007 target protein and GAM3185 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2007 and GAM3185

GR7115 AW974971 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7115(GR7115) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7115 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7115 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7115 gene encodes GR7115 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7115 precursor RNA folds spatially, forming GR7115 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7115 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7115 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7115 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3738 precursor RNA and GAM153004 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3738 RNA and GAM153004 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding

to GAM RNA of Fig. 8.

GAM3738 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3738 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3738 target RNA into GAM3738 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM153004 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM153004 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM153004 target RNA into GAM153004 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7115 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7115 gene: GAM3738 target protein and GAM153004 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3738 and GAM153004

GR7116 AI122797 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7116(GR7116) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7116 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7116 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7116 gene encodes GR7116 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7116 precursor RNA folds spatially, forming GR7116 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7116 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7116 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR7116 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM5544 precursor RNA, GAM95644 precursor RNA, GAM175836 precursor RNA and GAM227967 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5544 RNA, GAM95644 RNA, GAM175836 RNA and GAM227967 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5544 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5544 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5544 target RNA into GAM5544 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM95644 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM95644 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM95644 target RNA into GAM95644 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM175836 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM175836 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM175836 target RNA into GAM175836 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM227967 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM227967 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM227967 target RNA into GAM227967 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly

utilities, of GR7116 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7116 gene: GAM5544 target protein, GAM95644 target protein, GAM175836 target protein and GAM227967 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5544, GAM95644, GAM175836 and GAM227967

GR7117 AI672526 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7117(GR7117) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7117 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7117 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7117 gene encodes GR7117 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7117 precursor RNA folds spatially, forming GR7117 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7117 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7117 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7117 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM70593 precursor RNA and GAM249722 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM70593 RNA and GAM249722 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM70593 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM70593 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM70593 target RNA into GAM70593 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM249722 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM249722 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM249722 target RNA into GAM249722 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7117 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7117 gene: GAM70593 target protein and GAM249722 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM70593 and GAM249722

GR7118 AA293022 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7118(GR7118) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7118 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7118 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7118 gene encodes GR7118 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7118 precursor RNA folds spatially, forming GR7118 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7118 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7118 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7118 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM19725 precursor RNA and GAM281016 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3

FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM19725 RNA and GAM281016 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM19725 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM19725 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM19725 target RNA into GAM19725 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM281016 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM281016 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM281016 target RNA into GAM281016 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7118 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7118 gene: GAM19725 target protein and GAM281016 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM19725 and GAM281016

GR7119 AA363925 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7119(GR7119) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7119 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7119 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7119 gene encodes GR7119 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7119 precursor RNA folds spatially, forming GR7119 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7119 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7119 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7119 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM130236 precursor RNA and GAM163173 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM130236 RNA and GAM163173 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM130236 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM130236 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM130236 target RNA into GAM130236 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM163173 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM163173 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM163173 target RNA into GAM163173 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7119 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7119 gene: GAM130236 target protein and GAM163173 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM130236 and GAM163173

7120(GR7120) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7120 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7120 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7120 gene encodes GR7120 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7120 precursor RNA folds spatially, forming GR7120 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7120 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7120 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7120 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8671 precursor RNA and GAM253673 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8671 RNA and GAM253673 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8671 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8671 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8671 target RNA into GAM8671 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM253673 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM253673 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM253673 target RNA into GAM253673 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7120 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7120 gene: GAM8671 target protein and GAM253673 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8671 and GAM253673

GR7121 AI023733 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7121(GR7121) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7121 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7121 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7121 gene encodes GR7121 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7121 precursor RNA folds spatially, forming GR7121 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7121 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7121 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7121 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4859 precursor RNA and GAM237966 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4859 RNA and GAM237966 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4859 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM4859 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4859 target RNA into GAM4859 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM237966 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM237966 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM237966 target RNA into GAM237966 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7121 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7121 gene: GAM4859 target protein and GAM237966 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4859 and GAM237966

GR7122 BM174960 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7122(GR7122) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7122 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7122 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7122 gene encodes GR7122 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7122 precursor RNA folds spatially, forming GR7122 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7122 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7122 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7122 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3

separate GAM precursor RNAs, GAM183189 precursor RNA, GAM213717 precursor RNA and GAM332734 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM183189 RNA, GAM213717 RNA and GAM332734 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM183189 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM183189 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM183189 target RNA into GAM183189 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM213717 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM213717 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM213717 target RNA into GAM213717 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM332734 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM332734 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM332734 target RNA into GAM332734 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7122 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7122 gene: GAM183189 target protein, GAM213717 target protein and GAM332734 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM183189, GAM213717 and GAM332734

GR7123 AL712659 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7123(GR7123) gene, which encodes an `operon-like` cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7123 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7123 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7123 gene encodes GR7123 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7123 precursor RNA folds spatially, forming GR7123 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7123 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7123 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7123 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM20186 precursor RNA and GAM335965 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM20186 RNA and GAM335965 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM20186 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM20186 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM20186 target RNA into GAM20186 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM335965 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM335965 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM335965 target RNA into GAM335965 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7123 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7123 gene: GAM20186 target protein and GAM335965 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM20186 and GAM335965

GR7124 M62273 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7124(GR7124) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7124 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7124 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7124 gene encodes GR7124 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7124 precursor RNA folds spatially, forming GR7124 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7124 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7124 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7124 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM56410 precursor RNA and GAM79597 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM56410 RNA and GAM79597 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM56410 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM56410 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM56410 target RNA into GAM56410 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM79597 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM79597 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM79597 target RNA into GAM79597 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7124 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7124 gene: GAM56410 target protein and GAM79597 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM56410 and GAM79597

GR7125 AV764214 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7125(GR7125) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7125 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7125 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7125 gene encodes GR7125 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7125 precursor RNA folds spatially, forming GR7125 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7125 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7125 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7125 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM921 precursor RNA, GAM2327 precursor RNA,

GAM2499 precursor RNA and GAM7274 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM921 RNA, GAM2327 RNA, GAM2499 RNA and GAM7274 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM921 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM921 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM921 target RNA into GAM921 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM2327 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2327 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2327 target RNA into GAM2327 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM2499 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2499 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2499 target RNA into GAM2499 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7274 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7274 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7274 target RNA into GAM7274 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7125 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7125 gene: GAM921 target protein, GAM2327 target protein, GAM2499 target protein and GAM7274 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3

TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM921, GAM2327, GAM2499 and GAM7274

GR7126 AW770872 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7126(GR7126) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7126 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7126 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7126 gene encodes GR7126 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7126 precursor RNA folds spatially, forming GR7126 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7126 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7126 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7126 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3967 precursor RNA and GAM195522 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3967 RNA and GAM195522 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3967 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3967 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3967 target RNA into GAM3967 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM195522 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM195522 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM195522 target RNA into GAM195522 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7126 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7126 gene: GAM3967 target protein and GAM195522 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3967 and GAM195522

GR7127 AI885036 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7127(GR7127) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7127 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7127 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7127 gene encodes GR7127 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7127 precursor RNA folds spatially, forming GR7127 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7127 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7127 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7127 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3727 precursor RNA and GAM42101 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM3727 RNA and GAM42101 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3727 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3727 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3727 target RNA into GAM3727 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM42101 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM42101 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM42101 target RNA into GAM42101 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7127 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7127 gene: GAM3727 target protein and GAM42101 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3727 and GAM42101

GR7128 BE271546 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7128(GR7128) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7128 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7128 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7128 gene encodes GR7128 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7128 precursor RNA folds spatially, forming GR7128 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7128 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7128 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7128 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM94141 precursor RNA and GAM216331 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM94141 RNA and GAM216331 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM94141 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM94141 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM94141 target RNA into GAM94141 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM216331 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM216331 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM216331 target RNA into GAM216331 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7128 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7128 gene: GAM94141 target protein and GAM216331 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM94141 and GAM216331

GR7129 AI932986 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7129(GR7129) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7129 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7129 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7129 gene encodes GR7129 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7129 precursor RNA folds spatially, forming GR7129 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7129 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7129 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7129 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM70638 precursor RNA, GAM262396 precursor RNA and GAM272184 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM70638 RNA, GAM262396 RNA and GAM272184 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM70638 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM70638 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM70638 target RNA into GAM70638 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM262396 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM262396 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM262396 target RNA into GAM262396 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM272184 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM272184 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM272184 target RNA into GAM272184 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7129 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7129 gene: GAM70638 target protein, GAM262396 target protein and GAM272184 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM70638, GAM262396 and GAM272184

GR7130 AA527941 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7130(GR7130) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7130 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7130 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7130 gene encodes GR7130 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7130 precursor RNA folds spatially, forming GR7130 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7130 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7130 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7130 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM40279 precursor RNA and GAM150297 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM40279 RNA and GAM150297 RNA, herein schematically

represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM40279 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM40279 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM40279 target RNA into GAM40279 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM150297 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM150297 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM150297 target RNA into GAM150297 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7130 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7130 gene: GAM40279 target protein and GAM150297 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM40279 and GAM150297

GR7131 BF880955 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7131(GR7131) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7131 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7131 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7131 gene encodes GR7131 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7131 precursor RNA folds spatially, forming GR7131 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7131 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7131 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7131 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3532 precursor RNA, GAM3647 precursor RNA and GAM253172 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3532 RNA, GAM3647 RNA and GAM253172 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3532 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3532 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3532 target RNA into GAM3532 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM3647 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3647 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3647 target RNA into GAM3647 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM253172 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM253172 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM253172 target RNA into GAM253172 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7131 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7131 gene: GAM3532 target protein, GAM3647 target protein and GAM253172 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3532, GAM3647 and

GR7132 BI522497 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7132(GR7132) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7132 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7132 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7132 gene encodes GR7132 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7132 precursor RNA folds spatially, forming GR7132 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7132 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7132 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7132 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM242827 precursor RNA and GAM281020 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM242827 RNA and GAM281020 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM242827 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM242827 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM242827 target RNA into GAM242827 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM281020 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM281020 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM281020 target RNA into GAM281020 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7132 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7132 gene: GAM242827 target protein and GAM281020 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM242827 and GAM281020

GR7133 BF690254 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7133(GR7133) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7133 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7133 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7133 gene encodes GR7133 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7133 precursor RNA folds spatially, forming GR7133 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7133 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7133 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7133 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM19639 precursor RNA, GAM66284 precursor RNA and GAM93015 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM19639 RNA, GAM66284 RNA and GAM93015 RNA, herein

schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM19639 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM19639 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM19639 target RNA into GAM19639 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM66284 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM66284 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM66284 target RNA into GAM66284 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM93015 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM93015 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM93015 target RNA into GAM93015 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7133 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7133 gene: GAM19639 target protein, GAM66284 target protein and GAM93015 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM19639, GAM66284 and GAM93015

GR7134 AI718743 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7134(GR7134) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7134 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7134 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7134 gene encodes GR7134 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7134 precursor RNA folds spatially, forming GR7134 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7134 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7134 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7134 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM128844 precursor RNA and GAM270486 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM128844 RNA and GAM270486 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM128844 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM128844 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM128844 target RNA into GAM128844 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM270486 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM270486 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM270486 target RNA into GAM270486 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7134 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7134 gene: GAM128844 target protein and GAM270486 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM128844 and GAM270486

GR7135 AW365069 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7135(GR7135) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7135 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7135 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7135 gene encodes GR7135 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7135 precursor RNA folds spatially, forming GR7135 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7135 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7135 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7135 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4696 precursor RNA and GAM232338 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4696 RNA and GAM232338 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4696 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4696 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4696 target RNA into GAM4696 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM232338 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM232338 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM232338 target RNA into GAM232338 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7135 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7135 gene: GAM4696 target protein and GAM232338 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4696 and GAM232338

GR7136 BF246468 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7136(GR7136) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7136 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7136 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7136 gene encodes GR7136 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7136 precursor RNA folds spatially, forming GR7136 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7136 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7136 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7136 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM274004 precursor RNA and GAM315152 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM274004 RNA and GAM315152 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM274004 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM274004 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM274004 target RNA into GAM274004 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM315152 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM315152 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM315152 target RNA into GAM315152 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7136 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7136 gene: GAM274004 target protein and GAM315152 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM274004 and GAM315152

GR7137 AI001167 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7137(GR7137) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7137 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7137 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7137 gene encodes GR7137 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7137 precursor RNA folds spatially, forming GR7137 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7137 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7137 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7137 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM160434 precursor RNA and GAM180225 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM160434 RNA and GAM180225 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM160434 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM160434 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM160434 target RNA into GAM160434 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM180225 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM180225 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM180225 target RNA into GAM180225 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7137 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7137 gene: GAM160434 target protein and GAM180225 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM160434 and GAM180225

GR7138 BF826454 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7138(GR7138) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7138 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7138 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7138 gene encodes GR7138 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7138 precursor RNA folds spatially, forming GR7138 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7138 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7138 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7138 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1409 precursor RNA and GAM43682 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1409 RNA and GAM43682 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1409 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1409 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1409 target RNA into GAM1409 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM43682 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM43682 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM43682 target RNA into GAM43682 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7138 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7138 gene: GAM1409 target protein and GAM43682 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes

is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1409 and GAM43682

GR7139 BE545084 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7139(GR7139) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7139 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7139 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7139 gene encodes GR7139 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7139 precursor RNA folds spatially, forming GR7139 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7139 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7139 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7139 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5965 precursor RNA and GAM6611 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5965 RNA and GAM6611 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5965 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5965 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5965 target RNA into GAM5965 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6611 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM6611 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6611 target RNA into GAM6611 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7139 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7139 gene: GAM5965 target protein and GAM6611 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5965 and GAM6611

GR7140 BG722067 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7140(GR7140) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7140 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7140 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7140 gene encodes GR7140 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7140 precursor RNA folds spatially, forming GR7140 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7140 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7140 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7140 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM6371 precursor RNA, GAM108600 precursor RNA, GAM184307 precursor RNA and GAM289651 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM6371 RNA, GAM108600 RNA, GAM184307 RNA and GAM289651 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6371 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6371 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6371 target RNA into GAM6371 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM108600 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM108600 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM108600 target RNA into GAM108600 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM184307 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM184307 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM184307 target RNA into GAM184307 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM289651 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM289651 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM289651 target RNA into GAM289651 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7140 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7140 gene: GAM6371 target protein, GAM108600 target protein, GAM184307 target protein and GAM289651 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6371, GAM108600, GAM184307 and GAM289651

GR7141 AW836572 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7141(GR7141) gene, which encodes an `operon-like` cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7141 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7141 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7141 gene encodes GR7141 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7141 precursor RNA folds spatially, forming GR7141 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7141 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7141 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7141 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1810 precursor RNA, GAM45154 precursor RNA and GAM91775 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1810 RNA, GAM45154 RNA and GAM91775 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1810 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1810 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1810 target RNA into GAM1810 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM45154 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM45154 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM45154 target RNA into GAM45154 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM91775 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM91775 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM91775 target RNA into GAM91775 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7141 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7141 gene: GAM1810 target protein, GAM45154 target protein and GAM91775 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1810, GAM45154 and GAM91775

GR7142 AW205948 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7142(GR7142) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7142 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7142 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7142 gene encodes GR7142 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7142 precursor RNA folds spatially, forming GR7142 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7142 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7142 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7142 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM169092 precursor RNA, GAM178202 precursor RNA and GAM194688 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED

PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM169092 RNA, GAM178202 RNA and GAM194688 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM169092 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM169092 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM169092 target RNA into GAM169092 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM178202 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM178202 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM178202 target RNA into GAM178202 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM194688 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM194688 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM194688 target RNA into GAM194688 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7142 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7142 gene: GAM169092 target protein, GAM178202 target protein and GAM194688 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM169092, GAM178202 and GAM194688

GR7143 AA742544 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7143(GR7143) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7143 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7143 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7143 gene encodes GR7143 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7143 precursor RNA folds spatially, forming GR7143 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7143 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7143 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7143 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM169 precursor RNA and GAM247352 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM169 RNA and GAM247352 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM169 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM169 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM169 target RNA into GAM169 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM247352 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM247352 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM247352 target RNA into GAM247352 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7143 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR7143 gene: GAM169 target protein and GAM247352 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM169 and GAM247352

GR7144 BE837519 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7144(GR7144) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7144 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7144 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7144 gene encodes GR7144 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7144 precursor RNA folds spatially, forming GR7144 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7144 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7144 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7144 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM144602 precursor RNA and GAM217362 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM144602 RNA and GAM217362 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM144602 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM144602 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM144602 target RNA into GAM144602 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM217362 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM217362 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM217362 target RNA into GAM217362 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7144 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7144 gene: GAM144602 target protein and GAM217362 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM144602 and GAM217362

GR7145 AA641309 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7145(GR7145) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7145 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7145 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7145 gene encodes GR7145 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7145 precursor RNA folds spatially, forming GR7145 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7145 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7145 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7145 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM67943 precursor RNA and GAM218507 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM67943 RNA and GAM218507 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM67943 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM67943 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM67943 target RNA into GAM67943 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM218507 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM218507 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM218507 target RNA into GAM218507 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7145 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7145 gene: GAM67943 target protein and GAM218507 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM67943 and GAM218507

GR7146 AA492501 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7146(GR7146) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7146 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7146 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7146 gene encodes GR7146 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7146 precursor RNA folds spatially, forming GR7146 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7146 folded precursor RNA comprises a plurality of what is known in the

art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7146 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7146 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM19476 precursor RNA and GAM255985 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM19476 RNA and GAM255985 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM19476 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM19476 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM19476 target RNA into GAM19476 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM255985 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM255985 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM255985 target RNA into GAM255985 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7146 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7146 gene: GAM19476 target protein and GAM255985 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM19476 and GAM255985

GR7147 AA853986 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7147(GR7147) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR7147 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7147 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7147 gene encodes GR7147 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7147 precursor RNA folds spatially, forming GR7147 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7147 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7147 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7147 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM272098 precursor RNA and GAM276618 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM272098 RNA and GAM276618 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM272098 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM272098 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM272098 target RNA into GAM272098 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM276618 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM276618 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM276618 target RNA into GAM276618 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly

utilities, of GR7147 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7147 gene: GAM272098 target protein and GAM276618 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM272098 and GAM276618

GR7148 BE391662 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7148(GR7148) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7148 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7148 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7148 gene encodes GR7148 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7148 precursor RNA folds spatially, forming GR7148 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7148 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7148 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7148 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 5 separate GAM precursor RNAs, GAM1507 precursor RNA, GAM1742 precursor RNA, GAM112294 precursor RNA, GAM160175 precursor RNA and GAM291490 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1507 RNA, GAM1742 RNA, GAM112294 RNA, GAM160175 RNA and GAM291490 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1507 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1507 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds

to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1507 target RNA into GAM1507 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM1742 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1742 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1742 target RNA into GAM1742 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM112294 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM112294 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM112294 target RNA into GAM112294 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM160175 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM160175 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM160175 target RNA into GAM160175 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM291490 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM291490 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM291490 target RNA into GAM291490 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7148 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7148 gene: GAM1507 target protein, GAM1742 target protein, GAM112294 target protein, GAM160175 target protein and GAM291490 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1507, GAM1742, GAM112294, GAM160175 and GAM291490

GR7149 BG820310 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7149(GR7149) gene, which encodes an `operon-like` cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7149 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7149 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7149 gene encodes GR7149 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7149 precursor RNA folds spatially, forming GR7149 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7149 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7149 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7149 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM5619 precursor RNA, GAM131708 precursor RNA, GAM249009 precursor RNA and GAM269782 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5619 RNA, GAM131708 RNA, GAM249009 RNA and GAM269782 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5619 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5619 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5619 target RNA into GAM5619 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM131708 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM131708 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM131708 target RNA into GAM131708 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM249009 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM249009 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM249009 target RNA into GAM249009 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM269782 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM269782 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM269782 target RNA into GAM269782 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7149 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7149 gene: GAM5619 target protein, GAM131708 target protein, GAM249009 target protein and GAM269782 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5619, GAM131708, GAM249009 and GAM269782

GR7150 BM021478 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7150(GR7150) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7150 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7150 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7150 gene encodes GR7150 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7150 precursor RNA folds spatially, forming GR7150 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7150 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7150 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR7150 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM62796 precursor RNA and GAM110988 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM62796 RNA and GAM110988 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM62796 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM62796 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM62796 target RNA into GAM62796 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM110988 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM110988 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM110988 target RNA into GAM110988 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7150 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7150 gene: GAM62796 target protein and GAM110988 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM62796 and GAM110988

GR7151 BM749020 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7151(GR7151) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7151 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7151

gene was detected is described hereinabove with reference to Figs. 8-18.

GR7151 gene encodes GR7151 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7151 precursor RNA folds spatially, forming GR7151 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7151 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7151 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7151 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4378 precursor RNA and GAM113972 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4378 RNA and GAM113972 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4378 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4378 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4378 target RNA into GAM4378 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM113972 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM113972 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM113972 target RNA into GAM113972 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7151 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7151 gene: GAM4378 target protein and GAM113972 target protein, herein schematically represented by GAM1

TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4378 and GAM113972

GR7152 BG106935 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7152(GR7152) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7152 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7152 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7152 gene encodes GR7152 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7152 precursor RNA folds spatially, forming GR7152 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7152 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7152 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7152 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM6579 precursor RNA, GAM14411 precursor RNA, GAM219823 precursor RNA and GAM317852 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6579 RNA, GAM14411 RNA, GAM219823 RNA and GAM317852 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6579 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6579 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6579 target RNA into GAM6579 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM14411 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM14411 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM14411 target RNA into GAM14411 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM219823 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM219823 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM219823 target RNA into GAM219823 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM317852 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM317852 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM317852 target RNA into GAM317852 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7152 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7152 gene: GAM6579 target protein, GAM14411 target protein, GAM219823 target protein and GAM317852 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6579, GAM14411, GAM219823 and GAM317852

GR7153 AW969189 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7153(GR7153) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7153 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7153 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7153 gene encodes GR7153 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7153 precursor RNA folds spatially, forming GR7153 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7153 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7153 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7153 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3898 precursor RNA, GAM207058 precursor RNA and GAM332423 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3898 RNA, GAM207058 RNA and GAM332423 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3898 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3898 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3898 target RNA into GAM3898 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM207058 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM207058 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM207058 target RNA into GAM207058 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM332423 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM332423 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM332423 target RNA into GAM332423 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7153 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7153 gene: GAM3898 target protein, GAM207058 target protein and GAM332423 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3898, GAM207058 and GAM332423

GR7154 BI324862 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7154(GR7154) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7154 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7154 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7154 gene encodes GR7154 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7154 precursor RNA folds spatially, forming GR7154 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7154 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7154 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7154 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM6900 precursor RNA, GAM38701 precursor RNA and GAM70479 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6900 RNA, GAM38701 RNA and GAM70479 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6900 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6900 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds

to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6900 target RNA into GAM6900 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM38701 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM38701 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM38701 target RNA into GAM38701 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM70479 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM70479 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM70479 target RNA into GAM70479 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7154 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7154 gene: GAM6900 target protein, GAM38701 target protein and GAM70479 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6900, GAM38701 and GAM70479

GR7155 BG615907 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7155(GR7155) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7155 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7155 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7155 gene encodes GR7155 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7155 precursor RNA folds spatially, forming GR7155 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7155 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR7155 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7155 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM216062 precursor RNA and GAM250319 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM216062 RNA and GAM250319 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM216062 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM216062 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM216062 target RNA into GAM216062 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM250319 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM250319 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM250319 target RNA into GAM250319 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7155 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7155 gene: GAM216062 target protein and GAM250319 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM216062 and GAM250319

GR7156 AI150562 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7156(GR7156) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7156 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7156 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7156 gene encodes GR7156 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7156 precursor RNA folds spatially, forming GR7156 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7156 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7156 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7156 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM53439 precursor RNA and GAM67363 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM53439 RNA and GAM67363 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM53439 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM53439 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM53439 target RNA into GAM53439 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM67363 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM67363 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM67363 target RNA into GAM67363 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7156 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7156 gene: GAM53439 target protein and GAM67363 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM53439 and GAM67363

GR7157 AA627199 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7157(GR7157) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7157 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7157 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7157 gene encodes GR7157 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7157 precursor RNA folds spatially, forming GR7157 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7157 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7157 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7157 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2941 precursor RNA and GAM162494 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2941 RNA and GAM162494 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2941 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2941 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2941 target RNA into

GAM2941 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM162494 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM162494 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM162494 target RNA into GAM162494 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7157 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7157 gene: GAM2941 target protein and GAM162494 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2941 and GAM162494

GR7158 AI635603 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7158(GR7158) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7158 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7158 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7158 gene encodes GR7158 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7158 precursor RNA folds spatially, forming GR7158 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7158 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7158 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7158 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4258 precursor RNA and GAM101550 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4258 RNA and GAM101550 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4258 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4258 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4258 target RNA into GAM4258 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM101550 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM101550 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM101550 target RNA into GAM101550 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7158 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7158 gene: GAM4258 target protein and GAM101550 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4258 and GAM101550

GR7159 BF700015 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7159(GR7159) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7159 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7159 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7159 gene encodes GR7159 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7159 precursor RNA folds spatially, forming GR7159 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated

that GR7159 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7159 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7159 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4927 precursor RNA and GAM218163 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4927 RNA and GAM218163 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4927 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4927 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4927 target RNA into GAM4927 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM218163 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM218163 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM218163 target RNA into GAM218163 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7159 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7159 gene: GAM4927 target protein and GAM218163 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4927 and GAM218163

GR7160 BG473934 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7160(GR7160) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR7160 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7160 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7160 gene encodes GR7160 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7160 precursor RNA folds spatially, forming GR7160 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7160 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7160 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7160 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM2685 precursor RNA, GAM211263 precursor RNA, GAM219384 precursor RNA and GAM271302 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2685 RNA, GAM211263 RNA, GAM219384 RNA and GAM271302 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2685 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2685 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2685 target RNA into GAM2685 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM211263 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM211263 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM211263 target RNA into GAM211263 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM219384 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM219384 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM219384 target RNA into GAM219384 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM271302 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM271302 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM271302 target RNA into GAM271302 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7160 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7160 gene: GAM2685 target protein, GAM211263 target protein, GAM219384 target protein and GAM271302 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2685, GAM211263, GAM219384 and GAM271302

GR7161 AA507935 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7161(GR7161) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7161 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7161 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7161 gene encodes GR7161 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7161 precursor RNA folds spatially, forming GR7161 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7161 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7161 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7161 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM114417 precursor RNA and GAM222872 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM114417 RNA and GAM222872 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM114417 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM114417 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM114417 target RNA into GAM114417 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM222872 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM222872 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM222872 target RNA into GAM222872 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7161 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7161 gene: GAM114417 target protein and GAM222872 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM114417 and GAM222872

GR7162 BM685893 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7162(GR7162) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7162 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7162 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7162 gene encodes GR7162 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7162 precursor RNA folds spatially, forming GR7162 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7162 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7162 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7162 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM30327 precursor RNA, GAM160499 precursor RNA and GAM218990 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM30327 RNA, GAM160499 RNA and GAM218990 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM30327 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM30327 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM30327 target RNA into GAM30327 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM160499 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM160499 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM160499 target RNA into GAM160499 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM218990 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM218990 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM218990

target RNA into GAM218990 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7162 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7162 gene: GAM30327 target protein, GAM160499 target protein and GAM218990 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM30327, GAM160499 and GAM218990

GR7163 AW809289 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7163(GR7163) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7163 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7163 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7163 gene encodes GR7163 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7163 precursor RNA folds spatially, forming GR7163 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7163 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7163 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7163 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM184 precursor RNA, GAM2295 precursor RNA, GAM5904 precursor RNA and GAM307140 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM184 RNA, GAM2295 RNA, GAM5904 RNA and GAM307140 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM184 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM184 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM184 target RNA into GAM184 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM2295 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2295 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2295 target RNA into GAM2295 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5904 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5904 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5904 target RNA into GAM5904 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM307140 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM307140 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM307140 target RNA into GAM307140 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7163 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7163 gene: GAM184 target protein, GAM2295 target protein, GAM5904 target protein and GAM307140 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM184, GAM2295, GAM5904 and GAM307140

GR7164 BF670779 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7164(GR7164) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7164 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7164 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7164 gene encodes GR7164 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7164 precursor RNA folds spatially, forming GR7164 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7164 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7164 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7164 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM93707 precursor RNA, GAM321066 precursor RNA and GAM333521 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM93707 RNA, GAM321066 RNA and GAM333521 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM93707 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM93707 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM93707 target RNA into GAM93707 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM321066 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM321066 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM321066 target RNA into GAM321066 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM333521 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM333521 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM333521 target RNA into GAM333521 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7164 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7164 gene: GAM93707 target protein, GAM321066 target protein and GAM333521 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM93707, GAM321066 and GAM333521

GR7165 BE266357 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7165(GR7165) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7165 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7165 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7165 gene encodes GR7165 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7165 precursor RNA folds spatially, forming GR7165 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7165 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7165 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7165 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM223678 precursor RNA, GAM227263 precursor RNA and GAM260967 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM223678 RNA, GAM227263 RNA and GAM260967 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM223678 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM223678 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM223678 target RNA into GAM223678 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM227263 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM227263 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM227263 target RNA into GAM227263 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM260967 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM260967 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM260967 target RNA into GAM260967 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7165 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7165 gene: GAM223678 target protein, GAM227263 target protein and GAM260967 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM223678, GAM227263 and GAM260967

GR7166 BG959102 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7166(GR7166) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7166 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7166 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7166 gene encodes GR7166 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7166 precursor RNA folds spatially, forming GR7166 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7166 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7166 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7166 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5525 precursor RNA and GAM292206 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5525 RNA and GAM292206 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5525 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5525 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5525 target RNA into GAM5525 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM292206 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM292206 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM292206 target RNA into GAM292206 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7166 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7166 gene: GAM5525 target protein and GAM292206 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes

is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5525 and GAM292206

GR7167 BM922747 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7167(GR7167) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7167 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7167 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7167 gene encodes GR7167 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7167 precursor RNA folds spatially, forming GR7167 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7167 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7167 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7167 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2509 precursor RNA, GAM8453 precursor RNA and GAM64025 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2509 RNA, GAM8453 RNA and GAM64025 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2509 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2509 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2509 target RNA into GAM2509 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8453 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8453 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8453 target RNA into GAM8453 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM64025 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM64025 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM64025 target RNA into GAM64025 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7167 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7167 gene: GAM2509 target protein, GAM8453 target protein and GAM64025 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2509, GAM8453 and GAM64025

GR7168 BG184680 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7168(GR7168) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7168 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7168 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7168 gene encodes GR7168 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7168 precursor RNA folds spatially, forming GR7168 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7168 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7168 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7168 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8120 precursor RNA and GAM70228 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8120 RNA and GAM70228 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8120 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8120 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8120 target RNA into GAM8120 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM70228 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM70228 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM70228 target RNA into GAM70228 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7168 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7168 gene: GAM8120 target protein and GAM70228 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8120 and GAM70228

GR7169 BF347667 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7169(GR7169) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7169 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7169 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7169 gene encodes GR7169 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7169 precursor RNA folds spatially, forming GR7169 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7169 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7169 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7169 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM270046 precursor RNA and GAM318826 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM270046 RNA and GAM318826 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM270046 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM270046 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM270046 target RNA into GAM270046 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM318826 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM318826 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM318826 target RNA into GAM318826 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7169 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7169 gene: GAM270046 target protein and GAM318826 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference,

with references to GAM270046 and GAM318826

GR7170 BE675897 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7170(GR7170) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7170 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7170 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7170 gene encodes GR7170 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7170 precursor RNA folds spatially, forming GR7170 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7170 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7170 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7170 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM248532 precursor RNA, GAM294637 precursor RNA and GAM331786 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM248532 RNA, GAM294637 RNA and GAM331786 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM248532 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM248532 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM248532 target RNA into GAM248532 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM294637 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM294637 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM294637 target RNA into GAM294637 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM331786 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM331786 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM331786 target RNA into GAM331786 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7170 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7170 gene: GAM248532 target protein, GAM294637 target protein and GAM331786 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM248532, GAM294637 and GAM331786

GR7171 BI761117 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7171(GR7171) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7171 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7171 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7171 gene encodes GR7171 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7171 precursor RNA folds spatially, forming GR7171 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7171 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7171 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7171 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM5300 precursor RNA, GAM206195 precursor RNA, GAM223528 precursor RNA and GAM243802 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5300 RNA, GAM206195 RNA, GAM223528 RNA and GAM243802 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5300 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5300 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5300 target RNA into GAM5300 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM206195 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM206195 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM206195 target RNA into GAM206195 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM223528 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM223528 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM223528 target RNA into GAM223528 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM243802 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM243802 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM243802 target RNA into GAM243802 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7171 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7171 gene: GAM5300 target

protein, GAM206195 target protein, GAM223528 target protein and GAM243802 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5300, GAM206195, GAM223528 and GAM243802

GR7172 BG104450 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7172(GR7172) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7172 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7172 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7172 gene encodes GR7172 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7172 precursor RNA folds spatially, forming GR7172 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7172 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7172 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7172 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2751 precursor RNA, GAM7318 precursor RNA and GAM222474 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2751 RNA, GAM7318 RNA and GAM222474 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2751 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2751 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2751 target RNA into

GAM2751 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7318 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7318 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7318 target RNA into GAM7318 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM222474 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM222474 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM222474 target RNA into GAM222474 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7172 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7172 gene: GAM2751 target protein, GAM7318 target protein and GAM222474 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2751, GAM7318 and GAM222474

GR7173 BF888415 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7173(GR7173) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7173 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7173 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7173 gene encodes GR7173 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7173 precursor RNA folds spatially, forming GR7173 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7173 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7173 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7173 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM182255 precursor RNA, GAM197592 precursor RNA and GAM301281 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM182255 RNA, GAM197592 RNA and GAM301281 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM182255 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM182255 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM182255 target RNA into GAM182255 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM197592 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM197592 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM197592 target RNA into GAM197592 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM301281 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM301281 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM301281 target RNA into GAM301281 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7173 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7173 gene: GAM182255 target protein, GAM197592 target protein and GAM301281 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM182255, GAM197592 and

GR7174 BM461701 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7174(GR7174) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7174 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7174 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7174 gene encodes GR7174 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7174 precursor RNA folds spatially, forming GR7174 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7174 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7174 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7174 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM96901 precursor RNA and GAM302312 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM96901 RNA and GAM302312 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM96901 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM96901 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM96901 target RNA into GAM96901 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM302312 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM302312 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM302312 target RNA into GAM302312 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7174 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7174 gene: GAM96901 target protein and GAM302312 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM96901 and GAM302312

GR7175 BQ063103 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7175(GR7175) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7175 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7175 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7175 gene encodes GR7175 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7175 precursor RNA folds spatially, forming GR7175 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7175 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7175 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7175 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4666 precursor RNA and GAM190983 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4666 RNA and GAM190983 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding

to GAM RNA of Fig. 8.

GAM4666 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4666 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4666 target RNA into GAM4666 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM190983 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM190983 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM190983 target RNA into GAM190983 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7175 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7175 gene: GAM4666 target protein and GAM190983 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4666 and GAM190983

GR7176 H20654 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7176(GR7176) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7176 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7176 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7176 gene encodes GR7176 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7176 precursor RNA folds spatially, forming GR7176 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7176 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7176 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR7176 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4159 precursor RNA and GAM10748 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4159 RNA and GAM10748 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4159 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4159 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4159 target RNA into GAM4159 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM10748 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM10748 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM10748 target RNA into GAM10748 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7176 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7176 gene: GAM4159 target protein and GAM10748 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4159 and GAM10748

GR7177 BG576719 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7177(GR7177) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7177 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7177

gene was detected is described hereinabove with reference to Figs. 8-18.

GR7177 gene encodes GR7177 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7177 precursor RNA folds spatially, forming GR7177 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7177 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7177 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7177 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3225 precursor RNA and GAM142773 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3225 RNA and GAM142773 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3225 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3225 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3225 target RNA into GAM3225 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM142773 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM142773 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM142773 target RNA into GAM142773 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7177 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7177 gene: GAM3225 target protein and GAM142773 target protein, herein schematically represented by GAM1

TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3225 and GAM142773

GR7178 AV713230 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7178(GR7178) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7178 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7178 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7178 gene encodes GR7178 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7178 precursor RNA folds spatially, forming GR7178 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7178 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7178 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7178 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5296 precursor RNA and GAM264175 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5296 RNA and GAM264175 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5296 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5296 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5296 target RNA into GAM5296 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM264175 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM264175 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM264175 target RNA into GAM264175 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7178 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7178 gene: GAM5296 target protein and GAM264175 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5296 and GAM264175

GR7179 BM802758 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7179(GR7179) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7179 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7179 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7179 gene encodes GR7179 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7179 precursor RNA folds spatially, forming GR7179 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7179 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7179 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7179 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM182070 precursor RNA and GAM294091 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM182070 RNA and GAM294091 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM182070 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM182070 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM182070 target RNA into GAM182070 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM294091 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM294091 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM294091 target RNA into GAM294091 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7179 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7179 gene: GAM182070 target protein and GAM294091 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM182070 and GAM294091

GR7180 AW376691 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7180(GR7180) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7180 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7180 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7180 gene encodes GR7180 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7180 precursor RNA folds spatially, forming GR7180 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7180 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7180 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7180 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM179672 precursor RNA, GAM207423 precursor RNA and GAM251525 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM179672 RNA, GAM207423 RNA and GAM251525 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM179672 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM179672 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM179672 target RNA into GAM179672 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM207423 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM207423 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM207423 target RNA into GAM207423 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM251525 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM251525 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM251525 target RNA into GAM251525 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7180 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7180 gene: GAM179672 target protein, GAM207423 target protein and GAM251525 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6,

hereby incorporated by reference, with references to GAM179672, GAM207423 and GAM251525

GR7181 BF665990 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7181(GR7181) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7181 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7181 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7181 gene encodes GR7181 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7181 precursor RNA folds spatially, forming GR7181 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7181 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7181 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7181 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM84811 precursor RNA, GAM227817 precursor RNA and GAM316266 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM84811 RNA, GAM227817 RNA and GAM316266 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM84811 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM84811 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM84811 target RNA into GAM84811 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM227817 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM227817 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM227817 target RNA into GAM227817 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM316266 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM316266 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM316266 target RNA into GAM316266 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7181 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7181 gene: GAM84811 target protein, GAM227817 target protein and GAM316266 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM84811, GAM227817 and GAM316266

GR7182 AI284070 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7182(GR7182) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7182 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7182 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7182 gene encodes GR7182 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7182 precursor RNA folds spatially, forming GR7182 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7182 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7182 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7182 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM39240 precursor RNA and GAM258414 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM39240 RNA and GAM258414 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM39240 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM39240 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM39240 target RNA into GAM39240 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM258414 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM258414 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM258414 target RNA into GAM258414 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7182 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7182 gene: GAM39240 target protein and GAM258414 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM39240 and GAM258414

GR7183 BG460607 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7183(GR7183) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7183 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7183 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7183 gene encodes GR7183 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7183 precursor RNA folds spatially, forming GR7183 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7183 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7183 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7183 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM190310 precursor RNA and GAM240737 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM190310 RNA and GAM240737 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM190310 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM190310 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM190310 target RNA into GAM190310 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM240737 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM240737 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM240737 target RNA into GAM240737 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7183 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7183 gene: GAM190310 target protein and GAM240737 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference,

with references to GAM190310 and GAM240737

GR7184 BI544959 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7184(GR7184) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7184 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7184 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7184 gene encodes GR7184 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7184 precursor RNA folds spatially, forming GR7184 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7184 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7184 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7184 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM5853 precursor RNA, GAM189127 precursor RNA and GAM270927 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5853 RNA, GAM189127 RNA and GAM270927 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5853 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5853 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5853 target RNA into GAM5853 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM189127 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM189127 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM189127 target RNA into GAM189127 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM270927 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM270927 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM270927 target RNA into GAM270927 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7184 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7184 gene: GAM5853 target protein, GAM189127 target protein and GAM270927 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5853, GAM189127 and GAM270927

GR7185 BE384324 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7185(GR7185) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7185 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7185 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7185 gene encodes GR7185 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7185 precursor RNA folds spatially, forming GR7185 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7185 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7185 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7185 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM150049 precursor RNA and GAM307375 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM150049 RNA and GAM307375 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM150049 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM150049 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM150049 target RNA into GAM150049 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM307375 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM307375 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM307375 target RNA into GAM307375 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7185 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7185 gene: GAM150049 target protein and GAM307375 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM150049 and GAM307375

GR7186 BF131811 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7186(GR7186) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7186 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7186 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7186 gene encodes GR7186 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7186 precursor RNA folds spatially, forming GR7186 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7186 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7186 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7186 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM6356 precursor RNA, GAM82868 precursor RNA and GAM330270 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6356 RNA, GAM82868 RNA and GAM330270 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6356 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6356 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6356 target RNA into GAM6356 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM82868 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM82868 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM82868 target RNA into GAM82868 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM330270 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM330270 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM330270 target RNA into GAM330270 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7186 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7186 gene: GAM6356 target protein, GAM82868 target protein and GAM330270 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6356, GAM82868 and GAM330270

GR7187 BE086866 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7187(GR7187) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7187 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7187 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7187 gene encodes GR7187 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7187 precursor RNA folds spatially, forming GR7187 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7187 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7187 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7187 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM1117 precursor RNA, GAM170125 precursor RNA and GAM240777 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1117 RNA, GAM170125 RNA and GAM240777 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1117 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1117 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1117 target RNA into GAM1117 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM170125 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM170125 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM170125 target RNA into GAM170125 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM240777 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM240777 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM240777 target RNA into GAM240777 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7187 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7187 gene: GAM1117 target protein, GAM170125 target protein and GAM240777 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1117, GAM170125 and GAM240777

GR7188 BG939227 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7188(GR7188) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7188 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7188 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7188 gene encodes GR7188 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7188 precursor RNA folds spatially, forming GR7188 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7188 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7188 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7188 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM3704 precursor RNA, GAM8581 precursor RNA, GAM201096 precursor RNA and GAM327762 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3704 RNA, GAM8581 RNA, GAM201096 RNA and GAM327762 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3704 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3704 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3704 target RNA into GAM3704 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8581 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8581 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8581 target RNA into GAM8581 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM201096 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM201096 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM201096 target RNA into GAM201096 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM327762 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM327762 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM327762 target RNA into GAM327762 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7188 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7188 gene: GAM3704 target protein, GAM8581 target protein, GAM201096 target protein and GAM327762 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3704, GAM8581, GAM201096 and GAM327762

GR7189 AW583385 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7189(GR7189) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7189 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7189 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7189 gene encodes GR7189 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7189 precursor RNA folds spatially, forming GR7189 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7189 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7189 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7189 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM20053 precursor RNA and GAM78708 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM20053 RNA and GAM78708 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding

to GAM RNA of Fig. 8.

GAM20053 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM20053 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM20053 target RNA into GAM20053 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM78708 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM78708 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM78708 target RNA into GAM78708 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7189 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7189 gene: GAM20053 target protein and GAM78708 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM20053 and GAM78708

GR7190 AI869562 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7190(GR7190) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7190 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7190 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7190 gene encodes GR7190 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7190 precursor RNA folds spatially, forming GR7190 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7190 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7190 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR7190 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM92042 precursor RNA and GAM99275 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM92042 RNA and GAM99275 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM92042 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM92042 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM92042 target RNA into GAM92042 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM99275 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM99275 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM99275 target RNA into GAM99275 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7190 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7190 gene: GAM92042 target protein and GAM99275 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM92042 and GAM99275

GR7191 N50025 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7191(GR7191) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7191 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7191

gene was detected is described hereinabove with reference to Figs. 8-18.

GR7191 gene encodes GR7191 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7191 precursor RNA folds spatially, forming GR7191 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7191 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7191 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7191 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM32348 precursor RNA and GAM332452 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM32348 RNA and GAM332452 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM32348 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM32348 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM32348 target RNA into GAM32348 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM332452 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM332452 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM332452 target RNA into GAM332452 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7191 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7191 gene: GAM32348 target protein and GAM332452 target protein, herein schematically represented by GAM1

TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM32348 and GAM332452

GR7192 R35653 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7192(GR7192) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7192 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7192 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7192 gene encodes GR7192 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7192 precursor RNA folds spatially, forming GR7192 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7192 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7192 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7192 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM11376 precursor RNA and GAM126778 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM11376 RNA and GAM126778 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM11376 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM11376 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM11376 target RNA into GAM11376 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM126778 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM126778 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM126778 target RNA into GAM126778 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7192 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7192 gene: GAM11376 target protein and GAM126778 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM11376 and GAM126778

GR7193 BF241351 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7193(GR7193) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7193 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7193 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7193 gene encodes GR7193 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7193 precursor RNA folds spatially, forming GR7193 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7193 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7193 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7193 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7413 precursor RNA and GAM130677 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM7413 RNA and GAM130677 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7413 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7413 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7413 target RNA into GAM7413 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM130677 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM130677 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM130677 target RNA into GAM130677 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7193 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7193 gene: GAM7413 target protein and GAM130677 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7413 and GAM130677

GR7194 AW008987 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7194(GR7194) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7194 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7194 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7194 gene encodes GR7194 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7194 precursor RNA folds spatially, forming GR7194 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7194 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7194 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7194 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM188597 precursor RNA and GAM198327 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM188597 RNA and GAM198327 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM188597 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM188597 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM188597 target RNA into GAM188597 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM198327 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM198327 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM198327 target RNA into GAM198327 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7194 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7194 gene: GAM188597 target protein and GAM198327 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM188597 and GAM198327

GR7195 AW962394 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7195(GR7195) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7195 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7195 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7195 gene encodes GR7195 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7195 precursor RNA folds spatially, forming GR7195 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7195 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7195 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7195 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4096 precursor RNA and GAM104475 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4096 RNA and GAM104475 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4096 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4096 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4096 target RNA into GAM4096 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM104475 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM104475 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM104475 target RNA into GAM104475 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7195 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR7195 gene: GAM4096 target protein and GAM104475 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4096 and GAM104475

GR7196 BF512374 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7196(GR7196) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7196 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7196 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7196 gene encodes GR7196 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7196 precursor RNA folds spatially, forming GR7196 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7196 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7196 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7196 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM260 precursor RNA and GAM15272 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM260 RNA and GAM15272 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM260 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM260 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM260 target RNA into GAM260 target protein, herein schematically represented by GAM1 TARGET PROTEIN

through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM15272 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM15272 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM15272 target RNA into GAM15272 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7196 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7196 gene: GAM260 target protein and GAM15272 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM260 and GAM15272

GR7197 AL707942 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7197(GR7197) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7197 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7197 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7197 gene encodes GR7197 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7197 precursor RNA folds spatially, forming GR7197 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7197 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7197 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7197 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM310 precursor RNA, GAM2503 precursor RNA and GAM80409 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM310 RNA, GAM2503 RNA and GAM80409 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM310 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM310 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM310 target RNA into GAM310 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM2503 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2503 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2503 target RNA into GAM2503 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM80409 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM80409 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM80409 target RNA into GAM80409 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7197 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7197 gene: GAM310 target protein, GAM2503 target protein and GAM80409 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM310, GAM2503 and GAM80409

GR7198 BI061225 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7198(GR7198) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7198 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR7198 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7198 gene encodes GR7198 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7198 precursor RNA folds spatially, forming GR7198 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7198 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7198 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7198 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4598 precursor RNA and GAM70404 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4598 RNA and GAM70404 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4598 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4598 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4598 target RNA into GAM4598 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM70404 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM70404 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM70404 target RNA into GAM70404 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7198 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7198 gene: GAM4598 target

protein and GAM70404 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4598 and GAM70404

GR7199 BF105498 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7199(GR7199) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7199 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7199 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7199 gene encodes GR7199 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7199 precursor RNA folds spatially, forming GR7199 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7199 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7199 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7199 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3187 precursor RNA, GAM79043 precursor RNA and GAM148650 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3187 RNA, GAM79043 RNA and GAM148650 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3187 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3187 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3187 target RNA into GAM3187 target protein, herein schematically represented by GAM1 TARGET

PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM79043 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM79043 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM79043 target RNA into GAM79043 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM148650 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM148650 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM148650 target RNA into GAM148650 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7199 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7199 gene: GAM3187 target protein, GAM79043 target protein and GAM148650 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3187, GAM79043 and GAM148650

GR7200 BM796279 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7200(GR7200) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7200 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7200 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7200 gene encodes GR7200 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7200 precursor RNA folds spatially, forming GR7200 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7200 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7200 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR7200 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM47089 precursor RNA, GAM74998 precursor RNA and GAM154911 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM47089 RNA, GAM74998 RNA and GAM154911 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM47089 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM47089 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM47089 target RNA into GAM47089 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM74998 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM74998 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM74998 target RNA into GAM74998 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM154911 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM154911 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM154911 target RNA into GAM154911 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7200 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7200 gene: GAM47089 target protein, GAM74998 target protein and GAM154911 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM47089, GAM74998 and GAM154911

GR7201 AA166618 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7201(GR7201) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7201 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7201 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7201 gene encodes GR7201 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7201 precursor RNA folds spatially, forming GR7201 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7201 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7201 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7201 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM143307 precursor RNA, GAM266867 precursor RNA and GAM297455 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM143307 RNA, GAM266867 RNA and GAM297455 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM143307 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM143307 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM143307 target RNA into GAM143307 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM266867 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM266867 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM266867 target RNA into GAM266867 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM297455 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM297455 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM297455 target RNA into GAM297455 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7201 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7201 gene: GAM143307 target protein, GAM266867 target protein and GAM297455 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM143307, GAM266867 and GAM297455

GR7202 AI222245 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7202(GR7202) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7202 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7202 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7202 gene encodes GR7202 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7202 precursor RNA folds spatially, forming GR7202 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7202 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7202 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7202 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3

separate GAM precursor RNAs, GAM6694 precursor RNA, GAM176736 precursor RNA and GAM299192 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6694 RNA, GAM176736 RNA and GAM299192 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6694 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6694 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6694 target RNA into GAM6694 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM176736 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM176736 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM176736 target RNA into GAM176736 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM299192 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM299192 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM299192 target RNA into GAM299192 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7202 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7202 gene: GAM6694 target protein, GAM176736 target protein and GAM299192 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6694, GAM176736 and GAM299192

GR7203 BG912463 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7203(GR7203) gene, which encodes an `operon-like` cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7203 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7203 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7203 gene encodes GR7203 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7203 precursor RNA folds spatially, forming GR7203 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7203 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7203 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7203 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM34259 precursor RNA and GAM261399 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM34259 RNA and GAM261399 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM34259 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM34259 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM34259 target RNA into GAM34259 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM261399 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM261399 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM261399 target RNA into GAM261399 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7203 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7203 gene: GAM34259 target protein and GAM261399 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM34259 and GAM261399

GR7204 BG701437 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7204(GR7204) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7204 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7204 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7204 gene encodes GR7204 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7204 precursor RNA folds spatially, forming GR7204 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7204 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7204 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7204 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3048 precursor RNA, GAM3124 precursor RNA and GAM243941 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3048 RNA, GAM3124 RNA and GAM243941 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3048 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM3048 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3048 target RNA into GAM3048 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM3124 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3124 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3124 target RNA into GAM3124 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM243941 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM243941 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM243941 target RNA into GAM243941 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7204 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7204 gene: GAM3048 target protein, GAM3124 target protein and GAM243941 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3048, GAM3124 and GAM243941

GR7205 AA459590 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7205(GR7205) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7205 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7205 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7205 gene encodes GR7205 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7205 precursor RNA folds spatially, forming GR7205 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated

that GR7205 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7205 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7205 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM236761 precursor RNA and GAM291493 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM236761 RNA and GAM291493 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM236761 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM236761 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM236761 target RNA into GAM236761 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM291493 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM291493 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM291493 target RNA into GAM291493 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7205 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7205 gene: GAM236761 target protein and GAM291493 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM236761 and GAM291493

GR7206 AW937195 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7206(GR7206) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR7206 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7206 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7206 gene encodes GR7206 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7206 precursor RNA folds spatially, forming GR7206 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7206 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7206 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7206 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM135424 precursor RNA, GAM157251 precursor RNA and GAM314930 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM135424 RNA, GAM157251 RNA and GAM314930 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM135424 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM135424 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM135424 target RNA into GAM135424 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM157251 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM157251 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM157251 target RNA into GAM157251 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM314930 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM314930 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM314930 target RNA into GAM314930 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7206 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7206 gene: GAM135424 target protein, GAM157251 target protein and GAM314930 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM135424, GAM157251 and GAM314930

GR7207 BF317092 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7207(GR7207) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7207 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7207 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7207 gene encodes GR7207 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7207 precursor RNA folds spatially, forming GR7207 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7207 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7207 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7207 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM47207 precursor RNA, GAM99812 precursor RNA and GAM182182 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM47207 RNA, GAM99812 RNA and GAM182182 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM47207 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM47207 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM47207 target RNA into GAM47207 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM99812 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM99812 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM99812 target RNA into GAM99812 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM182182 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM182182 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM182182 target RNA into GAM182182 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7207 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7207 gene: GAM47207 target protein, GAM99812 target protein and GAM182182 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM47207, GAM99812 and GAM182182

GR7208 BE504919 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7208(GR7208) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7208 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR7208 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7208 gene encodes GR7208 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7208 precursor RNA folds spatially, forming GR7208 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7208 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7208 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7208 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3396 precursor RNA, GAM9816 precursor RNA and GAM295340 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3396 RNA, GAM9816 RNA and GAM295340 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3396 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3396 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3396 target RNA into GAM3396 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM9816 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM9816 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM9816 target RNA into GAM9816 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM295340 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM295340 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM295340 target RNA into GAM295340 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7208 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7208 gene: GAM3396 target protein, GAM9816 target protein and GAM295340 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3396, GAM9816 and GAM295340

GR7209 AA679029 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7209(GR7209) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7209 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7209 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7209 gene encodes GR7209 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7209 precursor RNA folds spatially, forming GR7209 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7209 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7209 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7209 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4274 precursor RNA and GAM63591 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4274 RNA and GAM63591 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding

to GAM RNA of Fig. 8.

GAM4274 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4274 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4274 target RNA into GAM4274 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM63591 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM63591 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM63591 target RNA into GAM63591 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7209 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7209 gene: GAM4274 target protein and GAM63591 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4274 and GAM63591

GR7210 BM993560 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7210(GR7210) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7210 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7210 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7210 gene encodes GR7210 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7210 precursor RNA folds spatially, forming GR7210 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7210 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7210 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR7210 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM84583 precursor RNA and GAM335914 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM84583 RNA and GAM335914 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM84583 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM84583 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM84583 target RNA into GAM84583 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM335914 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM335914 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM335914 target RNA into GAM335914 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7210 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7210 gene: GAM84583 target protein and GAM335914 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM84583 and GAM335914

GR7211 AA448642 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7211(GR7211) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7211 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7211

gene was detected is described hereinabove with reference to Figs. 8-18.

GR7211 gene encodes GR7211 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7211 precursor RNA folds spatially, forming GR7211 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7211 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7211 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7211 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM129 precursor RNA and GAM215810 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM129 RNA and GAM215810 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM129 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM129 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM129 target RNA into GAM129 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM215810 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM215810 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM215810 target RNA into GAM215810 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7211 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7211 gene: GAM129 target protein and GAM215810 target protein, herein schematically represented by GAM1

TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM129 and GAM215810

GR7212 BG706674 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7212(GR7212) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7212 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7212 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7212 gene encodes GR7212 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7212 precursor RNA folds spatially, forming GR7212 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7212 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7212 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7212 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4480 precursor RNA, GAM81685 precursor RNA and GAM172287 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4480 RNA, GAM81685 RNA and GAM172287 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4480 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4480 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4480 target RNA into GAM4480 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM81685 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM81685 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM81685 target RNA into GAM81685 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM172287 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM172287 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM172287 target RNA into GAM172287 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7212 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7212 gene: GAM4480 target protein, GAM81685 target protein and GAM172287 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4480, GAM81685 and GAM172287

GR7213 BM674695 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7213(GR7213) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7213 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7213 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7213 gene encodes GR7213 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7213 precursor RNA folds spatially, forming GR7213 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7213 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7213 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7213 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5571 precursor RNA and GAM6867 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5571 RNA and GAM6867 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5571 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5571 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5571 target RNA into GAM5571 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6867 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6867 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6867 target RNA into GAM6867 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7213 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7213 gene: GAM5571 target protein and GAM6867 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5571 and GAM6867

GR7214 BI600196 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7214(GR7214) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7214 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7214 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7214 gene encodes GR7214 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7214 precursor RNA folds spatially, forming GR7214 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7214 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7214 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7214 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM99014 precursor RNA, GAM210684 precursor RNA and GAM219815 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM99014 RNA, GAM210684 RNA and GAM219815 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM99014 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM99014 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM99014 target RNA into GAM99014 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM210684 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM210684 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM210684 target RNA into GAM210684 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM219815 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM219815 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM219815

target RNA into GAM219815 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7214 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7214 gene: GAM99014 target protein, GAM210684 target protein and GAM219815 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM99014, GAM210684 and GAM219815

GR7215 AL601192 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7215(GR7215) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7215 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7215 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7215 gene encodes GR7215 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7215 precursor RNA folds spatially, forming GR7215 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7215 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7215 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7215 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM232585 precursor RNA and GAM305981 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM232585 RNA and GAM305981 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM232585 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM232585 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM232585 target RNA into GAM232585 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM305981 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM305981 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM305981 target RNA into GAM305981 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7215 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7215 gene: GAM232585 target protein and GAM305981 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM232585 and GAM305981

GR7216 BF574318 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7216(GR7216) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7216 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7216 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7216 gene encodes GR7216 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7216 precursor RNA folds spatially, forming GR7216 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7216 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7216 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7216 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6967 precursor RNA and GAM7635 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6967 RNA and GAM7635 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6967 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6967 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6967 target RNA into GAM6967 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7635 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7635 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7635 target RNA into GAM7635 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7216 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7216 gene: GAM6967 target protein and GAM7635 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6967 and GAM7635

GR7217 BG927154 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7217(GR7217) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7217 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7217 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7217 gene encodes GR7217 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7217 precursor RNA folds spatially, forming GR7217 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7217 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7217 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7217 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM215010 precursor RNA and GAM300349 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM215010 RNA and GAM300349 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM215010 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM215010 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM215010 target RNA into GAM215010 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM300349 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM300349 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM300349 target RNA into GAM300349 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7217 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7217 gene: GAM215010 target protein and GAM300349 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference,

with references to GAM215010 and GAM300349

GR7218 BM011658 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7218(GR7218) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7218 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7218 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7218 gene encodes GR7218 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7218 precursor RNA folds spatially, forming GR7218 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7218 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7218 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7218 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 5 separate GAM precursor RNAs, GAM3701 precursor RNA, GAM75764 precursor RNA, GAM232315 precursor RNA, GAM331360 precursor RNA and GAM335897 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3701 RNA, GAM75764 RNA, GAM232315 RNA, GAM331360 RNA and GAM335897 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3701 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3701 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3701 target RNA into GAM3701 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM75764 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM75764 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM75764 target RNA into GAM75764 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM232315 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM232315 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM232315 target RNA into GAM232315 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM331360 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM331360 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM331360 target RNA into GAM331360 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM335897 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM335897 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM335897 target RNA into GAM335897 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7218 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7218 gene: GAM3701 target protein, GAM75764 target protein, GAM232315 target protein, GAM331360 target protein and GAM335897 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3701, GAM75764, GAM232315, GAM331360 and GAM335897

GR7219 BI198213 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7219(GR7219) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7219 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR7219 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7219 gene encodes GR7219 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7219 precursor RNA folds spatially, forming GR7219 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7219 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7219 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7219 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM99159 precursor RNA, GAM108524 precursor RNA and GAM206663 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM99159 RNA, GAM108524 RNA and GAM206663 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM99159 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM99159 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM99159 target RNA into GAM99159 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM108524 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM108524 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM108524 target RNA into GAM108524 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM206663 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM206663 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM206663 target RNA into GAM206663 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7219 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7219 gene: GAM99159 target protein, GAM108524 target protein and GAM206663 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM99159, GAM108524 and GAM206663

GR7220 AA970087 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7220(GR7220) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7220 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7220 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7220 gene encodes GR7220 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7220 precursor RNA folds spatially, forming GR7220 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7220 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7220 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7220 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3382 precursor RNA, GAM8492 precursor RNA and GAM219819 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3382 RNA, GAM8492 RNA and GAM219819 RNA, herein

schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3382 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3382 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3382 target RNA into GAM3382 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8492 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8492 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8492 target RNA into GAM8492 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM219819 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM219819 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM219819 target RNA into GAM219819 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7220 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7220 gene: GAM3382 target protein, GAM8492 target protein and GAM219819 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3382, GAM8492 and GAM219819

GR7221 BF972152 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7221(GR7221) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7221 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7221 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7221 gene encodes GR7221 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7221 precursor RNA folds spatially, forming GR7221 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7221 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7221 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7221 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3994 precursor RNA and GAM4004 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3994 RNA and GAM4004 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3994 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3994 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3994 target RNA into GAM3994 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM4004 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4004 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4004 target RNA into GAM4004 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7221 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7221 gene: GAM3994 target protein and GAM4004 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3994 and GAM4004

GR7222 AI814968 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7222(GR7222) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7222 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7222 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7222 gene encodes GR7222 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7222 precursor RNA folds spatially, forming GR7222 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7222 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7222 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7222 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5709 precursor RNA and GAM277652 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5709 RNA and GAM277652 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5709 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5709 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5709 target RNA into GAM5709 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM277652 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM277652 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM277652 target RNA into GAM277652 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7222 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7222 gene: GAM5709 target protein and GAM277652 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5709 and GAM277652

GR7223 AI190033 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7223(GR7223) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7223 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7223 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7223 gene encodes GR7223 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7223 precursor RNA folds spatially, forming GR7223 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7223 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7223 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7223 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM145823 precursor RNA and GAM180732 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM145823 RNA and GAM180732 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM145823 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM145823 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM145823 target RNA into GAM145823 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM180732 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM180732 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM180732 target RNA into GAM180732 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7223 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7223 gene: GAM145823 target protein and GAM180732 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM145823 and GAM180732

GR7224 BM981962 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7224(GR7224) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7224 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7224 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7224 gene encodes GR7224 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7224 precursor RNA folds spatially, forming GR7224 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7224 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7224 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7224 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM5315 precursor RNA, GAM119545 precursor RNA and GAM225209 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5315 RNA, GAM119545 RNA and GAM225209 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5315 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5315 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5315 target RNA into GAM5315 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM119545 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM119545 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM119545 target RNA into GAM119545 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM225209 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM225209 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM225209 target RNA into GAM225209 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7224 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7224 gene: GAM5315 target protein, GAM119545 target protein and GAM225209 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5315, GAM119545 and GAM225209

GR7225 BG168159 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7225(GR7225) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7225 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7225 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7225 gene encodes GR7225 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7225 precursor RNA folds spatially, forming GR7225 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7225 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7225 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7225 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM284 precursor RNA, GAM3807 precursor RNA, GAM5344 precursor RNA and GAM106823 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM284 RNA, GAM3807 RNA, GAM5344 RNA and GAM106823 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM284 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM284 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM284 target RNA into GAM284 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM3807 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3807 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds

to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3807 target RNA into GAM3807 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5344 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5344 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5344 target RNA into GAM5344 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM106823 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM106823 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM106823 target RNA into GAM106823 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7225 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7225 gene: GAM284 target protein, GAM3807 target protein, GAM5344 target protein and GAM106823 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM284, GAM3807, GAM5344 and GAM106823

GR7226 AA701969 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7226(GR7226) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7226 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7226 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7226 gene encodes GR7226 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7226 precursor RNA folds spatially, forming GR7226 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7226 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR7226 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7226 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM40833 precursor RNA and GAM207291 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM40833 RNA and GAM207291 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM40833 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM40833 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM40833 target RNA into GAM40833 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM207291 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM207291 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM207291 target RNA into GAM207291 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7226 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7226 gene: GAM40833 target protein and GAM207291 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM40833 and GAM207291

GR7227 BG492822 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7227(GR7227) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7227 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7227 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7227 gene encodes GR7227 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7227 precursor RNA folds spatially, forming GR7227 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7227 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7227 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7227 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2347 precursor RNA and GAM3641 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2347 RNA and GAM3641 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2347 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2347 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2347 target RNA into GAM2347 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM3641 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3641 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3641 target RNA into GAM3641 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7227 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7227 gene: GAM2347 target protein and GAM3641 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2347 and GAM3641

GR7228 BE767131 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7228(GR7228) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7228 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7228 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7228 gene encodes GR7228 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7228 precursor RNA folds spatially, forming GR7228 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7228 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7228 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7228 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM8432 precursor RNA, GAM15209 precursor RNA and GAM268538 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8432 RNA, GAM15209 RNA and GAM268538 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8432 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8432 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig. 8, thereby inhibiting translation of GAM8432 target RNA into GAM8432 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM15209 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM15209 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM15209 target RNA into GAM15209 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM268538 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM268538 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM268538 target RNA into GAM268538 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7228 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7228 gene: GAM8432 target protein, GAM15209 target protein and GAM268538 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8432, GAM15209 and GAM268538

GR7229 AA654407 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7229(GR7229) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7229 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7229 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7229 gene encodes GR7229 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7229 precursor RNA folds spatially, forming GR7229 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7229 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7229 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7229 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM340 precursor RNA, GAM3207 precursor RNA and GAM294733 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM340 RNA, GAM3207 RNA and GAM294733 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM340 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM340 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM340 target RNA into GAM340 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM3207 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3207 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3207 target RNA into GAM3207 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM294733 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM294733 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM294733 target RNA into GAM294733 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7229 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7229 gene: GAM340 target protein, GAM3207 target protein and GAM294733 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6,

hereby incorporated by reference, with references to GAM340, GAM3207 and GAM294733

GR7230 AV652093 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7230(GR7230) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7230 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7230 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7230 gene encodes GR7230 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7230 precursor RNA folds spatially, forming GR7230 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7230 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7230 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7230 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5552 precursor RNA and GAM5808 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5552 RNA and GAM5808 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5552 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5552 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5552 target RNA into GAM5552 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5808 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM5808 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5808 target RNA into GAM5808 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7230 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7230 gene: GAM5552 target protein and GAM5808 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5552 and GAM5808

GR7231 R45925 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7231 (GR7231) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7231 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7231 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7231 gene encodes GR7231 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7231 precursor RNA folds spatially, forming GR7231 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7231 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7231 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7231 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM177908 precursor RNA, GAM287832 precursor RNA and GAM320050 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22

nucleotides in length, GAM177908 RNA, GAM287832 RNA and GAM320050 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM177908 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM177908 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM177908 target RNA into GAM177908 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM287832 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM287832 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM287832 target RNA into GAM287832 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM320050 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM320050 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM320050 target RNA into GAM320050 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7231 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7231 gene: GAM177908 target protein, GAM287832 target protein and GAM320050 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM177908, GAM287832 and GAM320050

GR7232 AA719302 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7232(GR7232) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7232 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7232 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7232 gene encodes GR7232 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7232 precursor RNA folds spatially, forming GR7232 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7232 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7232 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7232 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3608 precursor RNA and GAM61274 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3608 RNA and GAM61274 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3608 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3608 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3608 target RNA into GAM3608 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM61274 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM61274 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM61274 target RNA into GAM61274 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7232 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7232 gene: GAM3608 target protein and GAM61274 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference,

with references to GAM3608 and GAM61274

GR7233 AW952867 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7233(GR7233) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7233 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7233 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7233 gene encodes GR7233 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7233 precursor RNA folds spatially, forming GR7233 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7233 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7233 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7233 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM37650 precursor RNA, GAM174201 precursor RNA and GAM181134 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM37650 RNA, GAM174201 RNA and GAM181134 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM37650 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM37650 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM37650 target RNA into GAM37650 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM174201 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM174201 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM174201 target RNA into GAM174201 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM181134 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM181134 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM181134 target RNA into GAM181134 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7233 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7233 gene: GAM37650 target protein, GAM174201 target protein and GAM181134 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM37650, GAM174201 and GAM181134

GR7234 AA984745 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7234(GR7234) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7234 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7234 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7234 gene encodes GR7234 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7234 precursor RNA folds spatially, forming GR7234 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7234 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7234 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7234 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7669 precursor RNA and GAM125669 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7669 RNA and GAM125669 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7669 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7669 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7669 target RNA into GAM7669 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM125669 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM125669 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM125669 target RNA into GAM125669 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7234 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7234 gene: GAM7669 target protein and GAM125669 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7669 and GAM125669

GR7235 AW867432 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7235(GR7235) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7235 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7235 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7235 gene encodes GR7235 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7235 precursor RNA folds spatially, forming GR7235 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7235 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7235 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7235 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4358 precursor RNA, GAM276547 precursor RNA and GAM278798 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4358 RNA, GAM276547 RNA and GAM278798 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4358 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4358 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4358 target RNA into GAM4358 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM276547 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM276547 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM276547 target RNA into GAM276547 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM278798 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM278798 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM278798 target RNA into GAM278798 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7235 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7235 gene: GAM4358 target protein, GAM276547 target protein and GAM278798 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4358, GAM276547 and GAM278798

GR7236 AA195750 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7236(GR7236) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7236 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7236 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7236 gene encodes GR7236 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7236 precursor RNA folds spatially, forming GR7236 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7236 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7236 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7236 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM22017 precursor RNA and GAM83331 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM22017 RNA and GAM83331 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM22017 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM22017 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM22017 target RNA into GAM22017 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM83331 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM83331 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM83331 target RNA into GAM83331 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7236 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7236 gene: GAM22017 target protein and GAM83331 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM22017 and GAM83331

GR7237 AI244667 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7237(GR7237) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7237 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7237 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7237 gene encodes GR7237 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7237 precursor RNA folds spatially, forming GR7237 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7237 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7237 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7237 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3

separate GAM precursor RNAs, GAM6969 precursor RNA, GAM38209 precursor RNA and GAM170029 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6969 RNA, GAM38209 RNA and GAM170029 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6969 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6969 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6969 target RNA into GAM6969 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM38209 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM38209 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM38209 target RNA into GAM38209 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM170029 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM170029 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM170029 target RNA into GAM170029 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7237 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7237 gene: GAM6969 target protein, GAM38209 target protein and GAM170029 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6969, GAM38209 and GAM170029

GR7238 BM819059 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7238(GR7238) gene, which encodes an `operon-like` cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7238 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7238 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7238 gene encodes GR7238 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7238 precursor RNA folds spatially, forming GR7238 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7238 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7238 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7238 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM177075 precursor RNA, GAM236719 precursor RNA and GAM307741 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM177075 RNA, GAM236719 RNA and GAM307741 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM177075 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM177075 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM177075 target RNA into GAM177075 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM236719 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM236719 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM236719 target RNA into GAM236719 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM307741 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM307741 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM307741 target RNA into GAM307741 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7238 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7238 gene: GAM177075 target protein, GAM236719 target protein and GAM307741 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM177075, GAM236719 and GAM307741

GR7239 AA910357 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7239(GR7239) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7239 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7239 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7239 gene encodes GR7239 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7239 precursor RNA folds spatially, forming GR7239 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7239 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7239 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7239 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM33266 precursor RNA, GAM144937 precursor RNA and GAM196772 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED

PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM33266 RNA, GAM144937 RNA and GAM196772 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM33266 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM33266 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM33266 target RNA into GAM33266 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM144937 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM144937 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM144937 target RNA into GAM144937 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM196772 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM196772 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM196772 target RNA into GAM196772 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7239 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7239 gene: GAM33266 target protein, GAM144937 target protein and GAM196772 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM33266, GAM144937 and GAM196772

GR7240 AL047571 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7240(GR7240) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7240 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7240 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7240 gene encodes GR7240 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7240 precursor RNA folds spatially, forming GR7240 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7240 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7240 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7240 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM128045 precursor RNA, GAM212701 precursor RNA, GAM249684 precursor RNA and GAM291918 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM128045 RNA, GAM212701 RNA, GAM249684 RNA and GAM291918 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM128045 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM128045 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM128045 target RNA into GAM128045 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM212701 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM212701 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM212701 target RNA into GAM212701 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM249684 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM249684 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM249684 target RNA into GAM249684 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM291918 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM291918 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM291918 target RNA into GAM291918 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7240 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7240 gene: GAM128045 target protein, GAM212701 target protein, GAM249684 target protein and GAM291918 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM128045, GAM212701, GAM249684 and GAM291918

GR7241 W65344 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7241(GR7241) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7241 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7241 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7241 gene encodes GR7241 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7241 precursor RNA folds spatially, forming GR7241 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7241 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7241 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7241 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2

separate GAM precursor RNAs, GAM6722 precursor RNA and GAM179571 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6722 RNA and GAM179571 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6722 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6722 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6722 target RNA into GAM6722 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM179571 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM179571 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM179571 target RNA into GAM179571 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7241 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7241 gene: GAM6722 target protein and GAM179571 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6722 and GAM179571

GR7242 BE537565 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7242(GR7242) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7242 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7242 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7242 gene encodes GR7242 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR7242 precursor RNA folds spatially, forming GR7242 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7242 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7242 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7242 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM116662 precursor RNA and GAM144655 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM116662 RNA and GAM144655 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM116662 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM116662 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM116662 target RNA into GAM116662 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM144655 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM144655 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM144655 target RNA into GAM144655 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7242 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7242 gene: GAM116662 target protein and GAM144655 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM116662 and GAM144655

GR7243 BF792059 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7243(GR7243) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7243 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7243 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7243 gene encodes GR7243 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7243 precursor RNA folds spatially, forming GR7243 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7243 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7243 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7243 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM5775 precursor RNA, GAM71755 precursor RNA and GAM200303 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5775 RNA, GAM71755 RNA and GAM200303 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5775 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5775 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5775 target RNA into GAM5775 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM71755 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM71755 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM71755 target RNA into GAM71755 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM200303 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM200303 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM200303 target RNA into GAM200303 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7243 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7243 gene: GAM5775 target protein, GAM71755 target protein and GAM200303 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5775, GAM71755 and GAM200303

GR7244 AW063436 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7244(GR7244) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7244 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7244 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7244 gene encodes GR7244 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7244 precursor RNA folds spatially, forming GR7244 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7244 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7244 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7244 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM255526 precursor RNA and GAM286405 precursor

RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM255526 RNA and GAM286405 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM255526 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM255526 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM255526 target RNA into GAM255526 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM286405 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM286405 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM286405 target RNA into GAM286405 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7244 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7244 gene: GAM255526 target protein and GAM286405 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM255526 and GAM286405

GR7245 AI499240 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7245(GR7245) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7245 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7245 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7245 gene encodes GR7245 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7245 precursor RNA folds spatially, forming GR7245 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7245 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7245 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7245 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM8595 precursor RNA, GAM26867 precursor RNA and GAM269801 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8595 RNA, GAM26867 RNA and GAM269801 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8595 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8595 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8595 target RNA into GAM8595 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM26867 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM26867 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM26867 target RNA into GAM26867 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM269801 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM269801 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM269801 target RNA into GAM269801 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly

utilities, of GR7245 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7245 gene: GAM8595 target protein, GAM26867 target protein and GAM269801 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8595, GAM26867 and GAM269801

GR7246 AW407686 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7246(GR7246) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7246 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7246 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7246 gene encodes GR7246 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7246 precursor RNA folds spatially, forming GR7246 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7246 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7246 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7246 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2409 precursor RNA, GAM5813 precursor RNA and GAM102934 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2409 RNA, GAM5813 RNA and GAM102934 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2409 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2409 target RNA, herein schematically represented by

GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2409 target RNA into GAM2409 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5813 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5813 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5813 target RNA into GAM5813 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM102934 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM102934 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM102934 target RNA into GAM102934 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7246 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7246 gene: GAM2409 target protein, GAM5813 target protein and GAM102934 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2409, GAM5813 and GAM102934

GR7247 R20920 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7247(GR7247) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7247 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7247 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7247 gene encodes GR7247 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7247 precursor RNA folds spatially, forming GR7247 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7247 folded precursor RNA comprises a plurality of what is known in the

art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7247 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7247 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4615 precursor RNA and GAM11651 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4615 RNA and GAM11651 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4615 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4615 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4615 target RNA into GAM4615 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM11651 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM11651 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM11651 target RNA into GAM11651 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7247 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7247 gene: GAM4615 target protein and GAM11651 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4615 and GAM11651

GR7248 BE730879 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7248(GR7248) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR7248 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7248 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7248 gene encodes GR7248 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7248 precursor RNA folds spatially, forming GR7248 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7248 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7248 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7248 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM72092 precursor RNA, GAM120395 precursor RNA and GAM245200 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM72092 RNA, GAM120395 RNA and GAM245200 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM72092 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM72092 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM72092 target RNA into GAM72092 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM120395 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM120395 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM120395 target RNA into GAM120395 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM245200 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM245200 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM245200 target RNA into GAM245200 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7248 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7248 gene: GAM72092 target protein, GAM120395 target protein and GAM245200 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM72092, GAM120395 and GAM245200

GR7249 BI768195 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7249(GR7249) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7249 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7249 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7249 gene encodes GR7249 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7249 precursor RNA folds spatially, forming GR7249 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7249 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7249 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7249 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8323 precursor RNA and GAM167657 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8323 RNA and GAM167657 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8323 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8323 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8323 target RNA into GAM8323 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM167657 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM167657 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM167657 target RNA into GAM167657 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7249 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7249 gene: GAM8323 target protein and GAM167657 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8323 and GAM167657

GR7250 BF736991 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7250(GR7250) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7250 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7250 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7250 gene encodes GR7250 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7250 precursor RNA folds spatially, forming GR7250 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7250 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR7250 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7250 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM6949 precursor RNA, GAM163625 precursor RNA, GAM223715 precursor RNA and GAM289202 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6949 RNA, GAM163625 RNA, GAM223715 RNA and GAM289202 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6949 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6949 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6949 target RNA into GAM6949 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM163625 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM163625 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM163625 target RNA into GAM163625 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM223715 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM223715 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM223715 target RNA into GAM223715 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM289202 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM289202 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM289202 target RNA into GAM289202 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7250 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7250 gene: GAM6949 target protein, GAM163625 target protein, GAM223715 target protein and GAM289202 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6949, GAM163625, GAM223715 and GAM289202

GR7251 AA436042 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7251(GR7251) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7251 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7251 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7251 gene encodes GR7251 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7251 precursor RNA folds spatially, forming GR7251 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7251 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7251 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7251 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 5 separate GAM precursor RNAs, GAM3284 precursor RNA, GAM132388 precursor RNA, GAM204998 precursor RNA, GAM209319 precursor RNA and GAM236195 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3284 RNA, GAM132388 RNA, GAM204998 RNA, GAM209319 RNA and GAM236195 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3284 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3284 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3284 target RNA into GAM3284 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM132388 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM132388 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM132388 target RNA into GAM132388 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM204998 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM204998 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM204998 target RNA into GAM204998 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM209319 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM209319 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM209319 target RNA into GAM209319 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM236195 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM236195 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM236195 target RNA into GAM236195 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7251 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7251 gene: GAM3284 target protein, GAM132388 target protein, GAM204998 target protein, GAM209319 target protein and GAM236195 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3284, GAM132388, GAM204998, GAM209319 and GAM236195

GR7252 BM665457 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7252(GR7252) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7252 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7252 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7252 gene encodes GR7252 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7252 precursor RNA folds spatially, forming GR7252 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7252 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7252 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7252 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7543 precursor RNA and GAM23779 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7543 RNA and GAM23779 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7543 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7543 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7543 target RNA into GAM7543 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM23779 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM23779 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM23779 target RNA into GAM23779 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7252 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7252 gene: GAM7543 target protein and GAM23779 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7543 and GAM23779

GR7253 AI767224 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7253(GR7253) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7253 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7253 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7253 gene encodes GR7253 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7253 precursor RNA folds spatially, forming GR7253 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7253 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7253 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7253 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM109194 precursor RNA, GAM181627 precursor RNA and GAM273205 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM109194 RNA, GAM181627 RNA and GAM273205 RNA, herein

schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM109194 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM109194 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM109194 target RNA into GAM109194 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM181627 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM181627 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM181627 target RNA into GAM181627 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM273205 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM273205 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM273205 target RNA into GAM273205 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7253 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7253 gene: GAM109194 target protein, GAM181627 target protein and GAM273205 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM109194, GAM181627 and GAM273205

GR7254 T90278 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7254(GR7254) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7254 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7254 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7254 gene encodes GR7254 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7254 precursor RNA folds spatially, forming GR7254 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7254 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7254 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7254 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM34471 precursor RNA and GAM67523 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM34471 RNA and GAM67523 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM34471 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM34471 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM34471 target RNA into GAM34471 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM67523 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM67523 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM67523 target RNA into GAM67523 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7254 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7254 gene: GAM34471 target protein and GAM67523 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM34471 and GAM67523

GR7255 BG337049 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7255(GR7255) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7255 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7255 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7255 gene encodes GR7255 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7255 precursor RNA folds spatially, forming GR7255 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7255 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7255 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7255 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4973 precursor RNA, GAM103047 precursor RNA and GAM214535 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4973 RNA, GAM103047 RNA and GAM214535 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4973 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4973 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4973 target RNA into GAM4973 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM103047 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM103047 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM103047 target RNA into GAM103047 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM214535 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM214535 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM214535 target RNA into GAM214535 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7255 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7255 gene: GAM4973 target protein, GAM103047 target protein and GAM214535 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4973, GAM103047 and GAM214535

GR7256 BE396179 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7256(GR7256) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7256 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7256 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7256 gene encodes GR7256 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7256 precursor RNA folds spatially, forming GR7256 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7256 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7256 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7256 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2

separate GAM precursor RNAs, GAM7333 precursor RNA and GAM56398 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM7333 RNA and GAM56398 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7333 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7333 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7333 target RNA into GAM7333 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM56398 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM56398 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM56398 target RNA into GAM56398 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7256 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7256 gene: GAM7333 target protein and GAM56398 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7333 and GAM56398

GR7257 H45131 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7257(GR7257) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7257 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7257 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7257 gene encodes GR7257 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR7257 precursor RNA folds spatially, forming GR7257 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7257 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7257 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7257 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5767 precursor RNA and GAM6310 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5767 RNA and GAM6310 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5767 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5767 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5767 target RNA into GAM5767 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6310 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6310 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6310 target RNA into GAM6310 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7257 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7257 gene: GAM5767 target protein and GAM6310 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5767 and GAM6310

GR7258 BF530598 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7258(GR7258) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7258 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7258 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7258 gene encodes GR7258 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7258 precursor RNA folds spatially, forming GR7258 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7258 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7258 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7258 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM99017 precursor RNA and GAM322869 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM99017 RNA and GAM322869 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM99017 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM99017 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM99017 target RNA into GAM99017 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM322869 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM322869 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM322869 target RNA into GAM322869 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7258 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7258 gene: GAM99017 target protein and GAM322869 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM99017 and GAM322869

GR7259 BM044733 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7259(GR7259) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7259 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7259 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7259 gene encodes GR7259 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7259 precursor RNA folds spatially, forming GR7259 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7259 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7259 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7259 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM68657 precursor RNA, GAM73070 precursor RNA, GAM238984 precursor RNA and GAM239789 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM68657 RNA, GAM73070 RNA, GAM238984 RNA and GAM239789 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM68657 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM68657 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM68657 target RNA into GAM68657 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM73070 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM73070 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM73070 target RNA into GAM73070 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM238984 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM238984 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM238984 target RNA into GAM238984 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM239789 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM239789 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM239789 target RNA into GAM239789 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7259 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7259 gene: GAM68657 target protein, GAM73070 target protein, GAM238984 target protein and GAM239789 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM68657, GAM73070, GAM238984 and GAM239789

GR7260 AW160748 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7260(GR7260) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7260 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7260 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7260 gene encodes GR7260 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7260 precursor RNA folds spatially, forming GR7260 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7260 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7260 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7260 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM84943 precursor RNA and GAM218109 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM84943 RNA and GAM218109 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM84943 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM84943 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM84943 target RNA into GAM84943 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM218109 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM218109 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM218109 target RNA into GAM218109 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7260 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7260 gene: GAM84943 target protein and GAM218109 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM84943 and GAM218109

GR7261 BG741187 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7261(GR7261) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7261 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7261 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7261 gene encodes GR7261 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7261 precursor RNA folds spatially, forming GR7261 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7261 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7261 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7261 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM164 precursor RNA, GAM110927 precursor RNA and GAM207078 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM164 RNA, GAM110927 RNA and GAM207078 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM164 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM164 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III of Fig. 8, thereby inhibiting translation of GAM164 target RNA into GAM164 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM110927 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM110927 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM110927 target RNA into GAM110927 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM207078 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM207078 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM207078 target RNA into GAM207078 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7261 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7261 gene: GAM164 target protein, GAM110927 target protein and GAM207078 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM164, GAM110927 and GAM207078

GR7262 BI551905 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7262(GR7262) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7262 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7262 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7262 gene encodes GR7262 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7262 precursor RNA folds spatially, forming GR7262 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7262 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7262 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7262 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6050 precursor RNA and GAM244747 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6050 RNA and GAM244747 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6050 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6050 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6050 target RNA into GAM6050 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM244747 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM244747 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM244747 target RNA into GAM244747 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7262 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7262 gene: GAM6050 target protein and GAM244747 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6050 and GAM244747

GR7263 C16807 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7263(GR7263) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7263 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7263 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7263 gene encodes GR7263 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7263 precursor RNA folds spatially, forming GR7263 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7263 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7263 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7263 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM60671 precursor RNA and GAM192304 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM60671 RNA and GAM192304 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM60671 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM60671 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM60671 target RNA into GAM60671 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM192304 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM192304 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM192304 target RNA into GAM192304 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7263 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR7263 gene: GAM60671 target protein and GAM192304 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM60671 and GAM192304

GR7264 BG478548 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7264(GR7264) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7264 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7264 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7264 gene encodes GR7264 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7264 precursor RNA folds spatially, forming GR7264 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7264 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7264 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7264 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM5065 precursor RNA, GAM38761 precursor RNA and GAM69038 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5065 RNA, GAM38761 RNA and GAM69038 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5065 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5065 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5065 target RNA into

GAM5065 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM38761 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM38761 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM38761 target RNA into GAM38761 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM69038 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM69038 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM69038 target RNA into GAM69038 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7264 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7264 gene: GAM5065 target protein, GAM38761 target protein and GAM69038 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5065, GAM38761 and GAM69038

GR7265 BI912021 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7265(GR7265) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7265 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7265 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7265 gene encodes GR7265 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7265 precursor RNA folds spatially, forming GR7265 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7265 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7265 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7265 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM380 precursor RNA, GAM3376 precursor RNA and GAM6400 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM380 RNA, GAM3376 RNA and GAM6400 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM380 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM380 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM380 target RNA into GAM380 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM3376 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3376 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3376 target RNA into GAM3376 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6400 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6400 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6400 target RNA into GAM6400 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7265 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7265 gene: GAM380 target protein, GAM3376 target protein and GAM6400 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM380, GAM3376 and

GR7266 BM829678 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7266(GR7266) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7266 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7266 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7266 gene encodes GR7266 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7266 precursor RNA folds spatially, forming GR7266 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7266 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7266 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7266 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM110121 precursor RNA and GAM183151 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM110121 RNA and GAM183151 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM110121 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM110121 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM110121 target RNA into GAM110121 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM183151 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM183151 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM183151 target RNA into GAM183151 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7266 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7266 gene: GAM110121 target protein and GAM183151 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM110121 and GAM183151

GR7267 BM930854 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7267(GR7267) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7267 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7267 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7267 gene encodes GR7267 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7267 precursor RNA folds spatially, forming GR7267 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7267 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7267 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7267 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM204873 precursor RNA and GAM273554 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM204873 RNA and GAM273554 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding

to GAM RNA of Fig. 8.

GAM204873 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM204873 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM204873 target RNA into GAM204873 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM273554 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM273554 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM273554 target RNA into GAM273554 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7267 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7267 gene: GAM204873 target protein and GAM273554 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM204873 and GAM273554

GR7268 BG675057 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7268(GR7268) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7268 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7268 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7268 gene encodes GR7268 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7268 precursor RNA folds spatially, forming GR7268 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7268 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7268 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR7268 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM78369 precursor RNA and GAM307878 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM78369 RNA and GAM307878 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM78369 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM78369 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM78369 target RNA into GAM78369 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM307878 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM307878 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM307878 target RNA into GAM307878 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7268 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7268 gene: GAM78369 target protein and GAM307878 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM78369 and GAM307878

GR7269 BG991862 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7269(GR7269) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7269 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7269

gene was detected is described hereinabove with reference to Figs. 8-18.

GR7269 gene encodes GR7269 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7269 precursor RNA folds spatially, forming GR7269 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7269 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7269 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7269 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1169 precursor RNA and GAM208643 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1169 RNA and GAM208643 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1169 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1169 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1169 target RNA into GAM1169 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM208643 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM208643 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM208643 target RNA into GAM208643 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7269 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7269 gene: GAM1169 target protein and GAM208643 target protein, herein schematically represented by GAM1

TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1169 and GAM208643

GR7270 R56530 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7270(GR7270) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7270 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7270 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7270 gene encodes GR7270 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7270 precursor RNA folds spatially, forming GR7270 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7270 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7270 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7270 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM980 precursor RNA and GAM7780 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM980 RNA and GAM7780 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM980 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM980 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM980 target RNA into GAM980 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7780 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7780 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7780 target RNA into GAM7780 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7270 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7270 gene: GAM980 target protein and GAM7780 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM980 and GAM7780

GR7271 BG540516 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7271(GR7271) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7271 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7271 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7271 gene encodes GR7271 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7271 precursor RNA folds spatially, forming GR7271 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7271 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7271 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7271 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM28849 precursor RNA, GAM185575 precursor RNA and GAM306439 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM28849 RNA, GAM185575 RNA and GAM306439 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM28849 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM28849 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM28849 target RNA into GAM28849 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM185575 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM185575 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM185575 target RNA into GAM185575 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM306439 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM306439 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM306439 target RNA into GAM306439 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7271 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7271 gene: GAM28849 target protein, GAM185575 target protein and GAM306439 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM28849, GAM185575 and GAM306439

GR7272 BI192668 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7272(GR7272) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7272 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7272 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7272 gene encodes GR7272 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7272 precursor RNA folds spatially, forming GR7272 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7272 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7272 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7272 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM258750 precursor RNA and GAM323240 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM258750 RNA and GAM323240 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM258750 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM258750 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM258750 target RNA into GAM258750 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM323240 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM323240 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM323240 target RNA into GAM323240 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7272 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7272 gene: GAM258750 target protein and GAM323240 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes

is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM258750 and GAM323240

GR7273 BM765703 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7273(GR7273) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7273 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7273 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7273 gene encodes GR7273 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7273 precursor RNA folds spatially, forming GR7273 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7273 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7273 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7273 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM120446 precursor RNA and GAM309391 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM120446 RNA and GAM309391 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM120446 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM120446 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM120446 target RNA into GAM120446 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM309391 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM309391 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM309391 target RNA into GAM309391 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7273 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7273 gene: GAM120446 target protein and GAM309391 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM120446 and GAM309391

GR7274 BI820492 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7274(GR7274) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7274 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7274 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7274 gene encodes GR7274 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7274 precursor RNA folds spatially, forming GR7274 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7274 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7274 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7274 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1833 precursor RNA and GAM184927 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1833 RNA and GAM184927 RNA, herein schematically

represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1833 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1833 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1833 target RNA into GAM1833 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM184927 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM184927 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM184927 target RNA into GAM184927 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7274 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7274 gene: GAM1833 target protein and GAM184927 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1833 and GAM184927

GR7275 BG402837 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7275(GR7275) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7275 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7275 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7275 gene encodes GR7275 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7275 precursor RNA folds spatially, forming GR7275 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7275 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7275 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7275 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM20392 precursor RNA and GAM99313 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM20392 RNA and GAM99313 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM20392 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM20392 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM20392 target RNA into GAM20392 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM99313 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM99313 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM99313 target RNA into GAM99313 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7275 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7275 gene: GAM20392 target protein and GAM99313 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM20392 and GAM99313

GR7276 BF676503 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7276(GR7276) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7276 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR7276 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7276 gene encodes GR7276 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7276 precursor RNA folds spatially, forming GR7276 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7276 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7276 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7276 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM148608 precursor RNA, GAM158260 precursor RNA and GAM269001 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM148608 RNA, GAM158260 RNA and GAM269001 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM148608 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM148608 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM148608 target RNA into GAM148608 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM158260 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM158260 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM158260 target RNA into GAM158260 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM269001 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM269001 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM269001 target RNA into GAM269001 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7276 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7276 gene: GAM148608 target protein, GAM158260 target protein and GAM269001 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM148608, GAM158260 and GAM269001

GR7277 BF306947 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7277(GR7277) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7277 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7277 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7277 gene encodes GR7277 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7277 precursor RNA folds spatially, forming GR7277 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7277 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7277 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7277 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM101836 precursor RNA, GAM118865 precursor RNA, GAM123382 precursor RNA and GAM252076 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM101836 RNA, GAM118865 RNA, GAM123382 RNA and

GAM252076 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM101836 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM101836 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM101836 target RNA into GAM101836 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM118865 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM118865 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM118865 target RNA into GAM118865 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM123382 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM123382 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM123382 target RNA into GAM123382 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM252076 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM252076 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM252076 target RNA into GAM252076 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7277 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7277 gene: GAM101836 target protein, GAM118865 target protein, GAM123382 target protein and GAM252076 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM101836, GAM118865, GAM123382 and GAM252076

GR7278 BI460369 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7278(GR7278) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR7278 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7278 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7278 gene encodes GR7278 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7278 precursor RNA folds spatially, forming GR7278 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7278 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7278 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7278 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4620 precursor RNA, GAM199959 precursor RNA and GAM205477 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4620 RNA, GAM199959 RNA and GAM205477 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4620 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4620 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4620 target RNA into GAM4620 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM199959 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM199959 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM199959 target RNA into GAM199959 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM205477 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM205477 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM205477 target RNA into GAM205477 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7278 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7278 gene: GAM4620 target protein, GAM199959 target protein and GAM205477 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4620, GAM199959 and GAM205477

GR7279 BQ017049 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7279(GR7279) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7279 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7279 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7279 gene encodes GR7279 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7279 precursor RNA folds spatially, forming GR7279 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7279 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7279 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7279 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM96350 precursor RNA, GAM102320 precursor RNA and GAM111405 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM96350 RNA, GAM102320 RNA and GAM111405 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM96350 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM96350 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM96350 target RNA into GAM96350 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM102320 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM102320 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM102320 target RNA into GAM102320 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM111405 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM111405 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM111405 target RNA into GAM111405 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7279 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7279 gene: GAM96350 target protein, GAM102320 target protein and GAM111405 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM96350, GAM102320 and GAM111405

GR7280 BF840455 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7280(GR7280) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7280 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR7280 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7280 gene encodes GR7280 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7280 precursor RNA folds spatially, forming GR7280 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7280 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7280 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7280 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM84263 precursor RNA and GAM151675 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM84263 RNA and GAM151675 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM84263 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM84263 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM84263 target RNA into GAM84263 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM151675 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM151675 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM151675 target RNA into GAM151675 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7280 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7280 gene: GAM84263 target

protein and GAM151675 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM84263 and GAM151675

GR7281 BE179953 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7281(GR7281) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7281 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7281 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7281 gene encodes GR7281 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7281 precursor RNA folds spatially, forming GR7281 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7281 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7281 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7281 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM89930 precursor RNA and GAM228224 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM89930 RNA and GAM228224 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM89930 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM89930 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM89930 target RNA into GAM89930 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM228224 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM228224 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM228224 target RNA into GAM228224 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7281 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7281 gene: GAM89930 target protein and GAM228224 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM89930 and GAM228224

GR7282 BE880399 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7282(GR7282) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7282 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7282 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7282 gene encodes GR7282 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7282 precursor RNA folds spatially, forming GR7282 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7282 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7282 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7282 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM100463 precursor RNA and GAM241284 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM100463 RNA and GAM241284 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM100463 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM100463 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM100463 target RNA into GAM100463 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM241284 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM241284 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM241284 target RNA into GAM241284 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7282 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7282 gene: GAM100463 target protein and GAM241284 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM100463 and GAM241284

GR7283 N95562 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7283(GR7283) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7283 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7283 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7283 gene encodes GR7283 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7283 precursor RNA folds spatially, forming GR7283 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7283 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR7283 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7283 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM104089 precursor RNA, GAM141937 precursor RNA and GAM272232 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM104089 RNA, GAM141937 RNA and GAM272232 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM104089 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM104089 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM104089 target RNA into GAM104089 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM141937 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM141937 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM141937 target RNA into GAM141937 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM272232 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM272232 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM272232 target RNA into GAM272232 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7283 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7283 gene: GAM104089 target protein, GAM141937 target protein and GAM272232 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN.

The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM104089, GAM141937 and GAM272232

GR7284 BG112878 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7284(GR7284) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7284 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7284 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7284 gene encodes GR7284 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7284 precursor RNA folds spatially, forming GR7284 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7284 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7284 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7284 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM160098 precursor RNA and GAM203275 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM160098 RNA and GAM203275 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM160098 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM160098 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM160098 target RNA into GAM160098 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM203275 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM203275 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM203275 target RNA into GAM203275 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7284 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7284 gene: GAM160098 target protein and GAM203275 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM160098 and GAM203275

GR7285 BG829529 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7285(GR7285) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7285 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7285 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7285 gene encodes GR7285 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7285 precursor RNA folds spatially, forming GR7285 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7285 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7285 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7285 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM7860 precursor RNA and GAM257675 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM7860 RNA and GAM257675 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM7860 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7860 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7860 target RNA into GAM7860 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM257675 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM257675 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM257675 target RNA into GAM257675 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7285 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7285 gene: GAM7860 target protein and GAM257675 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM7860 and GAM257675

GR7286 BM562247 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7286(GR7286) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7286 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7286 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7286 gene encodes GR7286 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7286 precursor RNA folds spatially, forming GR7286 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7286 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7286 precursor RNA comprises a plurality of

segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7286 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM20245 precursor RNA, GAM124390 precursor RNA and GAM333320 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM20245 RNA, GAM124390 RNA and GAM333320 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM20245 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM20245 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM20245 target RNA into GAM20245 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM124390 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM124390 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM124390 target RNA into GAM124390 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM333320 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM333320 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM333320 target RNA into GAM333320 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7286 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7286 gene: GAM20245 target protein, GAM124390 target protein and GAM333320 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6,

hereby incorporated by reference, with references to GAM20245, GAM124390 and GAM333320

GR7287 T77315 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7287(GR7287) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7287 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7287 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7287 gene encodes GR7287 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7287 precursor RNA folds spatially, forming GR7287 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7287 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7287 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7287 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM51218 precursor RNA and GAM159788 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM51218 RNA and GAM159788 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM51218 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM51218 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM51218 target RNA into GAM51218 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM159788 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM159788 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM159788 target RNA into GAM159788 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7287 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7287 gene: GAM51218 target protein and GAM159788 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM51218 and GAM159788

GR7288 BF203948 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7288(GR7288) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7288 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7288 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7288 gene encodes GR7288 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7288 precursor RNA folds spatially, forming GR7288 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7288 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7288 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7288 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM5945 precursor RNA, GAM163536 precursor RNA and GAM276124 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22

nucleotides in length, GAM5945 RNA, GAM163536 RNA and GAM276124 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5945 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5945 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5945 target RNA into GAM5945 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM163536 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM163536 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM163536 target RNA into GAM163536 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM276124 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM276124 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM276124 target RNA into GAM276124 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7288 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7288 gene: GAM5945 target protein, GAM163536 target protein and GAM276124 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5945, GAM163536 and GAM276124

GR7289 AW630039 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7289(GR7289) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7289 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7289 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7289 gene encodes GR7289 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7289 precursor RNA folds spatially, forming GR7289 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7289 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7289 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7289 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4847 precursor RNA and GAM150493 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4847 RNA and GAM150493 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4847 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4847 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4847 target RNA into GAM4847 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM150493 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM150493 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM150493 target RNA into GAM150493 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7289 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7289 gene: GAM4847 target protein and GAM150493 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference,

with references to GAM4847 and GAM150493

GR7290 BG201905 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7290(GR7290) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7290 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7290 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7290 gene encodes GR7290 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7290 precursor RNA folds spatially, forming GR7290 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7290 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7290 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7290 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM24507 precursor RNA and GAM63062 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM24507 RNA and GAM63062 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM24507 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM24507 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM24507 target RNA into GAM24507 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM63062 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM63062 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM63062 target RNA into GAM63062 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7290 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7290 gene: GAM24507 target protein and GAM63062 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM24507 and GAM63062

GR7291 BF754251 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7291(GR7291) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7291 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7291 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7291 gene encodes GR7291 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7291 precursor RNA folds spatially, forming GR7291 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7291 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7291 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7291 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3930 precursor RNA and GAM8283 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3930 RNA and GAM8283 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding

to GAM RNA of Fig. 8.

GAM3930 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3930 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3930 target RNA into GAM3930 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8283 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8283 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8283 target RNA into GAM8283 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7291 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7291 gene: GAM3930 target protein and GAM8283 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3930 and GAM8283

GR7292 BF570371 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7292(GR7292) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7292 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7292 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7292 gene encodes GR7292 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7292 precursor RNA folds spatially, forming GR7292 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7292 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7292 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR7292 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM63785 precursor RNA, GAM85452 precursor RNA and GAM210930 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM63785 RNA, GAM85452 RNA and GAM210930 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM63785 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM63785 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM63785 target RNA into GAM63785 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM85452 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM85452 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM85452 target RNA into GAM85452 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM210930 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM210930 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM210930 target RNA into GAM210930 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7292 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7292 gene: GAM63785 target protein, GAM85452 target protein and GAM210930 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM63785, GAM85452 and GAM210930

GR7293 BI009053 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7293(GR7293) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7293 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7293 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7293 gene encodes GR7293 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7293 precursor RNA folds spatially, forming GR7293 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7293 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7293 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7293 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM5124 precursor RNA, GAM154853 precursor RNA and GAM158081 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5124 RNA, GAM154853 RNA and GAM158081 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5124 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5124 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5124 target RNA into GAM5124 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM154853 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM154853 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM154853 target RNA into GAM154853 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM158081 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM158081 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM158081 target RNA into GAM158081 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7293 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7293 gene: GAM5124 target protein, GAM154853 target protein and GAM158081 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5124, GAM154853 and GAM158081

GR7294 AW085959 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7294(GR7294) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7294 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7294 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7294 gene encodes GR7294 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7294 precursor RNA folds spatially, forming GR7294 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7294 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7294 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7294 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2

separate GAM precursor RNAs, GAM5566 precursor RNA and GAM135952 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5566 RNA and GAM135952 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5566 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5566 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5566 target RNA into GAM5566 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM135952 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM135952 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM135952 target RNA into GAM135952 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7294 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7294 gene: GAM5566 target protein and GAM135952 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5566 and GAM135952

GR7295 BF378025 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7295(GR7295) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7295 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7295 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7295 gene encodes GR7295 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR7295 precursor RNA folds spatially, forming GR7295 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7295 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7295 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7295 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM11816 precursor RNA, GAM12931 precursor RNA and GAM136610 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM11816 RNA, GAM12931 RNA and GAM136610 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM11816 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM11816 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM11816 target RNA into GAM11816 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM12931 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM12931 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM12931 target RNA into GAM12931 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM136610 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM136610 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM136610 target RNA into GAM136610 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7295 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7295 gene: GAM11816 target protein, GAM12931 target protein and GAM136610 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM11816, GAM12931 and GAM136610

GR7296 BE410325 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7296(GR7296) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7296 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7296 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7296 gene encodes GR7296 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7296 precursor RNA folds spatially, forming GR7296 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7296 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7296 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7296 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6681 precursor RNA and GAM240226 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6681 RNA and GAM240226 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6681 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6681 target RNA, herein schematically represented by

GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6681 target RNA into GAM6681 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM240226 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM240226 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM240226 target RNA into GAM240226 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7296 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7296 gene: GAM6681 target protein and GAM240226 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6681 and GAM240226

GR7297 BM839399 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7297(GR7297) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7297 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7297 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7297 gene encodes GR7297 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7297 precursor RNA folds spatially, forming GR7297 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7297 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7297 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7297 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4529 precursor RNA, GAM6980 precursor RNA and

GAM311659 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4529 RNA, GAM6980 RNA and GAM311659 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4529 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4529 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4529 target RNA into GAM4529 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6980 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6980 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6980 target RNA into GAM6980 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM311659 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM311659 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM311659 target RNA into GAM311659 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7297 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7297 gene: GAM4529 target protein, GAM6980 target protein and GAM311659 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4529, GAM6980 and GAM311659

GR7298 BG284242 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7298(GR7298) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR7298 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7298 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7298 gene encodes GR7298 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7298 precursor RNA folds spatially, forming GR7298 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7298 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7298 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7298 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6252 precursor RNA and GAM144025 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6252 RNA and GAM144025 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6252 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6252 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6252 target RNA into GAM6252 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM144025 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM144025 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM144025 target RNA into GAM144025 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7298 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7298 gene: GAM6252 target protein and GAM144025 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6252 and GAM144025

GR7299 AW993249 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7299(GR7299) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7299 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7299 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7299 gene encodes GR7299 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7299 precursor RNA folds spatially, forming GR7299 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7299 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7299 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7299 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM17926 precursor RNA and GAM63296 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM17926 RNA and GAM63296 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM17926 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM17926 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM17926 target RNA into GAM17926 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM63296 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM63296 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM63296 target RNA into GAM63296 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7299 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7299 gene: GAM17926 target protein and GAM63296 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM17926 and GAM63296

GR7300 BE739570 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7300(GR7300) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7300 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7300 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7300 gene encodes GR7300 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7300 precursor RNA folds spatially, forming GR7300 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7300 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7300 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7300 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM224390 precursor RNA and GAM257910 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3

FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM224390 RNA and GAM257910 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM224390 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM224390 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM224390 target RNA into GAM224390 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM257910 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM257910 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM257910 target RNA into GAM257910 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7300 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7300 gene: GAM224390 target protein and GAM257910 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM224390 and GAM257910

GR7301 BG118450 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7301(GR7301) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7301 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7301 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7301 gene encodes GR7301 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7301 precursor RNA folds spatially, forming GR7301 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7301 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7301 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7301 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM131528 precursor RNA and GAM231137 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM131528 RNA and GAM231137 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM131528 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM131528 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM131528 target RNA into GAM131528 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM231137 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM231137 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM231137 target RNA into GAM231137 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7301 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7301 gene: GAM131528 target protein and GAM231137 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM131528 and GAM231137

7302(GR7302) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7302 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7302 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7302 gene encodes GR7302 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7302 precursor RNA folds spatially, forming GR7302 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7302 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7302 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7302 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4719 precursor RNA, GAM91809 precursor RNA and GAM192709 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4719 RNA, GAM91809 RNA and GAM192709 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4719 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4719 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4719 target RNA into GAM4719 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM91809 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM91809 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM91809

target RNA into GAM91809 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM192709 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM192709 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM192709 target RNA into GAM192709 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7302 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7302 gene: GAM4719 target protein, GAM91809 target protein and GAM192709 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4719, GAM91809 and GAM192709

GR7303 AW449558 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7303(GR7303) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7303 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7303 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7303 gene encodes GR7303 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7303 precursor RNA folds spatially, forming GR7303 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7303 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7303 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7303 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4515 precursor RNA, GAM178206 precursor RNA and GAM266137 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded

precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4515 RNA, GAM178206 RNA and GAM266137 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4515 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4515 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4515 target RNA into GAM4515 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM178206 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM178206 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM178206 target RNA into GAM178206 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM266137 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM266137 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM266137 target RNA into GAM266137 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7303 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7303 gene: GAM4515 target protein, GAM178206 target protein and GAM266137 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4515, GAM178206 and GAM266137

GR7304 BM052651 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7304(GR7304) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7304 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7304 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7304 gene encodes GR7304 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7304 precursor RNA folds spatially, forming GR7304 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7304 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7304 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7304 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6563 precursor RNA and GAM118854 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6563 RNA and GAM118854 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6563 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6563 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6563 target RNA into GAM6563 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM118854 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM118854 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM118854 target RNA into GAM118854 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7304 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7304 gene: GAM6563 target protein and GAM118854 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6563 and GAM118854

GR7305 BF855557 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7305(GR7305) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7305 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7305 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7305 gene encodes GR7305 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7305 precursor RNA folds spatially, forming GR7305 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7305 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7305 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7305 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM152068 precursor RNA and GAM275761 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM152068 RNA and GAM275761 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM152068 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM152068 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM152068

target RNA into GAM152068 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM275761 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM275761 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM275761 target RNA into GAM275761 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7305 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7305 gene: GAM152068 target protein and GAM275761 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM152068 and GAM275761

GR7306 BF310267 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7306(GR7306) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7306 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7306 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7306 gene encodes GR7306 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7306 precursor RNA folds spatially, forming GR7306 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7306 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7306 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7306 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8128 precursor RNA and GAM221628 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8128 RNA and GAM221628 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8128 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8128 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8128 target RNA into GAM8128 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM221628 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM221628 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM221628 target RNA into GAM221628 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7306 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7306 gene: GAM8128 target protein and GAM221628 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8128 and GAM221628

GR7307 R67306 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7307(GR7307) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7307 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7307 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7307 gene encodes GR7307 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7307 precursor RNA folds spatially, forming GR7307 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated

that GR7307 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7307 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7307 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM696 precursor RNA and GAM305314 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM696 RNA and GAM305314 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM696 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM696 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM696 target RNA into GAM696 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM305314 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM305314 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM305314 target RNA into GAM305314 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7307 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7307 gene: GAM696 target protein and GAM305314 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM696 and GAM305314

GR7308 BE613491 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7308(GR7308) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR7308 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7308 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7308 gene encodes GR7308 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7308 precursor RNA folds spatially, forming GR7308 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7308 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7308 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7308 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5216 precursor RNA and GAM319420 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5216 RNA and GAM319420 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5216 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5216 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5216 target RNA into GAM5216 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM319420 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM319420 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM319420 target RNA into GAM319420 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7308 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7308 gene: GAM5216 target protein and GAM319420 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5216 and GAM319420

GR7309 BE280831 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7309(GR7309) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7309 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7309 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7309 gene encodes GR7309 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7309 precursor RNA folds spatially, forming GR7309 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7309 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7309 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7309 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6570 precursor RNA and GAM7651 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6570 RNA and GAM7651 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6570 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6570 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds

to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6570 target RNA into GAM6570 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7651 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7651 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7651 target RNA into GAM7651 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7309 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7309 gene: GAM6570 target protein and GAM7651 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6570 and GAM7651

GR7310 AI684052 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7310(GR7310) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7310 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7310 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7310 gene encodes GR7310 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7310 precursor RNA folds spatially, forming GR7310 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7310 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7310 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7310 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM141896 precursor RNA and GAM203547 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3

FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM141896 RNA and GAM203547 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM141896 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM141896 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM141896 target RNA into GAM141896 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM203547 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM203547 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM203547 target RNA into GAM203547 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7310 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7310 gene: GAM141896 target protein and GAM203547 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM141896 and GAM203547

GR7311 BM704390 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7311(GR7311) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7311 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7311 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7311 gene encodes GR7311 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7311 precursor RNA folds spatially, forming GR7311 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7311 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7311 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7311 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5601 precursor RNA and GAM124336 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5601 RNA and GAM124336 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5601 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5601 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5601 target RNA into GAM5601 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM124336 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM124336 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM124336 target RNA into GAM124336 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7311 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7311 gene: GAM5601 target protein and GAM124336 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5601 and GAM124336

7312(GR7312) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7312 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7312 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7312 gene encodes GR7312 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7312 precursor RNA folds spatially, forming GR7312 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7312 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7312 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7312 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM97037 precursor RNA and GAM137395 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM97037 RNA and GAM137395 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM97037 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM97037 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM97037 target RNA into GAM97037 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM137395 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM137395 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM137395 target RNA into GAM137395 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7312 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7312 gene: GAM97037 target protein and GAM137395 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM97037 and GAM137395

GR7313 BG686477 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7313(GR7313) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7313 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7313 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7313 gene encodes GR7313 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7313 precursor RNA folds spatially, forming GR7313 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7313 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7313 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7313 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM196683 precursor RNA and GAM271774 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM196683 RNA and GAM271774 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM196683 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM196683 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM196683 target RNA into GAM196683 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM271774 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM271774 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM271774 target RNA into GAM271774 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7313 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7313 gene: GAM196683 target protein and GAM271774 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM196683 and GAM271774

GR7314 BF944827 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7314(GR7314) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7314 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7314 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7314 gene encodes GR7314 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7314 precursor RNA folds spatially, forming GR7314 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7314 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7314 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7314 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3

separate GAM precursor RNAs, GAM3518 precursor RNA, GAM58270 precursor RNA and GAM319761 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3518 RNA, GAM58270 RNA and GAM319761 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3518 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3518 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3518 target RNA into GAM3518 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM58270 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM58270 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM58270 target RNA into GAM58270 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM319761 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM319761 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM319761 target RNA into GAM319761 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7314 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7314 gene: GAM3518 target protein, GAM58270 target protein and GAM319761 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3518, GAM58270 and GAM319761

GR7315 BE930952 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7315(GR7315) gene, which encodes an `operon-like` cluster of novel micro

RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7315 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7315 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7315 gene encodes GR7315 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7315 precursor RNA folds spatially, forming GR7315 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7315 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7315 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7315 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5019 precursor RNA and GAM94814 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5019 RNA and GAM94814 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5019 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5019 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5019 target RNA into GAM5019 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM94814 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM94814 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM94814 target RNA into GAM94814 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7315 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7315 gene: GAM5019 target protein and GAM94814 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5019 and GAM94814

GR7316 AW088619 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7316(GR7316) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7316 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7316 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7316 gene encodes GR7316 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7316 precursor RNA folds spatially, forming GR7316 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7316 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7316 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7316 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM47461 precursor RNA and GAM236723 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM47461 RNA and GAM236723 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM47461 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM47461 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM47461 target RNA into GAM47461 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM236723 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM236723 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM236723 target RNA into GAM236723 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7316 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7316 gene: GAM47461 target protein and GAM236723 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM47461 and GAM236723

GR7317 AV658785 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7317(GR7317) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7317 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7317 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7317 gene encodes GR7317 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7317 precursor RNA folds spatially, forming GR7317 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7317 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7317 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7317 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM884 precursor RNA and GAM142001 precursor

RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM884 RNA and GAM142001 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM884 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM884 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM884 target RNA into GAM884 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM142001 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM142001 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM142001 target RNA into GAM142001 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7317 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7317 gene: GAM884 target protein and GAM142001 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM884 and GAM142001

GR7318 AI018133 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7318(GR7318) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7318 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7318 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7318 gene encodes GR7318 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7318 precursor RNA folds spatially, forming GR7318 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7318 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7318 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7318 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM18818 precursor RNA and GAM97584 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM18818 RNA and GAM97584 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM18818 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM18818 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM18818 target RNA into GAM18818 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM97584 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM97584 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM97584 target RNA into GAM97584 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7318 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7318 gene: GAM18818 target protein and GAM97584 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM18818 and GAM97584

bioinformatically detected regulatory gene, referred to here as Genomic Record 7319(GR7319) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7319 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7319 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7319 gene encodes GR7319 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7319 precursor RNA folds spatially, forming GR7319 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7319 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7319 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7319 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5233 precursor RNA and GAM220666 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5233 RNA and GAM220666 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5233 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5233 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5233 target RNA into GAM5233 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM220666 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM220666 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM220666

target RNA into GAM220666 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7319 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7319 gene: GAM5233 target protein and GAM220666 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5233 and GAM220666

GR7320 N22874 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7320(GR7320) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7320 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7320 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7320 gene encodes GR7320 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7320 precursor RNA folds spatially, forming GR7320 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7320 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7320 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7320 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM2118 precursor RNA and GAM149429 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2118 RNA and GAM149429 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2118 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2118 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2118 target RNA into GAM2118 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM149429 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM149429 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM149429 target RNA into GAM149429 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7320 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7320 gene: GAM2118 target protein and GAM149429 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2118 and GAM149429

GR7321 BG179710 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7321(GR7321) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7321 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7321 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7321 gene encodes GR7321 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7321 precursor RNA folds spatially, forming GR7321 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7321 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7321 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7321 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM6196 precursor RNA, GAM100255 precursor RNA and GAM123447 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6196 RNA, GAM100255 RNA and GAM123447 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6196 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6196 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6196 target RNA into GAM6196 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM100255 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM100255 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM100255 target RNA into GAM100255 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM123447 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM123447 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM123447 target RNA into GAM123447 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7321 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7321 gene: GAM6196 target protein, GAM100255 target protein and GAM123447 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6196, GAM100255 and GAM123447

7322(GR7322) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7322 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7322 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7322 gene encodes GR7322 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7322 precursor RNA folds spatially, forming GR7322 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7322 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7322 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7322 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM799 precursor RNA, GAM111159 precursor RNA and GAM288132 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM799 RNA, GAM111159 RNA and GAM288132 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM799 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM799 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM799 target RNA into GAM799 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM111159 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM111159 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM111159

target RNA into GAM111159 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM288132 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM288132 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM288132 target RNA into GAM288132 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7322 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7322 gene: GAM799 target protein, GAM111159 target protein and GAM288132 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM799, GAM111159 and GAM288132

GR7323 AI819918 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7323(GR7323) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7323 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7323 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7323 gene encodes GR7323 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7323 precursor RNA folds spatially, forming GR7323 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7323 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7323 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7323 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM149236 precursor RNA and GAM299755 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin

shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM149236 RNA and GAM299755 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM149236 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM149236 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM149236 target RNA into GAM149236 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM299755 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM299755 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM299755 target RNA into GAM299755 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7323 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7323 gene: GAM149236 target protein and GAM299755 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM149236 and GAM299755

GR7324 BM504555 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7324(GR7324) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7324 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7324 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7324 gene encodes GR7324 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7324 precursor RNA folds spatially, forming GR7324 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7324 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7324 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7324 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM6063 precursor RNA, GAM181442 precursor RNA and GAM298592 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6063 RNA, GAM181442 RNA and GAM298592 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6063 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6063 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6063 target RNA into GAM6063 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM181442 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM181442 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM181442 target RNA into GAM181442 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM298592 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM298592 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM298592 target RNA into GAM298592 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7324 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR7324 gene: GAM6063 target protein, GAM181442 target protein and GAM298592 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6063, GAM181442 and GAM298592

GR7325 BG913431 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7325(GR7325) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7325 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7325 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7325 gene encodes GR7325 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7325 precursor RNA folds spatially, forming GR7325 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7325 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7325 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7325 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM187230 precursor RNA and GAM235572 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM187230 RNA and GAM235572 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM187230 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM187230 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM187230

target RNA into GAM187230 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM235572 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM235572 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM235572 target RNA into GAM235572 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7325 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7325 gene: GAM187230 target protein and GAM235572 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM187230 and GAM235572

GR7326 AA994597 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7326(GR7326) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7326 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7326 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7326 gene encodes GR7326 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7326 precursor RNA folds spatially, forming GR7326 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7326 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7326 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7326 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM141128 precursor RNA, GAM168220 precursor RNA and GAM231336 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED

PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM141128 RNA, GAM168220 RNA and GAM231336 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM141128 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM141128 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM141128 target RNA into GAM141128 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM168220 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM168220 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM168220 target RNA into GAM168220 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM231336 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM231336 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM231336 target RNA into GAM231336 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7326 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7326 gene: GAM141128 target protein, GAM168220 target protein and GAM231336 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM141128, GAM168220 and GAM231336

GR7327 BF679909 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7327(GR7327) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7327 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7327 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7327 gene encodes GR7327 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7327 precursor RNA folds spatially, forming GR7327 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7327 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7327 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7327 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM47008 precursor RNA and GAM164337 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM47008 RNA and GAM164337 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM47008 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM47008 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM47008 target RNA into GAM47008 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM164337 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM164337 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM164337 target RNA into GAM164337 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7327 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR7327 gene: GAM47008 target protein and GAM164337 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM47008 and GAM164337

GR7328 BG701853 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7328(GR7328) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7328 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7328 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7328 gene encodes GR7328 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7328 precursor RNA folds spatially, forming GR7328 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7328 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7328 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7328 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM40121 precursor RNA, GAM95000 precursor RNA and GAM119975 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM40121 RNA, GAM95000 RNA and GAM119975 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM40121 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM40121 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM40121

target RNA into GAM40121 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM95000 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM95000 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM95000 target RNA into GAM95000 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM119975 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM119975 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM119975 target RNA into GAM119975 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7328 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7328 gene: GAM40121 target protein, GAM95000 target protein and GAM119975 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM40121, GAM95000 and GAM119975

GR7329 BF995958 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7329(GR7329) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7329 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7329 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7329 gene encodes GR7329 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7329 precursor RNA folds spatially, forming GR7329 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7329 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7329 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7329 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM61281 precursor RNA and GAM295315 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM61281 RNA and GAM295315 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM61281 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM61281 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM61281 target RNA into GAM61281 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM295315 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM295315 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM295315 target RNA into GAM295315 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7329 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7329 gene: GAM61281 target protein and GAM295315 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM61281 and GAM295315

GR7330 BM907607 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7330(GR7330) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7330 gene, herein designated GR GENE, is a novel bioinformatically

detected regulatory, non protein coding, RNA gene. The method by which GR7330 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7330 gene encodes GR7330 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7330 precursor RNA folds spatially, forming GR7330 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7330 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7330 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7330 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM11242 precursor RNA and GAM220979 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM11242 RNA and GAM220979 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM11242 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM11242 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM11242 target RNA into GAM11242 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM220979 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM220979 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM220979 target RNA into GAM220979 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7330 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7330 gene: GAM11242 target

protein and GAM220979 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM11242 and GAM220979

GR7331 BG707114 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7331 (GR7331) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7331 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7331 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7331 gene encodes GR7331 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7331 precursor RNA folds spatially, forming GR7331 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7331 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7331 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7331 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM49451 precursor RNA, GAM64613 precursor RNA and GAM322257 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM49451 RNA, GAM64613 RNA and GAM322257 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM49451 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM49451 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM49451 target RNA into GAM49451 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM64613 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM64613 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM64613 target RNA into GAM64613 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM322257 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM322257 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM322257 target RNA into GAM322257 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7331 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7331 gene: GAM49451 target protein, GAM64613 target protein and GAM322257 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM49451, GAM64613 and GAM322257

GR7332 BI906292 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7332(GR7332) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7332 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7332 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7332 gene encodes GR7332 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7332 precursor RNA folds spatially, forming GR7332 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7332 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7332 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR7332 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM44787 precursor RNA and GAM162318 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM44787 RNA and GAM162318 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM44787 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM44787 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM44787 target RNA into GAM44787 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM162318 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM162318 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM162318 target RNA into GAM162318 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7332 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7332 gene: GAM44787 target protein and GAM162318 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM44787 and GAM162318

GR7333 AA296547 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7333(GR7333) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7333 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7333

gene was detected is described hereinabove with reference to Figs. 8-18.

GR7333 gene encodes GR7333 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7333 precursor RNA folds spatially, forming GR7333 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7333 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7333 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7333 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM122030 precursor RNA and GAM169481 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM122030 RNA and GAM169481 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM122030 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM122030 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM122030 target RNA into GAM122030 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM169481 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM169481 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM169481 target RNA into GAM169481 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7333 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7333 gene: GAM122030 target protein and GAM169481 target protein, herein schematically represented by GAM1

TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM122030 and GAM169481

GR7334 BE961683 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7334(GR7334) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7334 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7334 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7334 gene encodes GR7334 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7334 precursor RNA folds spatially, forming GR7334 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7334 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7334 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7334 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM234590 precursor RNA, GAM264815 precursor RNA and GAM277820 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM234590 RNA, GAM264815 RNA and GAM277820 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM234590 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM234590 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM234590 target RNA into GAM234590 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM264815 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM264815 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM264815 target RNA into GAM264815 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM277820 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM277820 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM277820 target RNA into GAM277820 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7334 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7334 gene: GAM234590 target protein, GAM264815 target protein and GAM277820 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM234590, GAM264815 and GAM277820

GR7335 AV651184 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7335(GR7335) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7335 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7335 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7335 gene encodes GR7335 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7335 precursor RNA folds spatially, forming GR7335 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7335 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7335 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7335 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM349 precursor RNA, GAM70590 precursor RNA and GAM206953 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM349 RNA, GAM70590 RNA and GAM206953 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM349 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM349 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM349 target RNA into GAM349 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM70590 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM70590 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM70590 target RNA into GAM70590 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM206953 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM206953 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM206953 target RNA into GAM206953 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7335 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7335 gene: GAM349 target protein, GAM70590 target protein and GAM206953 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM349, GAM70590 and GAM206953

GR7336 BG505329 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7336(GR7336) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7336 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7336 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7336 gene encodes GR7336 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7336 precursor RNA folds spatially, forming GR7336 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7336 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7336 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7336 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM63752 precursor RNA and GAM142555 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM63752 RNA and GAM142555 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM63752 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM63752 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM63752 target RNA into GAM63752 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM142555 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM142555 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM142555 target RNA into GAM142555 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7336 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7336 gene: GAM63752 target protein and GAM142555 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM63752 and GAM142555

GR7337 AA533939 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7337(GR7337) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7337 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7337 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7337 gene encodes GR7337 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7337 precursor RNA folds spatially, forming GR7337 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7337 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7337 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7337 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM112231 precursor RNA, GAM154838 precursor RNA and GAM251160 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM112231 RNA, GAM154838 RNA and GAM251160 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM112231 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM112231 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM112231 target RNA into GAM112231 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM154838 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM154838 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM154838 target RNA into GAM154838 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM251160 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM251160 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM251160 target RNA into GAM251160 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7337 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7337 gene: GAM112231 target protein, GAM154838 target protein and GAM251160 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM112231, GAM154838 and GAM251160

GR7338 BF220070 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7338(GR7338) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7338 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7338 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7338 gene encodes GR7338 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7338 precursor RNA folds spatially, forming GR7338 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7338 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7338 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7338 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4325 precursor RNA and GAM101997 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4325 RNA and GAM101997 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4325 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4325 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4325 target RNA into GAM4325 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM101997 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM101997 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM101997 target RNA into GAM101997 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7338 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7338 gene: GAM4325 target protein and GAM101997 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4325 and GAM101997

bioinformatically detected regulatory gene, referred to here as Genomic Record 7339(GR7339) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7339 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7339 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7339 gene encodes GR7339 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7339 precursor RNA folds spatially, forming GR7339 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7339 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7339 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7339 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6605 precursor RNA and GAM286470 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6605 RNA and GAM286470 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6605 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6605 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6605 target RNA into GAM6605 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM286470 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM286470 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM286470

target RNA into GAM286470 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7339 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7339 gene: GAM6605 target protein and GAM286470 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6605 and GAM286470

GR7340 H79630 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7340(GR7340) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7340 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7340 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7340 gene encodes GR7340 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7340 precursor RNA folds spatially, forming GR7340 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7340 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7340 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7340 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3601 precursor RNA and GAM227213 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3601 RNA and GAM227213 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3601 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3601 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3601 target RNA into GAM3601 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM227213 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM227213 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM227213 target RNA into GAM227213 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7340 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7340 gene: GAM3601 target protein and GAM227213 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3601 and GAM227213

GR7341 BI195978 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7341(GR7341) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7341 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7341 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7341 gene encodes GR7341 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7341 precursor RNA folds spatially, forming GR7341 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7341 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7341 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7341 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3360 precursor RNA and GAM29753 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3360 RNA and GAM29753 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3360 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3360 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3360 target RNA into GAM3360 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM29753 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM29753 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM29753 target RNA into GAM29753 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7341 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7341 gene: GAM3360 target protein and GAM29753 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3360 and GAM29753

GR7342 BM465359 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7342(GR7342) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7342 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7342 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7342 gene encodes GR7342 precursor RNA, herein designated GR

PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7342 precursor RNA folds spatially, forming GR7342 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7342 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7342 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7342 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM76620 precursor RNA and GAM275308 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM76620 RNA and GAM275308 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM76620 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM76620 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM76620 target RNA into GAM76620 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM275308 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM275308 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM275308 target RNA into GAM275308 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7342 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7342 gene: GAM76620 target protein and GAM275308 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM76620 and GAM275308

GR7343 BF843864 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7343(GR7343) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7343 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7343 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7343 gene encodes GR7343 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7343 precursor RNA folds spatially, forming GR7343 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7343 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7343 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7343 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4735 precursor RNA, GAM115994 precursor RNA and GAM289360 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4735 RNA, GAM115994 RNA and GAM289360 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4735 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4735 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4735 target RNA into GAM4735 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM115994 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM115994 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM115994 target RNA into GAM115994 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM289360 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM289360 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM289360 target RNA into GAM289360 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7343 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7343 gene: GAM4735 target protein, GAM115994 target protein and GAM289360 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4735, GAM115994 and GAM289360

GR7344 AW887489 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7344(GR7344) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7344 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7344 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7344 gene encodes GR7344 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7344 precursor RNA folds spatially, forming GR7344 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7344 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7344 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7344 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2

separate GAM precursor RNAs, GAM6771 precursor RNA and GAM310546 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6771 RNA and GAM310546 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6771 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6771 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6771 target RNA into GAM6771 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM310546 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM310546 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM310546 target RNA into GAM310546 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7344 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7344 gene: GAM6771 target protein and GAM310546 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6771 and GAM310546

GR7345 BF672708 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7345(GR7345) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7345 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7345 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7345 gene encodes GR7345 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR7345 precursor RNA folds spatially, forming GR7345 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7345 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7345 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7345 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM3932 precursor RNA, GAM7240 precursor RNA and GAM263822 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3932 RNA, GAM7240 RNA and GAM263822 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3932 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3932 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3932 target RNA into GAM3932 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7240 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7240 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7240 target RNA into GAM7240 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM263822 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM263822 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM263822 target RNA into GAM263822 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7345 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7345 gene: GAM3932 target protein, GAM7240 target protein and GAM263822 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3932, GAM7240 and GAM263822

GR7346 BQ027229 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7346(GR7346) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7346 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7346 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7346 gene encodes GR7346 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7346 precursor RNA folds spatially, forming GR7346 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7346 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7346 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7346 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2095 precursor RNA, GAM178217 precursor RNA and GAM308207 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2095 RNA, GAM178217 RNA and GAM308207 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2095 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM2095 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2095 target RNA into GAM2095 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM178217 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM178217 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM178217 target RNA into GAM178217 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM308207 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM308207 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM308207 target RNA into GAM308207 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7346 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7346 gene: GAM2095 target protein, GAM178217 target protein and GAM308207 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2095, GAM178217 and GAM308207

GR7347 BF476482 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7347(GR7347) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7347 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7347 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7347 gene encodes GR7347 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7347 precursor RNA folds spatially, forming GR7347 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated

that GR7347 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7347 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7347 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM108795 precursor RNA and GAM230139 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM108795 RNA and GAM230139 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM108795 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM108795 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM108795 target RNA into GAM108795 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM230139 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM230139 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM230139 target RNA into GAM230139 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7347 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7347 gene: GAM108795 target protein and GAM230139 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM108795 and GAM230139

GR7348 BM353924 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7348(GR7348) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR7348 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7348 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7348 gene encodes GR7348 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7348 precursor RNA folds spatially, forming GR7348 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7348 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7348 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7348 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3421 precursor RNA and GAM127458 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3421 RNA and GAM127458 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3421 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3421 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3421 target RNA into GAM3421 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM127458 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM127458 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM127458 target RNA into GAM127458 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7348 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7348 gene: GAM3421 target protein and GAM127458 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3421 and GAM127458

GR7349 BF858616 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7349(GR7349) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7349 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7349 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7349 gene encodes GR7349 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7349 precursor RNA folds spatially, forming GR7349 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7349 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7349 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7349 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM156992 precursor RNA and GAM252925 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM156992 RNA and GAM252925 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM156992 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM156992 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM156992 target RNA into GAM156992 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM252925 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM252925 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM252925 target RNA into GAM252925 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7349 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7349 gene: GAM156992 target protein and GAM252925 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM156992 and GAM252925

GR7350 BM929805 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7350(GR7350) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7350 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7350 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7350 gene encodes GR7350 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7350 precursor RNA folds spatially, forming GR7350 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7350 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7350 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7350 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM34771 precursor RNA and GAM189259 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3

FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM34771 RNA and GAM189259 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM34771 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM34771 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM34771 target RNA into GAM34771 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM189259 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM189259 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM189259 target RNA into GAM189259 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7350 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7350 gene: GAM34771 target protein and GAM189259 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM34771 and GAM189259

GR7351 AA513944 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7351(GR7351) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7351 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7351 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7351 gene encodes GR7351 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7351 precursor RNA folds spatially, forming GR7351 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7351 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7351 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7351 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM63086 precursor RNA and GAM168905 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM63086 RNA and GAM168905 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM63086 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM63086 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM63086 target RNA into GAM63086 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM168905 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM168905 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM168905 target RNA into GAM168905 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7351 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7351 gene: GAM63086 target protein and GAM168905 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM63086 and GAM168905

7352(GR7352) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7352 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7352 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7352 gene encodes GR7352 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7352 precursor RNA folds spatially, forming GR7352 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7352 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7352 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7352 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4410 precursor RNA and GAM4901 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4410 RNA and GAM4901 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4410 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4410 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4410 target RNA into GAM4410 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM4901 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4901 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4901 target RNA into GAM4901 target protein, herein schematically represented by GAM1 TARGET

PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7352 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7352 gene: GAM4410 target protein and GAM4901 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4410 and GAM4901

GR7353 BG497210 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7353(GR7353) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7353 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7353 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7353 gene encodes GR7353 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7353 precursor RNA folds spatially, forming GR7353 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7353 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7353 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7353 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM54944 precursor RNA, GAM214665 precursor RNA and GAM231321 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM54944 RNA, GAM214665 RNA and GAM231321 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM54944 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM54944 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM54944 target RNA into GAM54944 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM214665 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM214665 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM214665 target RNA into GAM214665 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM231321 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM231321 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM231321 target RNA into GAM231321 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7353 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7353 gene: GAM54944 target protein, GAM214665 target protein and GAM231321 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM54944, GAM214665 and GAM231321

GR7354 AA778853 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7354(GR7354) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7354 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7354 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7354 gene encodes GR7354 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7354 precursor RNA folds spatially, forming GR7354 folded

precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7354 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7354 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7354 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM24094 precursor RNA, GAM125581 precursor RNA, GAM131015 precursor RNA and GAM202381 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM24094 RNA, GAM125581 RNA, GAM131015 RNA and GAM202381 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM24094 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM24094 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM24094 target RNA into GAM24094 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM125581 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM125581 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM125581 target RNA into GAM125581 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM131015 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM131015 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM131015 target RNA into GAM131015 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM202381 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM202381 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site

corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM202381 target RNA into GAM202381 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7354 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7354 gene: GAM24094 target protein, GAM125581 target protein, GAM131015 target protein and GAM202381 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM24094, GAM125581, GAM131015 and GAM202381

GR7355 BG402206 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7355(GR7355) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7355 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7355 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7355 gene encodes GR7355 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7355 precursor RNA folds spatially, forming GR7355 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7355 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7355 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7355 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM5510 precursor RNA, GAM282732 precursor RNA, GAM303239 precursor RNA and GAM333344 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5510 RNA, GAM282732 RNA, GAM303239 RNA and GAM333344

RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5510 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5510 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5510 target RNA into GAM5510 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM282732 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM282732 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM282732 target RNA into GAM282732 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM303239 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM303239 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM303239 target RNA into GAM303239 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM333344 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM333344 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM333344 target RNA into GAM333344 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7355 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7355 gene: GAM5510 target protein, GAM282732 target protein, GAM303239 target protein and GAM333344 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5510, GAM282732, GAM303239 and GAM333344

GR7356 AI829520 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7356(GR7356) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one

target gene, the function and utility of which at least one target gene is known in the art.

GR7356 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7356 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7356 gene encodes GR7356 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7356 precursor RNA folds spatially, forming GR7356 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7356 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7356 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7356 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM5686 precursor RNA, GAM159175 precursor RNA and GAM237492 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5686 RNA, GAM159175 RNA and GAM237492 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5686 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5686 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5686 target RNA into GAM5686 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM159175 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM159175 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM159175 target RNA into GAM159175 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM237492 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM237492 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM237492 target RNA into GAM237492 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7356 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7356 gene: GAM5686 target protein, GAM159175 target protein and GAM237492 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5686, GAM159175 and GAM237492

GR7357 BI860927 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7357(GR7357) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7357 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7357 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7357 gene encodes GR7357 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7357 precursor RNA folds spatially, forming GR7357 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7357 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7357 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7357 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6273 precursor RNA and GAM136769 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6273 RNA and GAM136769 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6273 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6273 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6273 target RNA into GAM6273 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM136769 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM136769 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM136769 target RNA into GAM136769 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7357 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7357 gene: GAM6273 target protein and GAM136769 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6273 and GAM136769

GR7358 AL042442 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7358(GR7358) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7358 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7358 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7358 gene encodes GR7358 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7358 precursor RNA folds spatially, forming GR7358 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7358 folded precursor RNA comprises a plurality of what is known in the

art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7358 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7358 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8150 precursor RNA and GAM233018 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8150 RNA and GAM233018 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8150 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8150 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8150 target RNA into GAM8150 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM233018 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM233018 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM233018 target RNA into GAM233018 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7358 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7358 gene: GAM8150 target protein and GAM233018 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8150 and GAM233018

GR7359 BG341211 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7359(GR7359) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is

known in the art.

GR7359 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7359 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7359 gene encodes GR7359 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7359 precursor RNA folds spatially, forming GR7359 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7359 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7359 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7359 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM65557 precursor RNA, GAM169743 precursor RNA and GAM267630 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM65557 RNA, GAM169743 RNA and GAM267630 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM65557 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM65557 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM65557 target RNA into GAM65557 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM169743 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM169743 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM169743 target RNA into GAM169743 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM267630 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM267630 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM267630 target RNA into GAM267630 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7359 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7359 gene: GAM65557 target protein, GAM169743 target protein and GAM267630 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM65557, GAM169743 and GAM267630

GR7360 BI090464 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7360(GR7360) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7360 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7360 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7360 gene encodes GR7360 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7360 precursor RNA folds spatially, forming GR7360 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7360 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7360 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7360 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM147761 precursor RNA and GAM248148 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER

COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM147761 RNA and GAM248148 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM147761 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM147761 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM147761 target RNA into GAM147761 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM248148 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM248148 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM248148 target RNA into GAM248148 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7360 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7360 gene: GAM147761 target protein and GAM248148 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM147761 and GAM248148

GR7361 BI600012 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7361(GR7361) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7361 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7361 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7361 gene encodes GR7361 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7361 precursor RNA folds spatially, forming GR7361 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7361 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact

that the nucleotide sequence of GR7361 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7361 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6647 precursor RNA and GAM112990 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6647 RNA and GAM112990 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6647 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6647 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6647 target RNA into GAM6647 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM112990 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM112990 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM112990 target RNA into GAM112990 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7361 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7361 gene: GAM6647 target protein and GAM112990 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6647 and GAM112990

GR7362 AV691461 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7362(GR7362) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7362 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7362 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7362 gene encodes GR7362 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7362 precursor RNA folds spatially, forming GR7362 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7362 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7362 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7362 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5261 precursor RNA and GAM7907 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5261 RNA and GAM7907 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5261 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5261 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5261 target RNA into GAM5261 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7907 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7907 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7907 target RNA into GAM7907 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7362 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7362 gene: GAM5261 target protein and GAM7907 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5261 and GAM7907

GR7363 BE082837 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7363(GR7363) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7363 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7363 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7363 gene encodes GR7363 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7363 precursor RNA folds spatially, forming GR7363 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7363 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7363 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7363 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM81 precursor RNA and GAM6546 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM81 RNA and GAM6546 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM81 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM81 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM81 target RNA into GAM81 target

protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6546 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6546 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6546 target RNA into GAM6546 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7363 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7363 gene: GAM81 target protein and GAM6546 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM81 and GAM6546

GR7364 BG008262 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7364(GR7364) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7364 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7364 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7364 gene encodes GR7364 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7364 precursor RNA folds spatially, forming GR7364 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7364 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7364 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7364 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM8392 precursor RNA and GAM144088 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8392 RNA and GAM144088 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8392 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8392 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8392 target RNA into GAM8392 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM144088 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM144088 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM144088 target RNA into GAM144088 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7364 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7364 gene: GAM8392 target protein and GAM144088 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8392 and GAM144088

GR7365 AI636556 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7365(GR7365) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7365 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7365 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7365 gene encodes GR7365 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7365 precursor RNA folds spatially, forming GR7365 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated

that GR7365 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7365 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7365 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM694 precursor RNA, GAM1253 precursor RNA and GAM71583 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM694 RNA, GAM1253 RNA and GAM71583 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM694 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM694 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM694 target RNA into GAM694 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM1253 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1253 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1253 target RNA into GAM1253 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM71583 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM71583 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM71583 target RNA into GAM71583 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7365 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7365 gene: GAM694 target

protein, GAM1253 target protein and GAM71583 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM694, GAM1253 and GAM71583

GR7366 BG170433 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7366(GR7366) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7366 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7366 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7366 gene encodes GR7366 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7366 precursor RNA folds spatially, forming GR7366 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7366 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7366 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7366 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM1125 precursor RNA and GAM6517 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1125 RNA and GAM6517 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1125 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1125 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1125 target RNA into GAM1125 target protein, herein schematically represented by GAM1 TARGET

PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6517 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6517 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6517 target RNA into GAM6517 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7366 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7366 gene: GAM1125 target protein and GAM6517 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1125 and GAM6517

GR7367 BE382818 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7367(GR7367) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7367 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7367 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7367 gene encodes GR7367 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7367 precursor RNA folds spatially, forming GR7367 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7367 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7367 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7367 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM5186 precursor RNA, GAM54746 precursor RNA, GAM122822 precursor RNA and GAM128425 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5186 RNA, GAM54746 RNA, GAM122822 RNA and GAM128425 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5186 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5186 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5186 target RNA into GAM5186 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM54746 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM54746 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM54746 target RNA into GAM54746 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM122822 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM122822 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM122822 target RNA into GAM122822 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM128425 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM128425 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM128425 target RNA into GAM128425 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7367 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7367 gene: GAM5186 target protein, GAM54746 target protein, GAM122822 target protein and GAM128425 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5186, GAM54746, GAM122822 and GAM128425

GR7368 BI547786 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7368(GR7368) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7368 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7368 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7368 gene encodes GR7368 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7368 precursor RNA folds spatially, forming GR7368 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7368 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7368 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7368 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM180028 precursor RNA and GAM269533 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM180028 RNA and GAM269533 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM180028 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM180028 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM180028 target RNA into GAM180028 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM269533 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM269533 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM269533 target RNA into GAM269533 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7368 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7368 gene: GAM180028 target protein and GAM269533 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM180028 and GAM269533

GR7369 BG484995 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7369(GR7369) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7369 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7369 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7369 gene encodes GR7369 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7369 precursor RNA folds spatially, forming GR7369 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7369 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7369 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7369 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM69124 precursor RNA and GAM229390 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM69124 RNA and GAM229390 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM69124 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM69124 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM69124 target RNA into GAM69124 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM229390 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM229390 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM229390 target RNA into GAM229390 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7369 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7369 gene: GAM69124 target protein and GAM229390 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM69124 and GAM229390

GR7370 BG025556 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7370(GR7370) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7370 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7370 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7370 gene encodes GR7370 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7370 precursor RNA folds spatially, forming GR7370 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7370 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7370 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7370 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM99962 precursor RNA, GAM252080 precursor RNA and GAM286926 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM99962 RNA, GAM252080 RNA and GAM286926 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM99962 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM99962 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM99962 target RNA into GAM99962 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM252080 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM252080 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM252080 target RNA into GAM252080 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM286926 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM286926 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM286926 target RNA into GAM286926 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7370 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7370 gene: GAM99962 target protein, GAM252080 target protein and GAM286926 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM99962, GAM252080 and GAM286926

bioinformatically detected regulatory gene, referred to here as Genomic Record 7371 (GR7371) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7371 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7371 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7371 gene encodes GR7371 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7371 precursor RNA folds spatially, forming GR7371 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7371 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7371 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7371 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM362 precursor RNA and GAM336792 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig. 8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig. 8, yielding respective short RNA segments of about 22 nucleotides in length, GAM362 RNA and GAM336792 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM362 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM362 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM362 target RNA into GAM362 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM336792 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM336792 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM336792

target RNA into GAM336792 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7371 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7371 gene: GAM362 target protein and GAM336792 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM362 and GAM336792

GR7372 BF882611 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7372(GR7372) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7372 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7372 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7372 gene encodes GR7372 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7372 precursor RNA folds spatially, forming GR7372 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7372 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7372 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7372 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM486 precursor RNA, GAM281295 precursor RNA and GAM305275 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM486 RNA, GAM281295 RNA and GAM305275 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM486 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM486 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM486 target RNA into GAM486 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM281295 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM281295 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM281295 target RNA into GAM281295 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM305275 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM305275 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM305275 target RNA into GAM305275 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7372 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7372 gene: GAM486 target protein, GAM281295 target protein and GAM305275 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM486, GAM281295 and GAM305275

GR7373 BG205211 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7373(GR7373) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7373 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7373 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7373 gene encodes GR7373 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7373 precursor RNA folds spatially, forming GR7373 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7373 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7373 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7373 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM6116 precursor RNA and GAM74387 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6116 RNA and GAM74387 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6116 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6116 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6116 target RNA into GAM6116 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM74387 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM74387 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM74387 target RNA into GAM74387 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7373 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7373 gene: GAM6116 target protein and GAM74387 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6116 and GAM74387

7374(GR7374) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7374 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7374 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7374 gene encodes GR7374 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7374 precursor RNA folds spatially, forming GR7374 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7374 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7374 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7374 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM11396 precursor RNA and GAM313161 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM11396 RNA and GAM313161 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM11396 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM11396 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM11396 target RNA into GAM11396 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM313161 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM313161 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM313161 target RNA into GAM313161 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7374 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7374 gene: GAM11396 target protein and GAM313161 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM11396 and GAM313161

GR7375 AA706930 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7375(GR7375) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7375 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7375 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7375 gene encodes GR7375 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7375 precursor RNA folds spatially, forming GR7375 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7375 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7375 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7375 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5707 precursor RNA and GAM7011 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5707 RNA and GAM7011 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5707 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM5707 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5707 target RNA into GAM5707 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7011 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7011 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7011 target RNA into GAM7011 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7375 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7375 gene: GAM5707 target protein and GAM7011 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5707 and GAM7011

GR7376 BG823583 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7376(GR7376) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7376 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7376 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7376 gene encodes GR7376 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7376 precursor RNA folds spatially, forming GR7376 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7376 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7376 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7376 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2

separate GAM precursor RNAs, GAM2192 precursor RNA and GAM8543 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2192 RNA and GAM8543 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2192 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2192 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2192 target RNA into GAM2192 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM8543 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8543 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8543 target RNA into GAM8543 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7376 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7376 gene: GAM2192 target protein and GAM8543 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2192 and GAM8543

GR7377 BG676092 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7377(GR7377) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7377 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7377 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7377 gene encodes GR7377 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR7377 precursor RNA folds spatially, forming GR7377 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7377 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7377 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7377 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 5 separate GAM precursor RNAs, GAM6174 precursor RNA, GAM6813 precursor RNA, GAM240366 precursor RNA, GAM243819 precursor RNA and GAM309563 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM6174 RNA, GAM6813 RNA, GAM240366 RNA, GAM243819 RNA and GAM309563 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM6174 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6174 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6174 target RNA into GAM6174 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM6813 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM6813 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM6813 target RNA into GAM6813 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM240366 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM240366 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM240366 target RNA into GAM240366 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM243819 RNA, herein schematically represented by GAM1 RNA through

GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM243819 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM243819 target RNA into GAM243819 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM309563 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM309563 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM309563 target RNA into GAM309563 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7377 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7377 gene: GAM6174 target protein, GAM6813 target protein, GAM240366 target protein, GAM243819 target protein and GAM309563 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM6174, GAM6813, GAM240366, GAM243819 and GAM309563

GR7378 BE865736 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7378(GR7378) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7378 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7378 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7378 gene encodes GR7378 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7378 precursor RNA folds spatially, forming GR7378 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7378 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7378 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7378 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM295722 precursor RNA and GAM330578 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM295722 RNA and GAM330578 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM295722 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM295722 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM295722 target RNA into GAM295722 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM330578 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM330578 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM330578 target RNA into GAM330578 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7378 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7378 gene: GAM295722 target protein and GAM330578 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM295722 and GAM330578

GR7379 BF514690 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7379(GR7379) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7379 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7379 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7379 gene encodes GR7379 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7379 precursor RNA folds spatially, forming GR7379 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7379 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7379 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7379 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM4601 precursor RNA and GAM5632 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4601 RNA and GAM5632 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4601 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4601 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4601 target RNA into GAM4601 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5632 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5632 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5632 target RNA into GAM5632 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7379 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7379 gene: GAM4601 target protein and GAM5632 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference,

with references to GAM4601 and GAM5632

GR7380 BF791868 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7380(GR7380) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7380 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7380 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7380 gene encodes GR7380 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7380 precursor RNA folds spatially, forming GR7380 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7380 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7380 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7380 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM133983 precursor RNA and GAM258147 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM133983 RNA and GAM258147 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM133983 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM133983 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM133983 target RNA into GAM133983 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM258147 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM258147 target RNA, herein schematically represented

by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM258147 target RNA into GAM258147 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7380 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7380 gene: GAM133983 target protein and GAM258147 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM133983 and GAM258147

GR7381 AI371038 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7381(GR7381) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7381 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7381 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7381 gene encodes GR7381 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7381 precursor RNA folds spatially, forming GR7381 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7381 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7381 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7381 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM92615 precursor RNA and GAM98460 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM92615 RNA and GAM98460 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding

to GAM RNA of Fig. 8.

GAM92615 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM92615 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM92615 target RNA into GAM92615 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM98460 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM98460 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM98460 target RNA into GAM98460 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7381 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7381 gene: GAM92615 target protein and GAM98460 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM92615 and GAM98460

GR7382 BF695574 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7382(GR7382) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7382 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7382 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7382 gene encodes GR7382 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7382 precursor RNA folds spatially, forming GR7382 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7382 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7382 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half

thereof, as is well known in the art.

GR7382 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM62084 precursor RNA and GAM310796 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM62084 RNA and GAM310796 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM62084 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM62084 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM62084 target RNA into GAM62084 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM310796 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM310796 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM310796 target RNA into GAM310796 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7382 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7382 gene: GAM62084 target protein and GAM310796 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM62084 and GAM310796

GR7383 AA101753 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7383(GR7383) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7383 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7383

gene was detected is described hereinabove with reference to Figs. 8-18.

GR7383 gene encodes GR7383 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7383 precursor RNA folds spatially, forming GR7383 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7383 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7383 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7383 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM3694 precursor RNA and GAM266612 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM3694 RNA and GAM266612 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM3694 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM3694 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM3694 target RNA into GAM3694 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM266612 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM266612 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM266612 target RNA into GAM266612 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7383 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7383 gene: GAM3694 target protein and GAM266612 target protein, herein schematically represented by GAM1

TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM3694 and GAM26612

GR7384 BG742790 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7384(GR7384) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7384 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7384 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7384 gene encodes GR7384 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7384 precursor RNA folds spatially, forming GR7384 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7384 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7384 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7384 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 4 separate GAM precursor RNAs, GAM1751 precursor RNA, GAM5645 precursor RNA, GAM42335 precursor RNA and GAM177703 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM1751 RNA, GAM5645 RNA, GAM42335 RNA and GAM177703 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM1751 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM1751 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM1751 target RNA into GAM1751 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM5645 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5645 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5645 target RNA into GAM5645 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM42335 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM42335 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM42335 target RNA into GAM42335 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM177703 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM177703 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM177703 target RNA into GAM177703 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7384 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7384 gene: GAM1751 target protein, GAM5645 target protein, GAM42335 target protein and GAM177703 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM1751, GAM5645, GAM42335 and GAM177703

GR7385 BE713407 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7385(GR7385) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7385 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7385 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7385 gene encodes GR7385 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7385 precursor RNA folds spatially, forming GR7385 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7385 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7385 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7385 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM2962 precursor RNA, GAM192518 precursor RNA and GAM327031 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM2962 RNA, GAM192518 RNA and GAM327031 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM2962 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM2962 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM2962 target RNA into GAM2962 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM192518 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM192518 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM192518 target RNA into GAM192518 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM327031 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM327031 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM327031 target RNA into GAM327031 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7385 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7385 gene: GAM2962 target protein, GAM192518 target protein and GAM327031 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM2962, GAM192518 and GAM327031

GR7386 BG423906 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7386(GR7386) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7386 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7386 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7386 gene encodes GR7386 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7386 precursor RNA folds spatially, forming GR7386 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7386 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7386 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7386 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM73207 precursor RNA and GAM261167 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM73207 RNA and GAM261167 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM73207 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM73207 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II

or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM73207 target RNA into GAM73207 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM261167 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM261167 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM261167 target RNA into GAM261167 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7386 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7386 gene: GAM73207 target protein and GAM261167 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM73207 and GAM261167

GR7387 BF965136 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7387(GR7387) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7387 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7387 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7387 gene encodes GR7387 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7387 precursor RNA folds spatially, forming GR7387 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7387 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7387 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7387 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM4356 precursor RNA, GAM7552 precursor RNA and GAM95355 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded

precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM4356 RNA, GAM7552 RNA and GAM95355 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM4356 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM4356 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM4356 target RNA into GAM4356 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM7552 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM7552 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM7552 target RNA into GAM7552 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM95355 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM95355 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM95355 target RNA into GAM95355 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7387 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7387 gene: GAM4356 target protein, GAM7552 target protein and GAM95355 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM4356, GAM7552 and GAM95355

GR7388 BE396228 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7388(GR7388) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7388 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7388 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7388 gene encodes GR7388 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7388 precursor RNA folds spatially, forming GR7388 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7388 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7388 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7388 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM120359 precursor RNA and GAM175388 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM120359 RNA and GAM175388 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM120359 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM120359 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM120359 target RNA into GAM120359 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM175388 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM175388 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM175388 target RNA into GAM175388 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7388 gene, herein designated GR GENE, correlate with, and may

be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7388 gene: GAM120359 target protein and GAM175388 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM120359 and GAM175388

GR7389 BF798246 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7389(GR7389) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7389 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7389 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7389 gene encodes GR7389 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7389 precursor RNA folds spatially, forming GR7389 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7389 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7389 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7389 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM777 precursor RNA and GAM19354 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM777 RNA and GAM19354 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM777 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM777 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM777 target RNA into

GAM777 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM19354 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM19354 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM19354 target RNA into GAM19354 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7389 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7389 gene: GAM777 target protein and GAM19354 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM777 and GAM19354

GR7390 BG120417 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7390(GR7390) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7390 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7390 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7390 gene encodes GR7390 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7390 precursor RNA folds spatially, forming GR7390 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7390 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7390 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7390 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM165661 precursor RNA, GAM197342 precursor RNA and GAM224886 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED

PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM165661 RNA, GAM197342 RNA and GAM224886 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM165661 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM165661 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM165661 target RNA into GAM165661 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM197342 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM197342 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM197342 target RNA into GAM197342 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM224886 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM224886 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM224886 target RNA into GAM224886 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7390 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7390 gene: GAM165661 target protein, GAM197342 target protein and GAM224886 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM165661, GAM197342 and GAM224886

GR7391 N54501 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7391(GR7391) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7391 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7391 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7391 gene encodes GR7391 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7391 precursor RNA folds spatially, forming GR7391 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7391 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7391 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7391 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM173974 precursor RNA and GAM326379 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM173974 RNA and GAM326379 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM173974 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM173974 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM173974 target RNA into GAM173974 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM326379 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM326379 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM326379 target RNA into GAM326379 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7391 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM

RNAs comprised in the `operon-like` cluster of GR7391 gene: GAM173974 target protein and GAM326379 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM173974 and GAM326379

GR7392 BG289483 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7392(GR7392) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7392 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7392 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7392 gene encodes GR7392 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7392 precursor RNA folds spatially, forming GR7392 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7392 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7392 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7392 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM8258 precursor RNA, GAM118492 precursor RNA and GAM269186 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8258 RNA, GAM118492 RNA and GAM269186 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8258 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8258 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8258 target RNA into

GAM8258 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM118492 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM118492 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM118492 target RNA into GAM118492 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM269186 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM269186 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM269186 target RNA into GAM269186 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7392 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7392 gene: GAM8258 target protein, GAM118492 target protein and GAM269186 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8258, GAM118492 and GAM269186

GR7393 BG541260 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7393(GR7393) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7393 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7393 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7393 gene encodes GR7393 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7393 precursor RNA folds spatially, forming GR7393 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7393 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7393 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence

which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7393 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM8140 precursor RNA, GAM157112 precursor RNA and GAM287706 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM8140 RNA, GAM157112 RNA and GAM287706 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM8140 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM8140 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM8140 target RNA into GAM8140 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM157112 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM157112 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM157112 target RNA into GAM157112 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM287706 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM287706 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM287706 target RNA into GAM287706 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7393 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7393 gene: GAM8140 target protein, GAM157112 target protein and GAM287706 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM8140, GAM157112 and

GR7394 AA227797 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7394(GR7394) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7394 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7394 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7394 gene encodes GR7394 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7394 precursor RNA folds spatially, forming GR7394 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7394 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7394 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7394 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM48581 precursor RNA, GAM252297 precursor RNA and GAM258099 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM48581 RNA, GAM252297 RNA and GAM258099 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM48581 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM48581 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM48581 target RNA into GAM48581 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM252297 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM252297 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM252297 target RNA into GAM252297 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM258099 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM258099 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM258099 target RNA into GAM258099 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7394 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7394 gene: GAM48581 target protein, GAM252297 target protein and GAM258099 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM48581, GAM252297 and GAM258099

GR7395 AA809894 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7395(GR7395) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7395 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7395 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7395 gene encodes GR7395 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7395 precursor RNA folds spatially, forming GR7395 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7395 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7395 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7395 folded precursor RNA, herein designated GR FOLDED PRECURSOR

RNA, is naturally processed by cellular enzymatic activity into at least 3 separate GAM precursor RNAs, GAM5625 precursor RNA, GAM63328 precursor RNA and GAM140225 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5625 RNA, GAM63328 RNA and GAM140225 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5625 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM5625 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5625 target RNA into GAM5625 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM63328 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM63328 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM63328 target RNA into GAM63328 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM140225 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM140225 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM140225 target RNA into GAM140225 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7395 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7395 gene: GAM5625 target protein, GAM63328 target protein and GAM140225 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5625, GAM63328 and GAM140225

7396(GR7396) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7396 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7396 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7396 gene encodes GR7396 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7396 precursor RNA folds spatially, forming GR7396 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7396 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7396 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7396 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM164544 precursor RNA and GAM219825 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM164544 RNA and GAM219825 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM164544 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM164544 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM164544 target RNA into GAM164544 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM219825 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM219825 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM219825 target RNA into GAM219825 target protein, herein schematically represented by

GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7396 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7396 gene: GAM164544 target protein and GAM219825 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM164544 and GAM219825

GR7397 BE176379 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7397(GR7397) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7397 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7397 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7397 gene encodes GR7397 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7397 precursor RNA folds spatially, forming GR7397 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7397 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7397 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7397 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM5173 precursor RNA and GAM162517 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM5173 RNA and GAM162517 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM5173 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an

untranslated region of GAM5173 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM5173 target RNA into GAM5173 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM162517 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM162517 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM162517 target RNA into GAM162517 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7397 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7397 gene: GAM5173 target protein and GAM162517 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM5173 and GAM162517

GR7398 BF669705 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7398(GR7398) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7398 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7398 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7398 gene encodes GR7398 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand nucleotides long.

GR7398 precursor RNA folds spatially, forming GR7398 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7398 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7398 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7398 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2

separate GAM precursor RNAs, GAM121130 precursor RNA and GAM220136 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM121130 RNA and GAM220136 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM121130 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM121130 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM121130 target RNA into GAM121130 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM220136 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM220136 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM220136 target RNA into GAM220136 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7398 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7398 gene: GAM121130 target protein and GAM220136 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM121130 and GAM220136

GR7399 AI807175 Fig. 16 further provides a conceptual description of novel bioinformatically detected regulatory gene, referred to here as Genomic Record 7399(GR7399) gene, which encodes an `operon-like` cluster of novel micro RNA-like genes, each of which in turn modulates expression of at least one target gene, the function and utility of which at least one target gene is known in the art.

GR7399 gene, herein designated GR GENE, is a novel bioinformatically detected regulatory, non protein coding, RNA gene. The method by which GR7399 gene was detected is described hereinabove with reference to Figs. 8-18.

GR7399 gene encodes GR7399 precursor RNA, herein designated GR PRECURSOR RNA, an RNA molecule, typically several hundred to several thousand

nucleotides long.

GR7399 precursor RNA folds spatially, forming GR7399 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA. It is appreciated that GR7399 folded precursor RNA comprises a plurality of what is known in the art as `hairpin` structures. These `hairpin` structures are due to the fact that the nucleotide sequence of GR7399 precursor RNA comprises a plurality of segments, the first half of each such segment having a nucleotide sequence which is at least a partial inversed-reversed sequence of the second half thereof, as is well known in the art.

GR7399 folded precursor RNA, herein designated GR FOLDED PRECURSOR RNA, is naturally processed by cellular enzymatic activity into at least 2 separate GAM precursor RNAs, GAM90426 precursor RNA and GAM166329 precursor RNA, herein schematically represented by GAM1 FOLDED PRECURSOR RNA through GAM3 FOLDED PRECURSOR RNA, each of which GAM folded precursor RNAs being a hairpin shaped RNA segment, corresponding to GAM FOLDED PRECURSOR RNA of Fig.8.

The above mentioned GAM folded precursor RNAs are diced by DICER COMPLEX of Fig.8, yielding respective short RNA segments of about 22 nucleotides in length, GAM90426 RNA and GAM166329 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, each of which GAM RNAs corresponding to GAM RNA of Fig. 8.

GAM90426 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM90426 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM90426 target RNA into GAM90426 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

GAM166329 RNA, herein schematically represented by GAM1 RNA through GAM3 RNA, binds complementarily to a target binding site located in an untranslated region of GAM166329 target RNA, herein schematically represented by GAM1 TARGET RNA through GAM3 TARGET RNA, which target binding site corresponds to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 8, thereby inhibiting translation of GAM166329 target RNA into GAM166329 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN, both of Fig. 8.

It is appreciated that specific functions, and accordingly utilities, of GR7399 gene, herein designated GR GENE, correlate with, and may be deduced from, the identity of the target genes, which are inhibited by GAM RNAs comprised in the `operon-like` cluster of GR7399 gene: GAM90426 target protein and GAM166329 target protein, herein schematically represented by GAM1 TARGET PROTEIN through GAM3 TARGET PROTEIN. The function of these target genes is elaborated with reference to Table 6, hereby incorporated by reference, with references to GAM90426 and GAM166329